Ian A Wilson

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5491764/publications.pdf Version: 2024-02-01



IAN A WUSON

| # | Article | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Neutralizing Antibodies to SARS oVâ€2 Selected from a Human Antibody Library Constructed Decades Ago. Advanced Science, 2022, 9, e2102181. | 11.2 | 14 |
| 2 | <i>N</i> -Glycolylneuraminic Acid Binding of Avian and Equine H7 Influenza A Viruses. Journal of Virology, 2022, 96, jvi0212021. | 3.4 | 14 |
| 3 | Amyloidogenic immunoglobulin light chain kinetic stabilizers comprising a simple urea linker module reveal a novel binding sub-site. Bioorganic and Medicinal Chemistry Letters, 2022, 60, 128571. | 2.2 | 5 |
| 4 | A human antibody reveals a conserved site on beta-coronavirus spike proteins and confers protection against SARS-CoV-2 infection. Science Translational Medicine, 2022, 14, eabi9215. | 12.4 | 123 |
| 5 | SARS-CoV-2 Beta variant infection elicits potent lineage-specific and cross-reactive antibodies. Science, 2022, 375, 782-787. | 12.6 | 60 |
| 6 | A novel CSP C-terminal epitope targeted by an antibody with protective activity against Plasmodium falciparum. PLoS Pathogens, 2022, 18, e1010409. | 4.7 | 14 |
| 7 | A large-scale systematic survey reveals recurring molecular features of public antibody responses to SARS-CoV-2. Immunity, 2022, 55, 1105-1117.e4. | 14.3 | 44 |
| 8 | Design of protein-binding proteins from the target structure alone. Nature, 2022, 605, 551-560. | 27.8 | 164 |
| 9 | Structural insights of a highly potent pan-neutralizing SARS-CoV-2 human monoclonal antibody. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2120976119. | 7.1 | 27 |
| 10 | Influenza chimeric hemagglutinin structures in complex with broadly protective antibodies to the stem and trimer interface. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 7.1 | 10 |
| 11 | Protective neutralizing epitopes in SARSâ€CoVâ€2. Immunological Reviews, 2022, 310, 76-92. | 6.0 | 23 |
| 12 | Targeted isolation of diverse human protective broadly neutralizing antibodies against SARS-like viruses. Nature Immunology, 2022, 23, 960-970. | 14.5 | 39 |
| 13 | Superimmunity by pan-sarbecovirus nanobodies. Cell Reports, 2022, 39, 111004. | 6.4 | 13 |
| 14 | Neutralizing Antibody Response to Sarbecovirus Is Delayed in Sequential Heterologous Immunization. Viruses, 2022, 14, 1382. | 3.3 | 2 |
| 15 | A broad and potent neutralization epitope in SARS-related coronaviruses. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 7.1 | 34 |
| 16 | Antigenic imprinting in SARS oVâ€2. Clinical and Translational Medicine, 2022, 12, . | 4.0 | 6 |
| 17 | Broadly neutralizing antibodies target the coronavirus fusion peptide. Science, 2022, 377, 728-735. | 12.6 | 111 |
| 18 | Recognition of the SARS-CoV-2 receptor binding domain by neutralizing antibodies. Biochemical and Biophysical Research Communications, 2021, 538, 192-203. | 2.1 | 165 |

| # | Article | IF | CITATIONS |
|----|---|------|-----------|
| 19 | 50ÂYears of structural immunology. Journal of Biological Chemistry, 2021, 296, 100745. | 3.4 | 15 |
| 20 | Structural and biophysical correlation of anti-NANP antibodies with in vivo protection against P. falciparum. Nature Communications, 2021, 12, 1063. | 12.8 | 30 |
| 21 | Structure-guided multivalent nanobodies block SARS-CoV-2 infection and suppress mutational escape. Science, 2021, 371, . | 12.6 | 304 |
| 22 | 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, . | 7.1 | 13 |
| 23 | A cross-neutralizing antibody between HIV-1 and influenza virus. PLoS Pathogens, 2021, 17, e1009407. | 4.7 | 23 |
| 24 | Single-component, self-assembling, protein nanoparticles presenting the receptor binding domain and stabilized spike as SARS-CoV-2 vaccine candidates. Science Advances, 2021, 7, . | 10.3 | 80 |
| 25 | Functional convergence of a germline-encoded neutralizing antibody response in rhesus macaques immunized with HCV envelope glycoproteins. Immunity, 2021, 54, 781-796.e4. | 14.3 | 23 |
| 26 | Dynamics of B cell repertoires and emergence of cross-reactive responses in patients with different severities of COVID-19. Cell Reports, 2021, 35, 109173. | 6.4 | 46 |
| 27 | Structural and functional ramifications of antigenic drift in recent SARS-CoV-2 variants. Science, 2021, 373, 818-823. | 12.6 | 309 |
| 28 | A combination of cross-neutralizing antibodies synergizes to prevent SARS-CoV-2 and SARS-CoV pseudovirus infection. Cell Host and Microbe, 2021, 29, 806-818.e6. | 11.0 | 49 |
| 29 | Selection of a picomolar antibody that targets CXCR2-mediated neutrophil activation and alleviates EAE symptoms. Nature Communications, 2021, 12, 2547. | 12.8 | 11 |
| 30 | Single-component multilayered self-assembling nanoparticles presenting rationally designed glycoprotein trimers as Ebola virus vaccines. Nature Communications, 2021, 12, 2633. | 12.8 | 25 |
| 31 | NMR Based SARS-CoV-2 Antibody Screening. Journal of the American Chemical Society, 2021, 143, 7930-7934. | 13.7 | 10 |
| 32 | Discovery of Potent Coumarin-Based Kinetic Stabilizers of Amyloidogenic Immunoglobulin Light Chains Using Structure-Based Design. Journal of Medicinal Chemistry, 2021, 64, 6273-6299. | 6.4 | 16 |
| 33 | Diverse immunoglobulin gene usage and convergent epitope targeting in neutralizing antibody responses to SARS-CoV-2. Cell Reports, 2021, 35, 109109. | 6.4 | 21 |
| 34 | Sequence signatures of two public antibody clonotypes that bind SARS-CoV-2 receptor binding domain. Nature Communications, 2021, 12, 3815. | 12.8 | 44 |
| 35 | Homologous and heterologous serological response to the Nâ€terminal domain of SARSâ€CoVâ€2 in humans and mice. European Journal of Immunology, 2021, 51, 2296-2305. | 2.9 | 7 |
| 36 | Neutralizing Antibodies Induced by First-Generation gp41-Stabilized HIV-1 Envelope Trimers and Nanoparticles. MBio, 2021, 12, e0042921. | 4.1 | 6 |

| # | Article | IF | CITATIONS |
|----|---|------|-----------|
| 37 | Functional human IgA targets a conserved site on malaria sporozoites. Science Translational Medicine, 2021, 13, . | 12.4 | 21 |
| 38 | Novel lamprey antibody recognizes terminal sulfated galactose epitopes on mammalian glycoproteins. Communications Biology, 2021, 4, 674. | 4.4 | 13 |
| 39 | Bispecific antibodies targeting distinct regions of the spike protein potently neutralize SARS-CoV-2 variants of concern. Science Translational Medicine, 2021, 13, eabj5413. | 12.4 | 79 |
| 40 | COVA1-18 neutralizing antibody protects against SARS-CoV-2 in three preclinical models. Nature Communications, 2021, 12, 6097. | 12.8 | 38 |
| 41 | Structural and Biochemical Characterization of Cysteinylation in Broadly Neutralizing Antibodies to HIV-1. Journal of Molecular Biology, 2021, 433, 167303. | 4.2 | 1 |
| 42 | Probing Affinity, Avidity, Anticooperativity, and Competition in Antibody and Receptor Binding to the SARS-CoV-2 Spike by Single Particle Mass Analyses. ACS Central Science, 2021, 7, 1863-1873. | 11.3 | 20 |
| 43 | A Novel Recombinant Influenza Virus Neuraminidase Vaccine Candidate Stabilized by a Measles Virus Phosphoprotein Tetramerization Domain Provides Robust Protection from Virus Challenge in the Mouse Model. MBio, 2021, 12, e0224121. | 4.1 | 21 |
