# Alexandra C Walls

List of Publications by Year
in descending order



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|---|---|---|---|
| 51 papers | 24,919 citations | 57758 44 h-index | 182427 51 g-index |
| 88 all docs | 88 docs citations | 88 times ranked | 29642 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | SARS-CoV-2 breakthrough infections elicit potent, broad, and durable neutralizing antibody responses. Cell, 2022, 185, 872-880.e3. | 28.9 | 165 |
| 2 | Antibody-mediated broad sarbecovirus neutralization through ACE2 molecular mimicry. Science, 2022, 375, 449-454. | 12.6 | 108 |
| 3 | Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts infectivity and fusogenicity. Nature, 2022, 603, 706-714. | 27.8 | 756 |
| 4 | ACE2 binding is an ancestral and evolvable trait of sarbecoviruses. Nature, 2022, 603, 913-918. | 27.8 | 109 |
| 5 | Broadly neutralizing antibodies overcome SARS-CoV-2 Omicron antigenic shift. Nature, 2022, 602, 664-670. | 27.8 | 917 |
| 6 | Structural basis of SARS-CoV-2 Omicron immune evasion and receptor engagement. Science, 2022, 375, 864-868. | 12.6 | 394 |
| 7 | Multivalent designed proteins neutralize SARS-CoV-2 variants of concern and confer protection against infection in mice. Science Translational Medicine, 2022, 14, eabn1252. | 12.4 | 68 |
| 8 | Thermodynamically coupled biosensors for detecting neutralizing antibodies against SARS-CoV-2 variants. Nature Biotechnology, 2022, 40, 1336-1340. | 17.5 | 23 |
| 9 | Adjuvanting a subunit SARS-CoV-2 vaccine with clinically relevant adjuvants induces durable protection in mice. Npj Vaccines, 2022, 7, . | 6.0 | 32 |
| 10 | Structure, receptor recognition, and antigenicity of the human coronavirus CCoV-HuPn-2018 spike glycoprotein. Cell, 2022, 185, 2279-2291.e17. | 28.9 | 25 |
| 11 | ACE2-binding exposes the SARS-CoV-2 fusion peptide to broadly neutralizing coronavirus antibodies. Science, 2022, 377, 735-742. | 12.6 | 85 |
| 12 | Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. Nature, 2021, 593, 136-141. | 27.8 | 648 |
| 13 | Adjuvanting a subunit COVID-19 vaccine to induce protective immunity. Nature, 2021, 594, 253-258. | 27.8 | 253 |
| 14 | Designed proteins assemble antibodies into modular nanocages. Science, 2021, 372, . | 12.6 | 104 |
| 15 | N-terminal domain antigenic mapping reveals a site of vulnerability for SARS-CoV-2. Cell, 2021, 184, 2332-2347.e16. | 28.9 | 784 |
| 16 | Structural basis for broad coronavirus neutralization. Nature Structural and Molecular Biology, 2021, 28, 478-486. | 8.2 | 152 |
| 17 | Stabilization of the SARS-CoV-2 Spike Receptor-Binding Domain Using Deep Mutational Scanning and Structure-Based Design. Frontiers in Immunology, 2021, 12, 710263. | 4.8 | 32 |
| 18 | Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. Nature, 2021, 595, 707-712. | 27.8 | 363 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | SARS-CoV-2 immune evasion by the B.1.427/B.1.429 variant of concern. Science, 2021, 373, 648-654. | 12.6 | 385 |
| 20 | Broad sarbecovirus neutralization by a human monoclonal antibody. Nature, 2021, 597, 103-108. | 27.8 | 220 |
| 21 | SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. Nature, 2021, 597, 97-102. | 27.8 | 385 |
| 22 | Discovery and Characterization of Spike Nâ€•Terminal Domainâ€•Binding Aptamers for Rapid SARSâ€•CoVâ€•2 Detection. Angewandte Chemie, 2021, 133, 21381-21385. | 2.0 | 14 |
| 23 | Lectins enhance SARS-CoV-2 infection and influence neutralizing antibodies. Nature, 2021, 598, 342-347. | 27.8 | 230 |
| 24 | Discovery and Characterization of Spike Nâ€•Terminal Domainâ€•Binding Aptamers for Rapid SARSâ€•CoVâ€•2 Detection. Angewandte Chemie - International Edition, 2021, 60, 21211-21215. | 13.8 | 62 |
| 25 | Elicitation of broadly protective sarbecovirus immunity by receptor-binding domain nanoparticle vaccines. Cell, 2021, 184, 5432-5447.e16. | 28.9 | 131 |
| 26 | Broad betacoronavirus neutralization by a stem helixâ€“specific human antibody. Science, 2021, 373, 1109-1116. | 12.6 | 262 |
| 27 | Molecular basis of immune evasion by the Delta and Kappa SARS-CoV-2 variants. Science, 2021, 374, 1621-1626. | 12.6 | 232 |
| 28 | Mapping Neutralizing and Immunodominant Sites on the SARS-CoV-2 Spike Receptor-Binding Domain by Structure-Guided High-Resolution Serology. Cell, 2020, 183, 1024-1042.e21. | 28.9 | 1,195 |
| 29 | An <i>Alphavirus</i> -derived replicon RNA vaccine induces SARS-CoV-2 neutralizing antibody and T cell responses in mice and nonhuman primates. Science Translational Medicine, 2020, 12, . | 12.4 | 181 |
| 30 | Structure-guided covalent stabilization of coronavirus spike glycoprotein trimers in the closed conformation. Nature Structural and Molecular Biology, 2020, 27, 942-949. | 8.2 | 153 |
| 31 | Deep Mutational Scanning of SARS-CoV-2 Receptor Binding Domain Reveals Constraints on Folding and ACE2 Binding. Cell, 2020, 182, 1295-1310.e20. | 28.9 | 1,726 |
| 32 | Elicitation of Potent Neutralizing Antibody Responses by Designed Protein Nanoparticle Vaccines for SARS-CoV-2. Cell, 2020, 183, 1367-1382.e17. | 28.9 | 420 |
| 33 | Serological identification of SARS-CoV-2 infections among children visiting a hospital during the initial Seattle outbreak. Nature Communications, 2020, 11, 4378. | 12.8 | 63 |
| 34 | De novo design of picomolar SARS-CoV-2 miniprotein inhibitors. Science, 2020, 370, 426-431. | 12.6 | 464 |
| 35 | Cross-neutralization of SARS-CoV-2 by a human monoclonal SARS-CoV antibody. Nature, 2020, 583, 290-295. | 27.8 | 1,695 |
| 36 | Structure, Function, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein. Cell, 2020, 181, 281-292.e6. | 28.9 | 6,979 |

