

David Veesler

List of Publications by Year in descending order

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Version: 2024-02-01

109
papers

30,772
citations

25014

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24961

109
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160
all docs

160
docs citations

160
times ranked

33332
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Structure, Function, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein. <i>Cell</i> , 2020, 181, 281-292.e6. | 13.5 | 6,979 |
| 2 | Deep Mutational Scanning of SARS-CoV-2 Receptor Binding Domain Reveals Constraints on Folding and ACE2 Binding. <i>Cell</i> , 2020, 182, 1295-1310.e20. | 13.5 | 1,726 |
| 3 | Cross-neutralization of SARS-CoV-2 by a human monoclonal SARS-CoV antibody. <i>Nature</i> , 2020, 583, 290-295. | 13.7 | 1,695 |
| 4 | Mapping Neutralizing and Immunodominant Sites on the SARS-CoV-2 Spike Receptor-Binding Domain by Structure-Guided High-Resolution Serology. <i>Cell</i> , 2020, 183, 1024-1042.e21. | 13.5 | 1,195 |
| 5 | Broadly neutralizing antibodies overcome SARS-CoV-2 Omicron antigenic shift. <i>Nature</i> , 2022, 602, 664-670. | 13.7 | 917 |
| 6 | N-terminal domain antigenic mapping reveals a site of vulnerability for SARS-CoV-2. <i>Cell</i> , 2021, 184, 2332-2347.e16. | 13.5 | 784 |
| 7 | Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts infectivity and fusogenicity. <i>Nature</i> , 2022, 603, 706-714. | 13.7 | 756 |
| 8 | Structural insights into coronavirus entry. <i>Advances in Virus Research</i> , 2019, 105, 93-116. | 0.9 | 669 |
| 9 | Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. <i>Nature</i> , 2021, 593, 136-141. | 13.7 | 648 |
| 10 | Protocol and Reagents for Pseudotyping Lentiviral Particles with SARS-CoV-2 Spike Protein for Neutralization Assays. <i>Viruses</i> , 2020, 12, 513. | 1.5 | 641 |
| 11 | Unexpected Receptor Functional Mimicry Elucidates Activation of Coronavirus Fusion. <i>Cell</i> , 2019, 176, 1026-1039.e15. | 13.5 | 558 |
| 12 | Ultrapotent human antibodies protect against SARS-CoV-2 challenge via multiple mechanisms. <i>Science</i> , 2020, 370, 950-957. | 6.0 | 504 |
| 13 | Tectonic conformational changes of a coronavirus spike glycoprotein promote membrane fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11157-11162. | 3.3 | 501 |
| 14 | Structural basis for human coronavirus attachment to sialic acid receptors. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 481-489. | 3.6 | 475 |
| 15 | De novo design of picomolar SARS-CoV-2 miniprotein inhibitors. <i>Science</i> , 2020, 370, 426-431. | 6.0 | 464 |
| 16 | Cryo-electron microscopy structure of a coronavirus spike glycoprotein trimer. <i>Nature</i> , 2016, 531, 114-117. | 13.7 | 453 |
| 17 | Elicitation of Potent Neutralizing Antibody Responses by Designed Protein Nanoparticle Vaccines for SARS-CoV-2. <i>Cell</i> , 2020, 183, 1367-1382.e17. | 13.5 | 420 |
| 18 | Structural basis of SARS-CoV-2 Omicron immune evasion and receptor engagement. <i>Science</i> , 2022, 375, 864-868. | 6.0 | 394 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | SARS-CoV-2 immune evasion by the B.1.427/B.1.429 variant of concern. <i>Science</i> , 2021, 373, 648-654. | 6.0 | 385 |
| 20 | SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. <i>Nature</i> , 2021, 597, 97-102. | 13.7 | 385 |
| 21 | Glycan shield and epitope masking of a coronavirus spike protein observed by cryo-electron microscopy. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 899-905. | 3.6 | 366 |
| 22 | Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. <i>Nature</i> , 2021, 595, 707-712. | 13.7 | 363 |
| 23 | Induction of Potent Neutralizing Antibody Responses by a Designed Protein Nanoparticle Vaccine for Respiratory Syncytial Virus. <i>Cell</i> , 2019, 176, 1420-1431.e17. | 13.5 | 339 |
| 24 | Tackling COVID-19 with neutralizing monoclonal antibodies. <i>Cell</i> , 2021, 184, 3086-3108. | 13.5 | 309 |
| 25 | Movies of Ice-Embedded Particles Enhance Resolution in Electron Cryo-Microscopy. <i>Structure</i> , 2012, 20, 1823-1828. | 1.6 | 277 |
| 26 | Broad betacoronavirus neutralization by a stem helix-specific human antibody. <i>Science</i> , 2021, 373, 1109-1116. | 6.0 | 262 |