| 44 | Vaccine innovations for emerging infectious diseases—a symposium report. Annals of the New York Academy of Sciences, 2020, 1462, 14-26. | 3.8 | 15 |
| 45 | Influenza Hemagglutinin Structures and Antibody Recognition. Cold Spring Harbor Perspectives in Medicine, 2020, 10, a038778. | 6.2 | 79 |
| 46 | Diverse Antibody Responses to Conserved Structural Motifs in Plasmodium falciparum Circumsporozoite Protein. Journal of Molecular Biology, 2020, 432, 1048-1063. | 4.2 | 28 |
| 47 | Structural Biology of Influenza Hemagglutinin: An Amaranthine Adventure. Viruses, 2020, 12, 1053. | 3.3 | 35 |
| 48 | A Therapeutic Non-self-reactive SARS-CoV-2 Antibody Protects from Lung Pathology in a COVID-19 Hamster Model. Cell, 2020, 183, 1058-1069.e19. | 28.9 | 305 |
| 49 | An Alternative Binding Mode of IGHV3-53 Antibodies to the SARS-CoV-2 Receptor Binding Domain. Cell Reports, 2020, 33, 108274. | 6.4 | 152 |
| 50 | An influenza A hemagglutinin small-molecule fusion inhibitor identified by a new high-throughput fluorescence polarization screen. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18431-18438. | 7.1 | 25 |
| 51 | Structural basis of a shared antibody response to SARS-CoV-2. Science, 2020, 369, 1119-1123. | 12.6 | 536 |
| 52 | Cross-Neutralization of a SARS-CoV-2 Antibody to a Functionally Conserved Site Is Mediated by Avidity. Immunity, 2020, 53, 1272-1280.e5. | 14.3 | 185 |
| 53 | An alternate conformation of HCV E2 neutralizing face as an additional vaccine target. Science Advances, 2020, 6, eabb5642. | 10.3 | 26 |
| 54 | A high-affinity antibody against the CSP N-terminal domain lacks <i>Plasmodium falciparum</i> inhibitory activity. Journal of Experimental Medicine, 2020, 217, . | 8.5 | 21 |

| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 55 | Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. PLoS Pathogens, 2020, 16, e1008753. | 4.7 | 61 |
| 56 | A V _H 1-69 antibody lineage from an infected Chinese donor potently neutralizes HIV-1 by targeting the V3 glycan supersite. Science Advances, 2020, 6, . | 10.3 | 19 |
| 57 | Serological assays for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), March 2020. Eurosurveillance, 2020, 25, . | 7.0 | 309 |
| 58 | Cross-reactive Antibody Response between SARS-CoV-2 and SARS-CoV Infections. Cell Reports, 2020, 31, 107725. | 6.4 | 353 |
| 59 | Innovations in structure-based antigen design and immune monitoring for next generation vaccines. Current Opinion in Immunology, 2020, 65, 50-56. | 5.5 | 43 |
| 60 | HIV-1 Envelope and MPER Antibody Structures in Lipid Assemblies. Cell Reports, 2020, 31, 107583. | 6.4 | 60 |
| 61 | Inhibitory antibodies identify unique sites of therapeutic vulnerability in rhinovirus and other enteroviruses. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13499-13508. | 7.1 | 7 |
| 62 | Vulnerabilities in coronavirus glycan shields despite extensive glycosylation. Nature Communications, 2020, 11, 2688. | 12.8 | 304 |
| 63 | Structural basis of broad HIV neutralization by a vaccine-induced cow antibody. Science Advances, 2020, 6, eaba0468. | 10.3 | 31 |
| 64 | Isolation of potent SARS-CoV-2 neutralizing antibodies and protection from disease in a small animal model. Science, 2020, 369, 956-963. | 12.6 | 1,287 |
| 65 | Different genetic barriers for resistance to HA stem antibodies in influenza H3 and H1 viruses. Science, 2020, 368, 1335-1340. | 12.6 | 51 |
| 66 | Structure and mechanism of monoclonal antibody binding to theÂjunctional epitope of Plasmodium falciparumÂcircumsporozoite protein. PLoS Pathogens, 2020, 16, e1008373. | 4.7 | 30 |
| 67 | Major antigenic site B of human influenza H3N2 viruses has an evolving local fitness landscape. Nature Communications, 2020, 11, 1233. | 12.8 | 40 |
| 68 | A highly conserved cryptic epitope in the receptor binding domains of SARS-CoV-2 and SARS-CoV. Science, 2020, 368, 630-633. | 12.6 | 1,379 |
| 69 | Structural basis for the stabilization of amyloidogenic immunoglobulin light chains by hydantoins. Bioorganic and Medicinal Chemistry Letters, 2020, 30, 127356. | 2.2 | 15 |
| 70 | Convergent Evolution in Breadth of Two VH6-1-Encoded Influenza Antibody Clonotypes from a Single Donor. Cell Host and Microbe, 2020, 28, 434-444.e4. | 11.0 | 16 |
| 71 | The Impact of Sustained Immunization Regimens on the Antibody Response to Oligomannose Glycans. ACS Chemical Biology, 2020, 15, 789-798. | 3.4 | 9 |
| 72 | Autologous Antibody Responses to an HIV Envelope Glycan Hole Are Not Easily Broadened in Rabbits. Journal of Virology, 2020, 94, . | 3.4 | 57 |

| # | Article | IF | CITATIONS |
|----|---|------|-----------|
| 73 | Proof of concept for rational design of hepatitis C virus E2 core nanoparticle vaccines. Science Advances, 2020, 6, eaaz6225. | 10.3 | 44 |
| 74 | Neutralizing Antibody Induction by HIV-1 Envelope Glycoprotein SOSIP Trimers on Iron Oxide Nanoparticles May Be Impaired by Mannose Binding Lectin. Journal of Virology, 2020, 94, . | 3.4 | 29 |
| 75 | A natural mutation between SARS-CoV-2 and SARS-CoV determines neutralization by a cross-reactive antibody. PLoS Pathogens, 2020, 16, e1009089. | 4.7 | 55 |
| 76 | Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. , 2020, 16, e1008753. | | 0 |
| 77 | Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. , 2020, 16, e1008753. | | 0 |
| 78 | Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. , 2020, 16, e1008753. | | 0 |
| 79 | Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. , 2020, 16, e1008753. | | 0 |
| 80 | Structures of singleâ€layer βâ€sheet proteins evolved from βâ€hairpin repeats. Protein Science, 2019, 28, 1676-1689. | 7.6 | 4 |
| 81 | A generalized HIV vaccine design strategy for priming of broadly neutralizing antibody responses. Science, 2019, 366, . | 12.6 | 172 |
| 82 | Broadly protective human antibodies that target the active site of influenza virus neuraminidase. Science, 2019, 366, 499-504. | 12.6 | 162 |
| 83 | Potent anti-influenza H7 human monoclonal antibody induces separation of hemagglutinin receptor-binding head domains. PLoS Biology, 2019, 17, e3000139. | 5.6 | 37 |
| 84 | Exploitation of glycosylation in enveloped virus pathobiology. Biochimica Et Biophysica Acta - General Subjects, 2019, 1863, 1480-1497. | 2.4 | 383 |
| 85 | Structural Insights into the Lipid A Transport Pathway in MsbA. Structure, 2019, 27, 1114-1123.e3. | 3.3 | 41 |
| 86 | Structure and immunogenicity of a stabilized HIV-1 envelope trimer based on a group-M consensus sequence. Nature Communications, 2019, 10, 2355. | 12.8 | 116 |
| 87 | Preventing an Antigenically Disruptive Mutation in Egg-Based H3N2 Seasonal Influenza Vaccines by Mutational Incompatibility. Cell Host and Microbe, 2019, 25, 836-844.e5. | 11.0 | 45 |
| 88 | N-Glycolylneuraminic Acid as a Receptor for Influenza A Viruses. Cell Reports, 2019, 27, 3284-3294.e6. | 6.4 | 78 |
| 89 | Conformational Plasticity in the HIV-1 Fusion Peptide Facilitates Recognition by Broadly Neutralizing Antibodies. Cell Host and Microbe, 2019, 25, 873-883.e5. | 11.0 | 42 |