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|---|---|---|---|
| 37 | Structural Studies of Coronavirus Fusion Proteins. Microscopy and Microanalysis, 2019, 25, 1300-1301. | 0.4 | 4 |
| 38 | Unexpected Receptor Functional Mimicry Elucidates Activation of Coronavirus Fusion. Cell, 2019, 176, 1026-1039.e15. | 28.9 | 558 |
| 39 | Structural basis for human coronavirus attachment to sialic acid receptors. Nature Structural and Molecular Biology, 2019, 26, 481-489. | 8.2 | 475 |
| 40 | Structures of MERS-CoV spike glycoprotein in complex with sialoside attachment receptors. Nature Structural and Molecular Biology, 2019, 26, 1151-1157. | 8.2 | 218 |
| 41 | Automatically Fixing Errors in Glycoprotein Structures with Rosetta. Structure, 2019, 27, 134-139.e3. | 3.3 | 93 |
| 42 | Glycan Shield and Fusion Activation of a Deltacoronavirus Spike Glycoprotein Fine-Tuned for Enteric Infections. Journal of Virology, 2018, 92, . | 3.4 | 124 |
| 43 | Vitrification after multiple rounds of sample application and blotting improves particle density on cryo-electron microscopy grids. Journal of Structural Biology, 2017, 198, 38-42. | 2.8 | 68 |
| 44 | RosettaES: a sampling strategy enabling automated interpretation of difficult cryo-EM maps. Nature Methods, 2017, 14, 797-800. | 19.0 | 118 |
| 45 | Tectonic conformational changes of a coronavirus spike glycoprotein promote membrane fusion. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11157-11162. | 7.1 | 501 |
| 46 | Crucial steps in the structure determination of a coronavirus spike glycoprotein using cryoâ€electron microscopy. Protein Science, 2017, 26, 113-121. | 7.6 | 31 |
| 47 | Glycan shield and epitope masking of a coronavirus spike protein observed by cryo-electron microscopy. Nature Structural and Molecular Biology, 2016, 23, 899-905. | 8.2 | 366 |
| 48 | Secreted Effectors Encoded within and outside of the Francisella Pathogenicity Island Promote Intramacrophage Growth. Cell Host and Microbe, 2016, 20, 573-583. | 11.0 | 68 |
| 49 | Subunit connectivity, assembly determinants and architecture of the yeast exocyst complex. Nature Structural and Molecular Biology, 2016, 23, 59-66. | 8.2 | 108 |
| 50 | Cryo-electron microscopy structure of a coronavirus spike glycoprotein trimer. Nature, 2016, 531, 114-117. | 27.8 | 453 |
| 51 | Broadly neutralizing antibodies overcome SARS-CoV-2 Omicron antigenic shift. Nature, 0, , . | 27.8 | 101 |