| 27 | Adjuvanting a subunit COVID-19 vaccine to induce protective immunity. <i>Nature</i> , 2021, 594, 253-258. | 13.7 | 253 |
| 28 | A Common Evolutionary Origin for Tailed-Bacteriophage Functional Modules and Bacterial Machineries. <i>Microbiology and Molecular Biology Reviews</i> , 2011, 75, 423-433. | 2.9 | 234 |
| 29 | Molecular basis of immune evasion by the Delta and Kappa SARS-CoV-2 variants. <i>Science</i> , 2021, 374, 1621-1626. | 6.0 | 232 |
| 30 | Lectins enhance SARS-CoV-2 infection and influence neutralizing antibodies. <i>Nature</i> , 2021, 598, 342-347. | 13.7 | 230 |
| 31 | Broad sarbecovirus neutralization by a human monoclonal antibody. <i>Nature</i> , 2021, 597, 103-108. | 13.7 | 220 |
| 32 | Structures of MERS-CoV spike glycoprotein in complex with sialoside attachment receptors. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1151-1157. | 3.6 | 218 |
| 33 | An <i>Alphavirus</i> -derived replicon RNA vaccine induces SARS-CoV-2 neutralizing antibody and T cell responses in mice and nonhuman primates. <i>Science Translational Medicine</i> , 2020, 12, . | 5.8 | 181 |
| 34 | Quadrivalent influenza nanoparticle vaccines induce broad protection. <i>Nature</i> , 2021, 592, 623-628. | 13.7 | 180 |
| 35 | Local protein kinase A action proceeds through intact holoenzymes. <i>Science</i> , 2017, 356, 1288-1293. | 6.0 | 165 |
| 36 | SARS-CoV-2 breakthrough infections elicit potent, broad, and durable neutralizing antibody responses. <i>Cell</i> , 2022, 185, 872-880.e3. | 13.5 | 165 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 37 | Studying 18Å...MDa Virus Assemblies with Native Mass Spectrometry. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 4020-4023. | 7.2 | 164 |
| 38 | 2.8 Å... resolution reconstruction of the <i>Thermoplasma acidophilum</i> 20S proteasome using cryo-electron microscopy. <i>ELife</i> , 2015, 4, . | 2.8 | 156 |
| 39 | Structure-guided covalent stabilization of coronavirus spike glycoprotein trimers in the closed conformation. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 942-949. | 3.6 | 153 |
| 40 | Structural basis for broad coronavirus neutralization. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 478-486. | 3.6 | 152 |
| 41 | Shifting mutational constraints in the SARS-CoV-2 receptor-binding domain during viral evolution. <i>Science</i> , 2022, 377, 420-424. | 6.0 | 140 |
| 42 | Elicitation of broadly protective sarbecovirus immunity by receptor-binding domain nanoparticle vaccines. <i>Cell</i> , 2021, 184, 5432-5447.e16. | 13.5 | 131 |
| 43 | Glycan Shield and Fusion Activation of a Deltacoronavirus Spike Glycoprotein Fine-Tuned for Enteric Infections. <i>Journal of Virology</i> , 2018, 92, . | 1.5 | 124 |
| 44 | Tailored design of protein nanoparticle scaffolds for multivalent presentation of viral glycoprotein antigens. <i>ELife</i> , 2020, 9, . | 2.8 | 123 |
| 45 | Structure of the phage TP901-1 1.8ÅMDa baseplate suggests an alternative host adhesion mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8954-8958. | 3.3 | 121 |
| 46 | RosettaES: a sampling strategy enabling automated interpretation of difficult cryo-EM maps. <i>Nature Methods</i> , 2017, 14, 797-800. | 9.0 | 118 |
| 47 | ACE2 binding is an ancestral and evolvable trait of sarbecoviruses. <i>Nature</i> , 2022, 603, 913-918. | 13.7 | 109 |
| 48 | Antibody-mediated broad sarbecovirus neutralization through ACE2 molecular mimicry. <i>Science</i> , 2022, 375, 449-454. | 6.0 | 108 |
| 49 | An Antibody Targeting the Fusion Machinery Neutralizes Dual-Tropic Infection and Defines a Site of Vulnerability on Epstein-Barr Virus. <i>Immunity</i> , 2018, 48, 799-811.e9. | 6.6 | 104 |
| 50 | Designed proteins assemble antibodies into modular nanocages. <i>Science</i> , 2021, 372, . | 6.0 | 104 |
| 51 | Broadly neutralizing antibodies overcome SARS-CoV-2 Omicron antigenic shift. <i>Nature</i> , 0, , . | 13.7 | 101 |
| 52 | Automatically Fixing Errors in Glycoprotein Structures with Rosetta. <i>Structure</i> , 2019, 27, 134-139.e3. | 1.6 | 93 |
| 53 | Structure, Adsorption to Host, and Infection Mechanism of Virulent Lactococcal Phage p2. <i>Journal of Virology</i> , 2013, 87, 12302-12312. | 1.5 | 85 |
| 54 | ACE2-binding exposes the SARS-CoV-2 fusion peptide to broadly neutralizing coronavirus antibodies. <i>Science</i> , 2022, 377, 735-742. | 6.0 | 85 |