| 90 | The Chimpanzee SIV Envelope Trimer: Structure and Deployment as an HIV Vaccine Template. Cell Reports, 2019, 27, 2426-2441.e6. | 6.4 | 35 |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 91 | A Site of Vulnerability on the Influenza Virus Hemagglutinin Head Domain Trimer Interface. Cell, 2019, 177, 1136-1152.e18. | 28.9 | 177 |
| 92 | Bacterial glycosyltransferase-mediated cell-surface chemoenzymatic glycan modification. Nature Communications, 2019, 10, 1799. | 12.8 | 46 |
| 93 | VH1-69 antiviral broadly neutralizing antibodies: genetics, structures, and relevance to rational vaccine design. Current Opinion in Virology, 2019, 34, 149-159. | 5.4 | 92 |
| 94 | Antibody responses to viral infections: a structural perspective across three different enveloped viruses. Nature Microbiology, 2019, 4, 734-747. | 13.3 | 158 |
| 95 | A small-molecule fusion inhibitor of influenza virus is orally active in mice. Science, 2019, 363, . | 12.6 | 98 |
| 96 | Stabilization of the V2 loop improves the presentation of V2 loop–associated broadly neutralizing antibody epitopes on HIV-1 envelope trimers. Journal of Biological Chemistry, 2019, 294, 5616-5631. | 3.4 | 16 |
| 97 | 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. | 7.1 | 52 |
| 98 | A pan-coronavirus fusion inhibitor targeting the HR1 domain of human coronavirus spike. Science Advances, 2019, 5, eaav4580. | 10.3 | 393 |
| 99 | Oligomannose Glycopeptide Conjugates Elicit Antibodies Targeting the Glycan Core Rather than Its Extremities. ACS Central Science, 2019, 5, 237-249. | 11.3 | 33 |
| 100 | Capturing the inherent structural dynamics of the HIV-1 envelope glycoprotein fusion peptide. Nature Communications, 2019, 10, 763. | 12.8 | 30 |
| 101 | Identification of Antibodies Targeting the H3N2 Hemagglutinin Receptor Binding Site following Vaccination of Humans. Cell Reports, 2019, 29, 4460-4470.e8. | 6.4 | 22 |
| 102 | An MPER antibody neutralizes HIV-1 using germline features shared among donors. Nature Communications, 2019, 10, 5389. | 12.8 | 44 |
| 103 | Structural Basis of Protection against H7N9 Influenza Virus by Human Anti-N9 Neuraminidase Antibodies. Cell Host and Microbe, 2019, 26, 729-738.e4. | 11.0 | 51 |
| 104 | Influenza H7N9 Virus Neuraminidase-Specific Human Monoclonal Antibodies Inhibit Viral Egress and Protect from Lethal Influenza Infection in Mice. Cell Host and Microbe, 2019, 26, 715-728.e8. | 11.0 | 49 |
| 105 | A Dynamic Switch in Inactive p38Î ³ Leads to an Excited State on the Pathway to an Active Kinase. Biochemistry, 2019, 58, 5160-5172. | 2.5 | 7 |
| 106 | Vaccine-Induced Protection from Homologous Tier 2 SHIV Challenge in Nonhuman Primates Depends on Serum-Neutralizing Antibody Titers. Immunity, 2019, 50, 241-252.e6. | 14.3 | 153 |
| 107 | Immunodominance and Antigenic Variation of Influenza Virus Hemagglutinin: Implications for Design of Universal Vaccine Immunogens. Journal of Infectious Diseases, 2019, 219, S38-S45. | 4.0 | 67 |
| 108 | Genetic and structural insights into broad neutralization of hepatitis C virus by human V _H 1-69 antibodies. Science Advances, 2019, 5, eaav1882. | 10.3 | 77 |

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 109 | Multistate design of influenza antibodies improves affinity and breadth against seasonal viruses. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1597-1602. | 7.1 | 23 |
| 110 | Closing and Opening Holes in the Glycan Shield of HIV-1 Envelope Glycoprotein SOSIP Trimers Can Redirect the Neutralizing Antibody Response to the Newly Unmasked Epitopes. Journal of Virology, 2019, 93, . | 3.4 | 66 |
| 111 | Novel Rigid Glycomimetics to Inhibit Influenza Infection. FASEB Journal, 2019, 33, . | 0.5 | 0 |
| 112 | Structural insights into the design of novel anti-influenza therapies. Nature Structural and Molecular Biology, 2018, 25, 115-121. | 8.2 | 81 |
| 113 | Integrity of Glycosylation Processing of a Glycan-Depleted Trimeric HIV-1 Immunogen Targeting Key B-Cell Lineages. Journal of Proteome Research, 2018, 17, 987-999. | 3.7 | 23 |
| 114 | "Inverse Drug Discovery―Strategy To Identify Proteins That Are Targeted by Latent Electrophiles As Exemplified by Aryl Fluorosulfates. Journal of the American Chemical Society, 2018, 140, 200-210. | 13.7 | 206 |
| 115 | Structure and Immune Recognition of the HIV Glycan Shield. Annual Review of Biophysics, 2018, 47, 499-523. | 10.0 | 115 |
| 116 | A complex epistatic network limits the mutational reversibility in the influenza hemagglutinin receptor-binding site. Nature Communications, 2018, 9, 1264. | 12.8 | 58 |
| 117 | A small-molecule fragment that emulates binding of receptor and broadly neutralizing antibodies to influenza A hemagglutinin. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4240-4245. | 7.1 | 25 |
| 118 | VLR Recognition of TLR5 Expands the Molecular Characterization of Protein Antigen Binding by Non-Ig-based Antibodies. Journal of Molecular Biology, 2018, 430, 1350-1367. | 4.2 | 12 |
| 119 | A public antibody lineage that potently inhibits malaria infection through dual binding to the circumsporozoite protein. Nature Medicine, 2018, 24, 401-407. | 30.7 | 183 |
| 120 | Stabilization of the gp120 V3 loop through hydrophobic interactions reduces the immunodominant V3-directed non-neutralizing response to HIV-1 envelope trimers. Journal of Biological Chemistry, 2018, 293, 1688-1701. | 3.4 | 40 |
| 121 | cGMP production and analysis of BG505 SOSIP.664, an extensively glycosylated, trimeric HIVâ€1 envelope glycoprotein vaccine candidate. Biotechnology and Bioengineering, 2018, 115, 885-899. | 3.3 | 75 |
| 122 | HIV-1 vaccine design through minimizing envelope metastability. Science Advances, 2018, 4, eaau6769. | 10.3 | 75 |
| 123 | Recurring and Adaptable Binding Motifs in Broadly Neutralizing Antibodies to Influenza Virus Are Encoded on the D3-9 Segment of the Ig Gene. Cell Host and Microbe, 2018, 24, 569-578.e4. | 11.0 | 32 |
| 124 | Cryo-EM structure of <i>P. falciparum</i> circumsporozoite protein with a vaccine-elicited antibody is stabilized by somatically mutated inter-Fab contacts. Science Advances, 2018, 4, eaau8529. | 10.3 | 70 |
| 125 | Structural Basis for Recognition of a Unique Epitope by a Human Anti-tau Antibody. Structure, 2018, 26, 1626-1634.e4. | 3.3 | 9 |
| 126 | Universal protection against influenza infection by a multidomain antibody to influenza hemagglutinin. Science, 2018, 362, 598-602. | 12.6 | 170 |

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 127 | Structure–Activity Relationships in Metal-Binding Pharmacophores for Influenza Endonuclease. Journal of Medicinal Chemistry, 2018, 61, 10206-10217. | 6.4 | 42 |
| 128 | Crystal structure of the post-fusion core of the <i>Human coronavirus 229E</i> spike protein at 1.86â€Ã resolution. Acta Crystallographica Section D: Structural Biology, 2018, 74, 841-851. | 2.3 | 18 |
| 129 | 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. | 7.1 | 18 |
| 130 | Structure of a cleavage-independent HIV Env recapitulates the glycoprotein architecture of the native cleaved trimer. Nature Communications, 2018, 9, 1956. | 12.8 | 50 |
| 131 | The Unusual Genetics and Biochemistry of Bovine Immunoglobulins. Advances in Immunology, 2018, 137, 135-164. | 2.2 | 36 |
| 132 | Immunogenetic and structural analysis of a class of HCV broadly neutralizing antibodies and their precursors. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7569-7574. | 7.1 | 14 |
| 133 | The human naive B cell repertoire contains distinct subclasses for a germline-targeting HIV-1 vaccine immunogen. Science Translational Medicine, 2018, 10, . | 12.4 | 113 |
| 134 | Electron-Microscopy-Based Epitope Mapping Defines Specificities of Polyclonal Antibodies Elicited during HIV-1 BG505 Envelope Trimer Immunization. Immunity, 2018, 49, 288-300.e8. | 14.3 | 175 |
| 135 | The Neutralizing Face of Hepatitis C Virus E2 Envelope Glycoprotein. Frontiers in Immunology, 2018, 9, 1315. | 4.8 | 56 |
| 136 | A multifunctional human monoclonal neutralizing antibody that targets a unique conserved epitope on influenza HA. Nature Communications, 2018, 9, 2669. | 12.8 | 67 |
| 137 | A common antigenic motif recognized by naturally occurring human VH5–51/VL4–1 anti-tau antibodies with distinct functionalities. Acta Neuropathologica Communications, 2018, 6, 43. | 5.2 | 15 |
| 138 | Co-evolution of HIV Envelope and Apex-Targeting Neutralizing Antibody Lineage Provides Benchmarks for Vaccine Design. Cell Reports, 2018, 23, 3249-3261. | 6.4 | 52 |
| 139 | Epitopes for neutralizing antibodies induced by HIV-1 envelope glycoprotein BG505 SOSIP trimers in rabbits and macaques. PLoS Pathogens, 2018, 14, e1006913. | 4.7 | 111 |
| 140 | The <scp>HIV</scp> â€1 envelope glycoprotein structure: nailing down a moving target. Immunological Reviews, 2017, 275, 21-32. | 6.0 | 251 |
| 141 | Unique Structural Features of Influenza Virus H15 Hemagglutinin. Journal of Virology, 2017, 91, . | 3.4 | 12 |
| 142 | The 150-Loop Restricts the Host Specificity of Human H10N8 Influenza Virus. Cell Reports, 2017, 19, 235-245. | 6.4 | 35 |
| 143 | A Broadly Neutralizing Antibody Targets the Dynamic HIV Envelope Trimer Apex via a Long, Rigidified, and Anionic β-Hairpin Structure. Immunity, 2017, 46, 690-702. | 14.3 | 216 |
| 144 | In vitro evolution of an influenza broadly neutralizing antibody is modulated by hemagglutinin receptor specificity. Nature Communications, 2017, 8, 15371. | 12.8 | 55 |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 145 | 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. | 14.3 | 96 |
| 146 | Elicitation of Robust Tier 2 Neutralizing Antibody Responses in Nonhuman Primates by HIV Envelope Trimer Immunization Using Optimized Approaches. Immunity, 2017, 46, 1073-1088.e6. | 14.3 | 286 |
| 147 | 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. | 7.1 | 56 |
| 148 | Reducing V3 Antigenicity and Immunogenicity on Soluble, Native-Like HIV-1 Env SOSIP Trimers. Journal of Virology, 2017, 91, . | 3.4 | 57 |
| 149 | Semi-quantitative models for identifying potent and selective transthyretin amyloidogenesis inhibitors. Bioorganic and Medicinal Chemistry Letters, 2017, 27, 3441-3449. | 2.2 | 8 |
| 150 | Computational design of trimeric influenza-neutralizing proteins targeting the hemagglutinin receptor binding site. Nature Biotechnology, 2017, 35, 667-671. | 17.5 | 108 |
| 151 | Genetically encoding phosphotyrosine and its nonhydrolyzable analog in bacteria. Nature Chemical Biology, 2017, 13, 845-849. | 8.0 | 105 |
| 152 | Diversity of Functionally Permissive Sequences in the Receptor-Binding Site of Influenza Hemagglutinin. Cell Host and Microbe, 2017, 21, 742-753.e8. | 11.0 | 59 |
| 153 | Improving the Expression and Purification of Soluble, Recombinant Native-Like HIV-1 Envelope Glycoprotein Trimers by Targeted Sequence Changes. Journal of Virology, 2017, 91, . | 3.4 | 27 |
| 154 | Immunological memory to hyperphosphorylated tau in asymptomatic individuals. Acta Neuropathologica, 2017, 133, 767-783. | 7.7 | 43 |
| 155 | Recent H3N2 Viruses Have Evolved Specificity for Extended, Branched Human-type Receptors, Conferring Potential for Increased Avidity. Cell Host and Microbe, 2017, 21, 23-34. | 11.0 | 163 |
| 156 | Structural basis of influenza virus fusion inhibition by the antiviral drug Arbidol. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 206-214. | 7.1 | 340 |
| 157 | Structural Insights into VLR Fine Specificity for Blood Group Carbohydrates. Structure, 2017, 25, 1667-1678.e4. | 3.3 | 27 |
| 158 | Elicitation of Neutralizing Antibodies Targeting the V2 Apex of the HIV Envelope Trimer in a Wild-Type Animal Model. Cell Reports, 2017, 21, 222-235. | 6.4 | 58 |
| 159 | Massively parallel de novo protein design for targeted therapeutics. Nature, 2017, 550, 74-79. | 27.8 | 354 |
| 160 | Potent peptidic fusion inhibitors of influenza virus. Science, 2017, 358, 496-502. | 12.6 | 135 |
| 161 | Improving the Immunogenicity of Native-like HIV-1 Envelope Trimers by Hyperstabilization. Cell Reports, 2017, 20, 1805-1817. | 6.4 | 171 |
| 162 | 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. | 8.5 | 151 |

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 163 | Antibody 27F3 Broadly Targets Influenza A Group 1 and 2 Hemagglutinins through a Further Variation in VH1-69 Antibody Orientation on the HA Stem. Cell Reports, 2017, 20, 2935-2943. | 6.4 | 103 |
| 164 | Selection of nanobodies with broad neutralizing potential against primary HIV-1 strains using soluble subtype C gp140 envelope trimers. Scientific Reports, 2017, 7, 8390. | 3.3 | 31 |
| 165 | Defining the Structural Basis for Allosteric Product Release from <i>E. coli</i> Dihydrofolate Reductase Using NMR Relaxation Dispersion. Journal of the American Chemical Society, 2017, 139, 11233-11240. | 13.7 | 27 |
| 166 | Rapid elicitation of broadly neutralizing antibodies to HIV by immunization in cows. Nature, 2017, 548, 108-111. | 27.8 | 154 |
| 167 | A single mutation in Taiwanese H6N1 influenza hemagglutinin switches binding to humanâ€ŧype receptors. EMBO Molecular Medicine, 2017, 9, 1314-1325. | 6.9 | 44 |
| 168 | HIV Envelope Glycoform Heterogeneity and Localized Diversity Govern the Initiation and Maturation of a V2 Apex Broadly Neutralizing Antibody Lineage. Immunity, 2017, 47, 990-1003.e9. | 14.3 | 90 |
| 169 | Crystal structure of an anti-idiotype variable lymphocyte receptor. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 682-687. | 0.8 | 3 |
| 170 | Bacterially derived synthetic mimetics of mammalian oligomannose prime antibody responses that neutralize HIV infectivity. Nature Communications, 2017, 8, 1601. | 12.8 | 33 |
| 171 | Structural basis for antibody recognition of the NANP repeats in <i>Plasmodium falciparum</i> circumsporozoite protein. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E10438-E10445. | 7.1 | 116 |
| 172 | A Perspective on the Structural and Functional Constraints for Immune Evasion: Insights from Influenza Virus. Journal of Molecular Biology, 2017, 429, 2694-2709. | 4.2 | 133 |
| 173 | Open and closed structures reveal allostery and pliability in the HIV-1 envelope spike. Nature, 2017, 547, 360-363. | 27.8 | 217 |
| 174 | Structure-based optimization and synthesis of antiviral drug Arbidol analogues with significantly improved affinity to influenza hemagglutinin. Bioorganic and Medicinal Chemistry Letters, 2017, 27, 3744-3748. | 2.2 | 48 |