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|----|---|-----|-----------|
| 55 | Virus Maturation. <i>Annual Review of Biophysics</i> , 2012, 41, 473-496. | 4.5 | 80 |
| 56 | Atomic structure of the 75 MDa extremophile <i>Sulfolobus</i> turreted icosahedral virus determined by CryoEM and X-ray crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5504-5509. | 3.3 | 77 |
| 57 | Crystal Structure of Bacteriophage SPP1 Distal Tail Protein (gp19.1). <i>Journal of Biological Chemistry</i> , 2010, 285, 36666-36673. | 1.6 | 70 |
| 58 | An antibody against the F glycoprotein inhibits Nipah and Hendra virus infections. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 980-987. | 3.6 | 69 |
| 59 | Secreted Effectors Encoded within and outside of the Francisella Pathogenicity Island Promote Intramacrophage Growth. <i>Cell Host and Microbe</i> , 2016, 20, 573-583. | 5.1 | 68 |
| 60 | Vitrification after multiple rounds of sample application and blotting improves particle density on cryo-electron microscopy grids. <i>Journal of Structural Biology</i> , 2017, 198, 38-42. | 1.3 | 68 |
| 61 | Multivalent designed proteins neutralize SARS-CoV-2 variants of concern and confer protection against infection in mice. <i>Science Translational Medicine</i> , 2022, 14, eabn1252. | 5.8 | 68 |
| 62 | Cryo-EM structure of human adenovirus D26 reveals the conservation of structural organization among human adenoviruses. <i>Science Advances</i> , 2017, 3, e1602670. | 4.7 | 64 |
| 63 | Structures and host-adhesion mechanisms of lactococcal siphophages. <i>Frontiers in Microbiology</i> , 2014, 5, 3. | 1.5 | 63 |
| 64 | Role of bacteriophage T4 baseplate in regulating assembly and infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2654-2659. | 3.3 | 63 |
| 65 | Serological identification of SARS-CoV-2 infections among children visiting a hospital during the initial Seattle outbreak. <i>Nature Communications</i> , 2020, 11, 4378. | 5.8 | 63 |
| 66 | Discovery and Characterization of Spike N-Terminal Domain Binding Aptamers for Rapid SARS-CoV-2 Detection. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 21211-21215. | 7.2 | 62 |
| 67 | Crystal Structure and Function of a DARPIn Neutralizing Inhibitor of Lactococcal Phage TP901-1. <i>Journal of Biological Chemistry</i> , 2009, 284, 30718-30726. | 1.6 | 55 |
| 68 | Structure and Molecular Assignment of Lactococcal Phage TP901-1 Baseplate. <i>Journal of Biological Chemistry</i> , 2010, 285, 39079-39086. | 1.6 | 55 |
| 69 | Visualizing a Complete Siphoviridae Member by Single-Particle Electron Microscopy: the Structure of Lactococcal Phage TP901-1. <i>Journal of Virology</i> , 2013, 87, 1061-1068. | 1.5 | 55 |
| 70 | CryoEM structure of a prokaryotic cyclic nucleotide-gated ion channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4430-4435. | 3.3 | 51 |
| 71 | Design of multi-scale protein complexes by hierarchical building block fusion. <i>Nature Communications</i> , 2021, 12, 2294. | 5.8 | 48 |
| 72 | A SARS-CoV-2 variant elicits an antibody response with a shifted immunodominance hierarchy. <i>PLoS Pathogens</i> , 2022, 18, e1010248. | 2.1 | 48 |