| 175 | An HIV-1 antibody from an elite neutralizer implicates the fusion peptide as a site of vulnerability. Nature Microbiology, 2017, 2, 16199. | 13.3 | 144 |
| 176 | Three mutations switch H7N9 influenza to human-type receptor specificity. PLoS Pathogens, 2017, 13, e1006390. | 4.7 | 83 |
| 177 | A structural explanation for the low effectiveness of the seasonal influenza H3N2 vaccine. PLoS Pathogens, 2017, 13, e1006682. | 4.7 | 188 |
| 178 | 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. | 4.7 | 58 |
| 179 | Probing the antigenicity of hepatitis C virus envelope glycoprotein complex by high-throughput mutagenesis. PLoS Pathogens, 2017, 13, e1006735. | 4.7 | 66 |
| 180 | A Computationally Designed Hemagglutinin Stem-Binding Protein Provides In Vivo Protection from Influenza Independent of a Host Immune Response. PLoS Pathogens, 2016, 12, e1005409. | 4.7 | 49 |

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 181 | Minimally Mutated HIV-1 Broadly Neutralizing Antibodies to Guide Reductionist Vaccine Design. PLoS Pathogens, 2016, 12, e1005815. | 4.7 | 104 |
| 182 | Uncleaved prefusion-optimized gp140 trimers derived from analysis of HIV-1 envelope metastability. Nature Communications, 2016, 7, 12040. | 12.8 | 134 |
| 183 | Presenting native-like trimeric HIV-1 antigens with self-assembling nanoparticles. Nature Communications, 2016, 7, 12041. | 12.8 | 146 |
| 184 | UHM–ULM interactions in the RBM39–U2AF65 splicing-factor complex. Acta Crystallographica Section D: Structural Biology, 2016, 72, 497-511. | 2.3 | 36 |
| 185 | HIV's Achilles' Heel. Scientific American, 2016, 315, 50-55. | 1.0 | 6 |
| 186 | Key gp120 Glycans Pose Roadblocks to the Rapid Development of VRC01-Class Antibodies in an HIV-1-Infected Chinese Donor. Immunity, 2016, 44, 939-950. | 14.3 | 85 |
| 187 | Early Antibody Lineage Diversification and Independent Limb Maturation Lead to Broad HIV-1 Neutralization Targeting the Env High-Mannose Patch. Immunity, 2016, 44, 1215-1226. | 14.3 | 138 |
| 188 | Arylfluorosulfates Inactivate Intracellular Lipid Binding Protein(s) through Chemoselective SuFEx Reaction with a Binding Site Tyr Residue. Journal of the American Chemical Society, 2016, 138, 7353-7364. | 13.7 | 212 |
| 189 | A Distinct Type of Pilus from the Human Microbiome. Cell, 2016, 165, 690-703. | 28.9 | 78 |
| 190 | Stabilizing the C _H 2 Domain of an Antibody by Engineering in an Enhanced Aromatic Sequon. ACS Chemical Biology, 2016, 11, 1852-1861. | 3.4 | 40 |
| 191 | Tailored Immunogens Direct Affinity Maturation toward HIV Neutralizing Antibodies. Cell, 2016, 166, 1459-1470.e11. | 28.9 | 230 |
| 192 | HIV Vaccine Design to Target Germline Precursors of Glycan-Dependent Broadly Neutralizing Antibodies. Immunity, 2016, 45, 483-496. | 14.3 | 335 |
| 193 | Holes in the Glycan Shield of the Native HIV Envelope Are a Target of Trimer-Elicited Neutralizing Antibodies. Cell Reports, 2016, 16, 2327-2338. | 6.4 | 216 |
| 194 | Dynamic Local Polymorphisms in the Gbx1 Homeodomain Induced by DNA Binding. Structure, 2016, 24, 1372-1379. | 3.3 | 2 |
| 195 | A Prominent Site of Antibody Vulnerability on HIV Envelope Incorporates a Motif Associated with CCR5 Binding and Its Camouflaging Glycans. Immunity, 2016, 45, 31-45. | 14.3 | 129 |
| 196 | HMGB1 Activates Proinflammatory Signaling via TLR5 Leading to Allodynia. Cell Reports, 2016, 17, 1128-1140. | 6.4 | 125 |
| 197 | Structural flexibility at a major conserved antibody target on hepatitis C virus E2 antigen. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12768-12773. | 7.1 | 78 |
| 198 | Conservation and diversity in the ultralong third heavy-chain complementarity-determining region of bovine antibodies. Science Immunology, 2016, 1, . | 11.9 | 52 |

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 199 | HIV-1 broadly neutralizing antibody precursor B cells revealed by germline-targeting immunogen. Science, 2016, 351, 1458-1463. | 12.6 | 382 |
| 200 | Dlx5 Homeodomain:DNA Complex: Structure, Binding and Effect of Mutations Related to Split Hand and Foot Malformation Syndrome. Journal of Molecular Biology, 2016, 428, 1130-1141. | 4.2 | 10 |
| 201 | Composition and Antigenic Effects of Individual Glycan Sites of a Trimeric HIV-1 Envelope Glycoprotein. Cell Reports, 2016, 14, 2695-2706. | 6.4 | 250 |
| 202 | Crystal Structure and Activity Studies of the C11 Cysteine Peptidase from Parabacteroides merdae in the Human Gut Microbiome. Journal of Biological Chemistry, 2016, 291, 9482-9491. | 3.4 | 15 |
| 203 | Crystallographic Identification of Lipid as an Integral Component of the Epitope of HIV Broadly Neutralizing Antibody 4E10. Immunity, 2016, 44, 21-31. | 14.3 | 87 |
| 204 | H7N9 influenza virus neutralizing antibodies that possess few somatic mutations. Journal of Clinical Investigation, 2016, 126, 1482-1494. | 8.2 | 62 |
| 205 | Sequential and Simultaneous Immunization of Rabbits with HIV-1 Envelope Glycoprotein SOSIP.664 Trimers from Clades A, B and C. PLoS Pathogens, 2016, 12, e1005864. | 4.7 | 138 |
| 206 | Approaching rational epitope vaccine design for hepatitis C virus with meta-server and multivalent scaffolding. Scientific Reports, 2015, 5, 12501. | 3.3 | 68 |
| 207 | Structural Basis for a Switch in Receptor Binding Specificity of Two H5N1 Hemagglutinin Mutants. Cell Reports, 2015, 13, 1683-1691. | 6.4 | 18 |
| 208 | A Fluorogenic Aryl Fluorosulfate for Intraorganellar Transthyretin Imaging in Living Cells and in <i>Caenorhabditis elegans</i> . Journal of the American Chemical Society, 2015, 137, 7404-7414. | 13.7 | 86 |
| 209 | Immunogenicity of Stabilized HIV-1 Envelope Trimers with Reduced Exposure of Non-neutralizing Epitopes. Cell, 2015, 163, 1702-1715. | 28.9 | 341 |
| 210 | Affinity Maturation of a Potent Family of HIV Antibodies Is Primarily Focused on Accommodating or Avoiding Glycans. Immunity, 2015, 43, 1053-1063. | 14.3 | 200 |
| 211 | Structural Constraints Determine the Glycosylation of HIV-1 Envelope Trimers. Cell Reports, 2015, 11, 1604-1613. | 6.4 | 135 |
| 212 | Antibody potency relates to the ability to recognize the closed, pre-fusion form of HIV Env. Nature Communications, 2015, 6, 6144. | 12.8 | 130 |
| 213 | Insights into the trimeric HIV-1 envelope glycoprotein structure. Trends in Biochemical Sciences, 2015, 40, 101-107. | 7.5 | 95 |
| 214 | HIV-1 neutralizing antibodies induced by native-like envelope trimers. Science, 2015, 349, aac4223. | 12.6 | 482 |
| 215 | Structure of Hepatitis C Virus Envelope Glycoprotein E1 Antigenic Site 314–324 in Complex with Antibody IGH526. Journal of Molecular Biology, 2015, 427, 2617-2628. | 4.2 | 44 |
| 216 | Comprehensive Antigenic Map of a Cleaved Soluble HIV-1 Envelope Trimer. PLoS Pathogens, 2015, 11, e1004767. | 4.7 | 100 |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 217 | Capitalizing on knowledge of hepatitis C virus neutralizing epitopes for rational vaccine design. Current Opinion in Virology, 2015, 11, 148-157. | 5.4 | 54 |
| 218 | Structure of the apo anti-influenza CH65 Fab. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 145-148. | 0.8 | 5 |
| 219 | Structure-based discovery of NANOG variant with enhanced properties to promote self-renewal and reprogramming of pluripotent stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4666-4671. | 7.1 | 43 |
| 220 | A Native-Like SOSIP.664 Trimer Based on an HIV-1 Subtype B <i>env</i> Gene. Journal of Virology, 2015, 89, 3380-3395. | 3.4 | 247 |
| 221 | A Human-Infecting H10N8 Influenza Virus Retains a Strong Preference for Avian-type Receptors. Cell Host and Microbe, 2015, 17, 377-384. | 11.0 | 54 |
| 222 | Structure and Receptor Binding of the Hemagglutinin from a Human H6N1 Influenza Virus. Cell Host and Microbe, 2015, 17, 369-376. | 11.0 | 44 |
| 223 | Design and Structure of an Engineered Disulfide-Stabilized Influenza Virus Hemagglutinin Trimer. Journal of Virology, 2015, 89, 7417-7420. | 3.4 | 32 |
| 224 | 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 |
| 225 | Insights into Substrate Specificity of NlpC/P60 Cell Wall Hydrolases Containing Bacterial SH3 Domains. MBio, 2015, 6, e02327-14. | 4.1 | 46 |
| 226 | Antibodies to a conformational epitope on gp41 neutralize HIV-1 by destabilizing the Env spike. Nature Communications, 2015, 6, 8167. | 12.8 | 87 |
| 227 | A stable trimeric influenza hemagglutinin stem as a broadly protective immunogen. Science, 2015, 349, 1301-1306. | 12.6 | 480 |
| 228 | A General Method for Insertion of Functional Proteins within Proteins via Combinatorial Selection of Permissive Junctions. Chemistry and Biology, 2015, 22, 1134-1143. | 6.0 | 9 |
| 229 | Design and structure of two HIV-1 clade C SOSIP.664 trimers that increase the arsenal of native-like Env immunogens. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11947-11952. | 7.1 | 127 |
| 230 | Influences on the Design and Purification of Soluble, Recombinant Native-Like HIV-1 Envelope Glycoprotein Trimers. Journal of Virology, 2015, 89, 12189-12210. | 3.4 | 88 |
| 231 | Two Classes of Broadly Neutralizing Antibodies within a Single Lineage Directed to the High-Mannose Patch of HIV Envelope. Journal of Virology, 2015, 89, 1105-1118. | 3.4 | 80 |
| 232 | Crystal structure of the HIV neutralizing antibody 2G12 in complex with a bacterial oligosaccharide analog of mammalian oligomannose. Glycobiology, 2015, 25, 412-419. | 2.5 | 27 |
| 233 | Soluble human TLR2 ectodomain binds diacylglycerol from microbial lipopeptides and glycolipids. Innate Immunity, 2015, 21, 175-193. | 2.4 | 25 |
| 234 | Redesigned HIV antibodies exhibit enhanced neutralizing potency and breadth. Journal of Clinical Investigation, 2015, 125, 2523-2531. | 8.2 | 31 |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 235 | Crystal Structure of a Two-Subunit TrkA Octameric Gating Ring Assembly. PLoS ONE, 2015, 10, e0122512. | 2.5 | 2 |
| 236 | Structural Insights into the Recognition of Phosphopeptide by the FHA Domain of Kanadaptin. PLoS ONE, 2014, 9, e107309. | 2.5 | 6 |
| 237 | Promiscuous Glycan Site Recognition by Antibodies to the High-Mannose Patch of gp120 Broadens Neutralization of HIV. Science Translational Medicine, 2014, 6, 236ra63. | 12.4 | 160 |
| 238 | Receptor mimicry by antibody F045–092 facilitates universal binding to the H3 subtype of influenza virus. Nature Communications, 2014, 5, 3614. | 12.8 | 175 |
| 239 | Recombinant HIV envelope trimer selects for quaternary-dependent antibodies targeting the trimer apex. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17624-17629. | 7.1 | 324 |
| 240 | STRUCTURAL BASIS FOR HOST/COMMENSAL-MICROBE INTERACTIONS IN THE HUMAN DISTAL GUT MICROBIOME. , 2014, , . | | 0 |
| 241 | Stapled HIV-1 peptides recapitulate antigenic structures and engage broadly neutralizing antibodies. Nature Structural and Molecular Biology, 2014, 21, 1058-1067. | 8.2 | 69 |
| 242 | Structure-Guided Functional Characterization of DUF1460 Reveals a Highly Specific NlpC/P60 Amidase Family. Structure, 2014, 22, 1799-1809. | 3.3 | 10 |
| 243 | Stable 293ÂT and CHO cell lines expressing cleaved, stable HIV-1 envelope glycoprotein trimers for structural and vaccine studies. Retrovirology, 2014, 11, 33. | 2.0 | 46 |
| 244 | 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. | 3.4 | 67 |
| 245 | Structures of a Bifunctional Cell Wall Hydrolase CwlT Containing a Novel Bacterial Lysozyme and an NlpC/P60 dl-Endopeptidase. Journal of Molecular Biology, 2014, 426, 169-184. | 4.2 | 25 |
| 246 | Broadly Neutralizing HIV Antibodies Define a Glycan-Dependent Epitope on the Prefusion Conformation of gp41 on Cleaved Envelope Trimers. Immunity, 2014, 40, 657-668. | 14.3 | 342 |
| 247 | A Structurally Distinct Human Mycoplasma Protein that Generically Blocks Antigen-Antibody Union. Science, 2014, 343, 656-661. | 12.6 | 85 |
| 248 | Developmental pathway for potent V1V2-directed HIV-neutralizing antibodies. Nature, 2014, 509, 55-62. | 27.8 | 681 |
| 249 | Structural Delineation of a Quaternary, Cleavage-Dependent Epitope at the gp41-gp120 Interface on Intact HIV-1 Env Trimers. Immunity, 2014, 40, 669-680. | 14.3 | 323 |
| 250 | Hemagglutinin Receptor Specificity and Structural Analyses of Respiratory Droplet-Transmissible H5N1 Viruses. Journal of Virology, 2014, 88, 768-773. | 3.4 | 61 |
| 251 | A common solution to group 2 influenza virus neutralization. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 445-450. | 7.1 | 187 |
| 252 | Characterization of a Broadly Neutralizing Monoclonal Antibody That Targets the Fusion Domain of Group 2 Influenza A Virus Hemagglutinin. Journal of Virology, 2014, 88, 13580-13592. | 3.4 | 110 |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 253 | Structural Evolution of Glycan Recognition by a Family of Potent HIV Antibodies. Cell, 2014, 159, 69-79. | 28.9 | 161 |
| 254 | Structural Characterization of Viral Epitopes Recognized by Broadly Cross-Reactive Antibodies. Current Topics in Microbiology and Immunology, 2014, 386, 323-341. | 1.1 | 83 |
| 255 | Differential binding of neutralizing and non-neutralizing antibodies to native-like soluble HIV-1 Env trimers, uncleaved Env proteins, and monomeric subunits. Retrovirology, 2014, 11, 41. | 2.0 | 139 |
| 256 | Alternative Recognition of the Conserved Stem Epitope in Influenza A Virus Hemagglutinin by a V _H 3-30-Encoded Heterosubtypic Antibody. Journal of Virology, 2014, 88, 7083-7092. | 3.4 | 62 |
| 257 | CD4-Induced Activation in a Soluble HIV-1 Env Trimer. Structure, 2014, 22, 974-984. | 3.3 | 108 |
| 258 | Antibody Structure. Microbiology Spectrum, 2014, 2, . | 3.0 | 31 |
| 259 | HIV ENVELOPE AND INFLUENZA HEMAGGLUTININ FUSION GLYCOPROTEINS AND THE QUEST FOR A UNIVERSAL VACCINE. , 2014, , . | | 0 |
| 260 | Bifunctional coumarin derivatives that inhibit transthyretin amyloidogenesis and serve as fluorescent transthyretin folding sensors. Chemical Communications, 2013, 49, 9188. | 4.1 | 35 |
| 261 | Crystal Structure of a Soluble Cleaved HIV-1 Envelope Trimer. Science, 2013, 342, 1477-1483. | 12.6 | 793 |
| 262 | Cryo-EM Structure of a Fully Glycosylated Soluble Cleaved HIV-1 Envelope Trimer. Science, 2013, 342, 1484-1490. | 12.6 | 662 |
| 263 | A Unique and Conserved Neutralization Epitope in H5N1 Influenza Viruses Identified by an Antibody against the A/Goose/Guangdong/1/96 Hemagglutinin. Journal of Virology, 2013, 87, 12619-12635. | 3.4 | 51 |