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|----|--|-----|-----------|
| 73 | Structure and Functional Analysis of the Host Recognition Device of Lactococcal Phage Tuc2009. <i>Journal of Virology</i> , 2013, 87, 8429-8440. | 1.5 | 46 |
| 74 | Viral infection modulation and neutralization by camelid nanobodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1371-9. | 3.3 | 45 |
| 75 | The Opening of the SPP1 Bacteriophage Tail, a Prevalent Mechanism in Gram-positive-infecting Siphophages. <i>Journal of Biological Chemistry</i> , 2011, 286, 25397-25405. | 1.6 | 40 |
| 76 | A Cross-Reactive Humanized Monoclonal Antibody Targeting Fusion Glycoprotein Function Protects Ferrets Against Lethal Nipah Virus and Hendra Virus Infection. <i>Journal of Infectious Diseases</i> , 2020, 221, S471-S479. | 1.9 | 39 |
| 77 | Structure of the type VI secretion system TssKâ€“TssFâ€“TssG baseplate subcomplex revealed by cryo-electron microscopy. <i>Nature Communications</i> , 2018, 9, 5385. | 5.8 | 37 |
| 78 | Architecture of a dsDNA Viral Capsid in Complex with Its Maturation Protease. <i>Structure</i> , 2014, 22, 230-237. | 1.6 | 34 |
| 79 | Single-particle EM reveals plasticity of interactions between the adenovirus penton base and integrin $\beta 3$. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8815-8819. | 3.3 | 33 |
| 80 | Broadly neutralizing antibody cocktails targeting Nipah virus and Hendra virus fusion glycoproteins. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 426-434. | 3.6 | 33 |
| 81 | Architecture and antigenicity of the Nipah virus attachment glycoprotein. <i>Science</i> , 2022, 375, 1373-1378. | 6.0 | 33 |
| 82 | Computational design of mechanically coupled axle-rotor protein assemblies. <i>Science</i> , 2022, 376, 383-390. | 6.0 | 33 |
| 83 | Stabilization of the SARS-CoV-2 Spike Receptor-Binding Domain Using Deep Mutational Scanning and Structure-Based Design. <i>Frontiers in Immunology</i> , 2021, 12, 710263. | 2.2 | 32 |
| 84 | Germline VRC01 antibody recognition of a modified clade C HIV-1 envelope trimer and a glycosylated HIV-1 gp120 core. <i>ELife</i> , 2018, 7, . | 2.8 | 32 |
| 85 | Adjuvanting a subunit SARS-CoV-2 vaccine with clinically relevant adjuvants induces durable protection in mice. <i>Npj Vaccines</i> , 2022, 7, . | 2.9 | 32 |
| 86 | Crucial steps in the structure determination of a coronavirus spike glycoprotein using cryo-electron microscopy. <i>Protein Science</i> , 2017, 26, 113-121. | 3.1 | 31 |
| 87 | Maximizing the potential of electron cryomicroscopy data collected using direct detectors. <i>Journal of Structural Biology</i> , 2013, 184, 193-202. | 1.3 | 30 |
| 88 | HIV-1 VRC01 Germline-Targeting Immunogens Select Distinct Epitope-Specific B Cell Receptors. <i>Immunity</i> , 2020, 53, 840-851.e6. | 6.6 | 27 |
| 89 | Overcoming Steric Restrictions of VRC01 HIV-1 Neutralizing Antibodies through Immunization. <i>Cell Reports</i> , 2019, 29, 3060-3072.e7. | 2.9 | 26 |
| 90 | Generation of ordered protein assemblies using rigid three-body fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 3.3 | 25 |