| 264 | Hepatitis C Virus E2 Envelope Glycoprotein Core Structure. Science, 2013, 342, 1090-1094. | 12.6 | 374 |
| 265 | Antibody Recognition of the Pandemic H1N1 Influenza Virus Hemagglutinin Receptor Binding Site. Journal of Virology, 2013, 87, 12471-12480. | 3.4 | 139 |
| 266 | Preferential Recognition of Avian-Like Receptors in Human Influenza A H7N9 Viruses. Science, 2013, 342, 1230-1235. | 12.6 | 133 |
| 267 | Structural Characterization of Cleaved, Soluble HIV-1 Envelope Glycoprotein Trimers. Journal of Virology, 2013, 87, 9865-9872. | 3.4 | 71 |
| 268 | A recurring motif for antibody recognition of the receptor-binding site of influenza hemagglutinin. Nature Structural and Molecular Biology, 2013, 20, 363-370. | 8.2 | 141 |
| 269 | Broadly neutralizing antibodies against influenza viruses. Antiviral Research, 2013, 98, 476-483. | 4.1 | 136 |
| 270 | Rational HIV Immunogen Design to Target Specific Germline B Cell Receptors. Science, 2013, 340, 711-716. | 12.6 | 680 |

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 271 | Supersite of immune vulnerability on the glycosylated face of HIV-1 envelope glycoprotein gp120. Nature Structural and Molecular Biology, 2013, 20, 796-803. | 8.2 | 314 |
| 272 | Reshaping Antibody Diversity. Cell, 2013, 153, 1379-1393. | 28.9 | 179 |
| 273 | Broadly Neutralizing Antibody PGT121 Allosterically Modulates CD4 Binding via Recognition of the HIV-1 gp120 V3 Base and Multiple Surrounding Glycans. PLoS Pathogens, 2013, 9, e1003342. | 4.7 | 267 |
| 274 | A Next-Generation Cleaved, Soluble HIV-1 Env Trimer, BG505 SOSIP.664 gp140, Expresses Multiple Epitopes for Broadly Neutralizing but Not Non-Neutralizing Antibodies. PLoS Pathogens, 2013, 9, e1003618. | 4.7 | 835 |
| 275 | New World Bats Harbor Diverse Influenza A Viruses. PLoS Pathogens, 2013, 9, e1003657. | 4.7 | 1,050 |
| 276 | Asymmetric recognition of the HIV-1 trimer by broadly neutralizing antibody PG9. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4351-4356. | 7.1 | 236 |
| 277 | Cleavage strongly influences whether soluble HIV-1 envelope glycoprotein trimers adopt a native-like conformation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18256-18261. | 7.1 | 188 |
| 278 | Influences on Trimerization and Aggregation of Soluble, Cleaved HIV-1 SOSIP Envelope Glycoprotein. Journal of Virology, 2013, 87, 9873-9885. | 3.4 | 76 |
| 279 | Hemagglutinin homologue from H17N10 bat influenza virus exhibits divergent receptor-binding and pH-dependent fusion activities. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1458-1463. | 7.1 | 135 |
| 280 | Structure and Function of the DUF2233 Domain in Bacteria and in the Human Mannose 6-Phosphate Uncovering Enzyme. Journal of Biological Chemistry, 2013, 288, 16789-16799. | 3.4 | 7 |
| 281 | Structure of a Classical Broadly Neutralizing Stem Antibody in Complex with a Pandemic H2 Influenza Virus Hemagglutinin. Journal of Virology, 2013, 87, 7149-7154. | 3.4 | 114 |
| 282 | Influenza Human Monoclonal Antibody 1F1 Interacts with Three Major Antigenic Sites and Residues Mediating Human Receptor Specificity in H1N1 Viruses. PLoS Pathogens, 2012, 8, e1003067. | 4.7 | 80 |
| 283 | Heterosubtypic antibody recognition of the influenza virus hemagglutinin receptor binding site enhanced by avidity. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17040-17045. | 7.1 | 159 |
| 284 | Highly Conserved Protective Epitopes on Influenza B Viruses. Science, 2012, 337, 1343-1348. | 12.6 | 705 |
| 285 | Structure of Hepatitis C Virus Envelope Glycoprotein E2 Antigenic Site 412 to 423 in Complex with Antibody AP33. Journal of Virology, 2012, 86, 13085-13088. | 3.4 | 79 |
| 286 | A Blueprint for HIV Vaccine Discovery. Cell Host and Microbe, 2012, 12, 396-407. | 11.0 | 348 |
| 287 | Structural insights into key sites of vulnerability on <scp>HIV</scp> â€1 Env and influenza <scp>HA</scp> . Immunological Reviews, 2012, 250, 180-198. | 6.0 | 84 |
| 288 | Cross-neutralization of influenza A viruses mediated by a single antibody loop. Nature, 2012, 489, 526-532. | 27.8 | 434 |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 289 | Structural Characterization of the Hemagglutinin Receptor Specificity from the 2009 H1N1 Influenza Pandemic. Journal of Virology, 2012, 86, 982-990. | 3.4 | 155 |
| 290 | Structural Basis of TLR5-Flagellin Recognition and Signaling. Science, 2012, 335, 859-864. | 12.6 | 454 |
| 291 | Broadly Neutralizing Antibodies Present New Prospects to Counter Highly Antigenically Diverse Viruses. Science, 2012, 337, 183-186. | 12.6 | 394 |
| 292 | Structural basis of hepatitis C virus neutralization by broadly neutralizing antibody HCV1. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9499-9504. | 7.1 | 135 |
| 293 | Optimization of affinity, specificity and function of designed influenza inhibitors using deep sequencing. Nature Biotechnology, 2012, 30, 543-548. | 17.5 | 342 |
| 294 | Variable Lymphocyte Receptor Recognition of the Immunodominant Glycoprotein of Bacillus anthracis Spores. Structure, 2012, 20, 479-486. | 3.3 | 47 |
| 295 | A Dynamic Knockout Reveals That Conformational Fluctuations Influence the Chemical Step of Enzyme Catalysis. Science, 2011, 332, 234-238. | 12.6 | 414 |
| 296 | Broad neutralization coverage of HIV by multiple highly potent antibodies. Nature, 2011, 477, 466-470. | 27.8 | 1,397 |
| 297 | A structural analysis of M protein in coronavirus assembly and morphology. Journal of Structural Biology, 2011, 174, 11-22. | 2.8 | 625 |
| 298 | A Potent and Broad Neutralizing Antibody Recognizes and Penetrates the HIV Glycan Shield. Science, 2011, 334, 1097-1103. | 12.6 | 644 |
| 299 | A Highly Conserved Neutralizing Epitope on Group 2 Influenza A Viruses. Science, 2011, 333, 843-850. | 12.6 | 772 |
| 300 | Computational Design of Proteins Targeting the Conserved Stem Region of Influenza Hemagglutinin. Science, 2011, 332, 816-821. | 12.6 | 527 |
| 301 | Structure of HIV-1 gp120 V1/V2 domain with broadly neutralizing antibody PG9. Nature, 2011, 480, 336-343. | 27.8 | 794 |
| 302 | Structural Characterization of an Early Fusion Intermediate of Influenza Virus Hemagglutinin. Journal of Virology, 2011, 85, 5172-5182. | 3.4 | 113 |
| 303 | Trimeric HIV-1 glycoprotein gp140 immunogens and native HIV-1 envelope glycoproteins display the same closed and open quaternary molecular architectures. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11440-11445. | 7.1 | 149 |
| 304 | Structure of the Î ³ - <scp>D</scp> -glutamyl- <scp>L</scp> -diamino acid endopeptidase YkfC from <i>Bacillus cereus</i> in complex with <scp>L</scp> -Ala-Î ³ - <scp>D</scp> -Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1354-1364. | 0.7 | 64 |
| 305 | The JCSC high-throughput structural biology pipeline. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1137-1142. | 0.7 | 99 |
| 306 | Structural Basis of Preexisting Immunity to the 2009 H1N1 Pandemic Influenza Virus. Science, 2010, 328, 357-360. | 12.6 | 521 |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 307 | Structure, Receptor Binding, and Antigenicity of Influenza Virus Hemagglutinins from the 1957 H2N2 Pandemic. Journal of Virology, 2010, 84, 1715-1721. | 3.4 | 90 |