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|-----|--|------|-----------|
| 91 | Structure, receptor recognition, and antigenicity of the human coronavirus CCoV-HuPn-2018 spike glycoprotein. <i>Cell</i> , 2022, 185, 2279-2291.e17. | 13.5 | 25 |
| 92 | The Therapeutic Antibody LM609 Selectively Inhibits Ligand Binding to Human $\alpha 5 \beta 1$ Integrin via Steric Hindrance. <i>Structure</i> , 2017, 25, 1732-1739.e5. | 1.6 | 24 |
| 93 | Thermodynamically coupled biosensors for detecting neutralizing antibodies against SARS-CoV-2 variants. <i>Nature Biotechnology</i> , 2022, 40, 1336-1340. | 9.4 | 23 |
| 94 | In silico detection of SARS-CoV-2 specific B-cell epitopes and validation in ELISA for serological diagnosis of COVID-19. <i>Scientific Reports</i> , 2021, 11, 4290. | 1.6 | 22 |
| 95 | Intrinsic disorder within AKAP79 fine-tunes anchored phosphatase activity toward substrates and drug sensitivity. <i>ELife</i> , 2017, 6, . | 2.8 | 22 |
| 96 | Structure-based design of stabilized recombinant influenza neuraminidase tetramers. <i>Nature Communications</i> , 2022, 13, 1825. | 5.8 | 21 |
| 97 | Maturation in Action: CryoEM Study of a Viral Capsid Caught during Expansion. <i>Structure</i> , 2012, 20, 1384-1390. | 1.6 | 20 |
| 98 | Production and biophysical characterization of the CorA transporter from <i>Methanosarcina mazei</i> . <i>Analytical Biochemistry</i> , 2009, 388, 115-121. | 1.1 | 18 |
| 99 | Functional Analysis of the Fusion and Attachment Glycoproteins of Mojang Henipavirus. <i>Viruses</i> , 2021, 13, 517. | 1.5 | 15 |
| 100 | Discovery and Characterization of Spike N-Terminal Domain-Binding Aptamers for Rapid SARS-CoV-2 Detection. <i>Angewandte Chemie</i> , 2021, 133, 21381-21385. | 1.6 | 14 |
| 101 | Crystal structure of <i>Bacillus subtilis</i> SPP1 phage gp22 shares fold similarity with a domain of lactococcal phage p2 RBP. <i>Protein Science</i> , 2010, 19, 1439-1443. | 3.1 | 12 |
| 102 | Immunization with a self-assembling nanoparticle vaccine displaying EBV gH/gL protects humanized mice against lethal viral challenge. <i>Cell Reports Medicine</i> , 2022, 3, 100658. | 3.3 | 12 |
| 103 | Potent monoclonal antibody-mediated neutralization of a divergent Hendra virus variant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, . | 3.3 | 11 |
| 104 | Effect of the viral protease on the dynamics of bacteriophage HK97 maturation intermediates characterized by variance analysis of cryo EM particle ensembles. <i>Journal of Structural Biology</i> , 2016, 193, 188-195. | 1.3 | 7 |
| 105 | Allosteric effects in bacteriophage HK97 procapsids revealed directly from covariance analysis of cryo EM data. <i>Journal of Structural Biology</i> , 2018, 202, 129-141. | 1.3 | 5 |
| 106 | Structural Studies of Coronavirus Fusion Proteins. <i>Microscopy and Microanalysis</i> , 2019, 25, 1300-1301. | 0.2 | 4 |
| 107 | Cystovirus Maturation at Atomic Resolution. <i>Structure</i> , 2013, 21, 1266-1268. | 1.6 | 3 |
| 108 | Integration of X-ray crystallography and electron cryo-microscopy in the analysis of virus structure and function. <i>Crystallography Reviews</i> , 2016, 22, 102-127. | 0.4 | 3 |

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|-----|--|-----|-----------|
| 109 | Cryo-EM Structure of Nipah Virus Fusion Glycoprotein in Complex with a Monoclonal Antibody Reveals Mechanism of Neutralization. <i>Microscopy and Microanalysis</i> , 2019, 25, 1328-1329. | 0.2 | 0 |