| 308 | 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. | 3.4 | 92 |
| 309 | Structural Basis of Murein Peptide Specificity of a γ-D-Glutamyl-L-Diamino Acid Endopeptidase. Structure, 2009, 17, 303-313. | 3.3 | 73 |
| 310 | Antibody Recognition of a Highly Conserved Influenza Virus Epitope. Science, 2009, 324, 246-251. | 12.6 | 1,220 |
| 311 | Recent Avian H5N1 Viruses Exhibit Increased Propensity for Acquiring Human Receptor Specificity. Journal of Molecular Biology, 2008, 381, 1382-1394. | 4.2 | 192 |
| 312 | Structural Characterization of the 1918 Influenza Virus H1N1 Neuraminidase. Journal of Virology, 2008, 82, 10493-10501. | 3.4 | 241 |
| 313 | A Glycoconjugate Antigen Based on the Recognition Motif of a Broadly Neutralizing Human Immunodeficiency Virus Antibody, 2G12, Is Immunogenic but Elicits Antibodies Unable To Bind to the Self Glycans of gp120. Journal of Virology, 2008, 82, 6359-6368. | 3.4 | 112 |
| 314 | Antigen Recognition by Variable Lymphocyte Receptors. Science, 2008, 321, 1834-1837. | 12.6 | 163 |
| 315 | Structural Basis of Enhanced Binding of Extended and Helically Constrained Peptide Epitopes of the Broadly Neutralizing HIV-1 Antibody 4E10. Journal of Molecular Biology, 2007, 365, 1533-1544. | 4.2 | 121 |
| 316 | The challenge of protein structure determination—lessons from structural genomics. Protein Science, 2007, 16, 2472-2482. | 7.6 | 135 |
| 317 | Structure and Receptor Specificity of the Hemagglutinin from an H5N1 Influenza Virus. Science, 2006, 312, 404-410. | 12.6 | 865 |
| 318 | Glycan Microarray Analysis of the Hemagglutinins from Modern and Pandemic Influenza Viruses Reveals Different Receptor Specificities. Journal of Molecular Biology, 2006, 355, 1143-1155. | 4.2 | 570 |
| 319 | Antibody Elbow Angles are Influenced by their Light Chain Class. Journal of Molecular Biology, 2006, 357, 1566-1574. | 4.2 | 229 |
| 320 | Glycan microarray technologies: tools to survey host specificity of influenza viruses. Nature Reviews Microbiology, 2006, 4, 857-864. | 28.6 | 319 |
| 321 | Toward a Carbohydrate-Based HIV-1 Vaccine. ACS Symposium Series, 2006, , 161-185. | 0.5 | 3 |
| 322 | Crystal structure of the IL-2 signaling complex: Paradigm for a heterotrimeric cytokine receptor. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2788-2793. | 7.1 | 225 |
| 323 | Antibody vs. HIV in a clash of evolutionary titans. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14943-14948. | 7.1 | 268 |
| 324 | A Single Amino Acid Substitution in 1918 Influenza Virus Hemagglutinin Changes Receptor Binding Specificity. Journal of Virology, 2005, 79, 11533-11536. | 3.4 | 356 |

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 325 | Dissection of the carbohydrate specificity of the broadly neutralizing anti-HIV-1 antibody 2G12. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13372-13377. | 7.1 | 291 |
| 326 | Crystal Structure of Human Toll-Like Receptor 3 (TLR3) Ectodomain. Science, 2005, 309, 581-585. | 12.6 | 545 |
| 327 | Broadly Neutralizing Anti-HIV Antibody 4E10 Recognizes a Helical Conformation of a Highly Conserved Fusion-Associated Motif in gp41. Immunity, 2005, 22, 163-173. | 14.3 | 410 |
| 328 | Printed covalent glycan array for ligand profiling of diverse glycan binding proteins. Proceedings of the United States of America, 2004, 101, 17033-17038. | 7.1 | 1,039 |
| 329 | HIV vaccine design and the neutralizing antibody problem. Nature Immunology, 2004, 5, 233-236. | 14.5 | 721 |
| 330 | Crystal Structure of a Shark Single-Domain Antibody V Region in Complex with Lysozyme. Science, 2004, 305, 1770-1773. | 12.6 | 282 |
| 331 | Monoglucosylated glycans in the secreted human complement component C3: implications for protein biosynthesis and structure. FEBS Letters, 2004, 566, 270-274. | 2.8 | 47 |
| 332 | Structure of the Uncleaved Human H1 Hemagglutinin from the Extinct 1918 Influenza Virus. Science, 2004, 303, 1866-1870. | 12.6 | 440 |
| 333 | Fine Mapping of the Interaction of Neutralizing and Nonneutralizing Monoclonal Antibodies with the CD4 Binding Site of Human Immunodeficiency Virus Type 1 gp120. Journal of Virology, 2003, 77, 642-658. | 3.4 | 237 |
| 334 | Antibody Domain Exchange Is an Immunological Solution to Carbohydrate Cluster Recognition. Science, 2003, 300, 2065-2071. | 12.6 | 736 |
| 335 | The Carbohydrate Epitope of the Neutralizing Anti-HIV-1 Antibody 2G12. Advances in Experimental Medicine and Biology, 2003, 535, 205-218. | 1.6 | 65 |
| 336 | Structural genomics of the Thermotoga maritima proteome implemented in a high-throughput structure determination pipeline. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11664-11669. | 7.1 | 397 |
| 337 | The Broadly Neutralizing Anti-Human Immunodeficiency Virus Type 1 Antibody 2G12 Recognizes a Cluster of 1±1→2 Mannose Residues on the Outer Face of gp120. Journal of Virology, 2002, 76, 7306-7321. | 3.4 | 664 |
| 338 | Crystal Structure of a Neutralizing Human IgG Against HIV-1: A Template for Vaccine Design. Science, 2001, 293, 1155-1159. | 12.6 | 870 |
| 339 | Global Efforts in Structural Genomics. Science, 2001, 294, 89-92. | 12.6 | 195 |
| 340 | Crystal structure of Sar1-GDP at 1.7 AÌŠ resolution and the role of the NH2 terminus in ER export. Journal of Cell Biology, 2001, 155, 937-948. | 5.2 | 149 |
| 341 | A New Functional Domain of Guanine Nucleotide Dissociation Inhibitor (α-GDI) Involved in Rab Recycling. Traffic, 2000, 1, 270-281. | 2.7 | 37 |
| 342 | STRUCTURAL BASIS OF T CELL RECOGNITION. Annual Review of Immunology, 1999, 17, 369-397. | 21.8 | 488 |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 343 | Engineering protein for Xâ€ray crystallography: The murine major histocompatibility complex class II molecule lâ€A ^d . Protein Science, 1998, 7, 413-418. | 7.6 | 18 |
| 344 | Structural Basis of Plasticity in T Cell Receptor Recognition of a Self Peptide-MHC Antigen. Science, 1998, 279, 1166-1172. | 12.6 | 641 |
| 345 | Antibody-antigen interactions: new structures and new conformational changes. Current Opinion in Structural Biology, 1994, 4, 857-867. | 5.7 | 505 |
| 346 | Major antigen-induced domain rearrangements in an antibody. Structure, 1993, 1, 83-93. | 3.3 | 216 |
| 347 | Three-dimensional Structure of an Anti-steroid Fab′ and Progesterone-Fab′ Complex. Journal of Molecular Biology, 1993, 231, 103-118. | 4.2 | 154 |
| 348 | X-Ray Crystallographic Studies of Antibody–Peptide Complexes. ImmunoMethods, 1993, 3, 211-221. | 0.8 | 24 |
| 349 | Antibody-antigen interactions. Current Opinion in Structural Biology, 1993, 3, 113-118. | 5.7 | 279 |
| 350 | Applications of the streak seeding technique in protein crystallization. Journal of Crystal Growth, 1991, 110, 270-282. | 1.5 | 147 |
| 351 | Analytical and production seeding techniques. Methods, 1990, 1, 38-49. | 3.8 | 98 |
| 352 | Antibody Structure. , 0, , 49-62. | | 1 |
| 353 | Dynamics of B-Cell Repertoires and Emergence of Cross-Reactive Responses in COVID-19 Patients with Different Disease Severity, SSRN Electronic Journal O | 0.4 | 2 |