

# David Veessler

## List of Publications by Year in Descending Order

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**Version:** 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

143  
papers

17,089  
citations

53  
h-index

130  
g-index

160  
ext. papers

25,083  
ext. citations

22.2  
avg, IF

7.65  
L-index

#	Paper	IF	Citations
143	Structural changes in the SARS-CoV-2 spike E406W mutant escaping a clinical monoclonal antibody cocktail. <b>2022</b> ,		2
142	SARS-CoV-2 breakthrough infections elicit potent, broad, and durable neutralizing antibody responses.. <i>Cell</i> , <b>2022</b> ,	56.2	21
141	Antibody-mediated broad sarbecovirus neutralization through ACE2 molecular mimicry.. <i>Science</i> , <b>2022</b> , 375, eabm8143	33.3	23
140	Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts tropism and fusogenicity.. <i>Nature</i> , <b>2022</b> ,	50.4	95
139	ACE2 binding is an ancestral and evolvable trait of sarbecoviruses.. <i>Nature</i> , <b>2022</b> ,	50.4	19
138	A SARS-CoV-2 variant elicits an antibody response with a shifted immunodominance hierarchy.. <i>PLoS Pathogens</i> , <b>2022</b> , 18, e1010248	7.6	7
137	Structural basis of SARS-CoV-2 Omicron immune evasion and receptor engagement.. <i>Science</i> , <b>2022</b> , 375, eabn8652	33.3	71
136	Omicron BA.1 and BA.2 neutralizing activity elicited by a comprehensive panel of human vaccines. <b>2022</b> ,		3
135	Architecture and antigenicity of the Nipah virus attachment glycoprotein.. <i>Science</i> , <b>2022</b> , eabm5561	33.3	2
134	Structure-based design of stabilized recombinant influenza neuraminidase tetramers.. <i>Nature Communications</i> , <b>2022</b> , 13, 1825	17.4	0
133	Multivalent designed proteins neutralize SARS-CoV-2 variants of concern and confer protection against infection in mice.. <i>Science Translational Medicine</i> , <b>2022</b> , 14, eabn1252	17.5	3
132	Computational design of mechanically coupled axle-rotor protein assemblies.. <i>Science</i> , <b>2022</b> , 376, 383-390,	33.3	2
131	Broadly neutralizing antibodies overcome SARS-CoV-2 Omicron antigenic shift.. <i>Nature</i> , <b>2021</b> ,	50.4	204
130	Broadly neutralizing antibodies overcome SARS-CoV-2 Omicron antigenic shift. <b>2021</b> ,		16
129	SARS-CoV-2 spike conformation determines plasma neutralizing activity. <b>2021</b> ,		6
128	Molecular basis of immune evasion by the Delta and Kappa SARS-CoV-2 variants. <i>Science</i> , <b>2021</b> , eabl8506,	33.3	65
127	Antibody-mediated broad sarbecovirus neutralization through ACE2 molecular mimicry <b>2021</b> ,		7

126	A SARS-CoV-2 variant elicits an antibody response with a shifted immunodominance hierarchy <b>2021</b> ,		5
125	Emergence and spread of a SARS-CoV-2 variant through Europe in the summer of 2020 <b>2021</b> ,		142
124	Structural basis for broad coronavirus neutralization <b>2021</b> ,		14
123	Functional Analysis of the Fusion and Attachment Glycoproteins of Mojiang Henipavirus. <i>Viruses</i> , <b>2021</b> , 13,	6.2	3
122	Elicitation of broadly protective sarbecovirus immunity by receptor-binding domain nanoparticle vaccines <b>2021</b> ,		12
121	Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. <i>Nature</i> , <b>2021</b> , 593, 136-141	50.4	376
120	Quadrivalent influenza nanoparticle vaccines induce broad protection. <i>Nature</i> , <b>2021</b> , 592, 623-628	50.4	40
119	Adjuvanting a subunit COVID-19 vaccine to induce protective immunity. <i>Nature</i> , <b>2021</b> , 594, 253-258	50.4	92
118	Designed proteins assemble antibodies into modular nanocages. <i>Science</i> , <b>2021</b> , 372,	33.3	35
117	N-terminal domain antigenic mapping reveals a site of vulnerability for SARS-CoV-2. <i>Cell</i> , <b>2021</b> , 184, 2332-2347, 316	50.4	316
116	Broadly neutralizing antibody cocktails targeting Nipah virus and Hendra virus fusion glycoproteins. <i>Nature Structural and Molecular Biology</i> , <b>2021</b> , 28, 426-434	17.6	7
115	SARS-CoV-2 immune evasion by variant B.1.427/B.1.429 <b>2021</b> ,		62
114	Design of multi-scale protein complexes by hierarchical building block fusion. <i>Nature Communications</i> , <b>2021</b> , 12, 2294	17.4	14
113	Structural basis for broad sarbecovirus neutralization by a human monoclonal antibody <b>2021</b> ,		14
112	Antibodies to the SARS-CoV-2 receptor-binding domain that maximize breadth and resistance to viral escape <b>2021</b> ,		12
111	Structural basis for broad coronavirus neutralization. <i>Nature Structural and Molecular Biology</i> , <b>2021</b> , 28, 478-486	17.6	65
110	Detection of antibodies neutralizing historical and emerging SARS-CoV-2 strains using a thermodynamically coupled de novo biosensor system <b>2021</b> ,		1
109	Stabilization of the SARS-CoV-2 Spike Receptor-Binding Domain Using Deep Mutational Scanning and Structure-Based Design. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 710263	8.4	7

108	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> , <b>2021</b> , 118,	11.5	6
107	Tackling COVID-19 with neutralizing monoclonal antibodies. <i>Cell</i> , <b>2021</b> , 184, 3086-3108	56.2	108
106	Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. <i>Nature</i> , <b>2021</b> , 595, 707-712	50.4	168
105	SARS-CoV-2 immune evasion by the B.1.427/B.1.429 variant of concern. <i>Science</i> , <b>2021</b> , 373, 648-654	33.3	197
104	N-terminal domain antigenic mapping reveals a site of vulnerability for SARS-CoV-2 <b>2021</b> ,		34
103	Adjuvanting a subunit SARS-CoV-2 nanoparticle vaccine to induce protective immunity in non-human primates <b>2021</b> ,		7
102	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> , <b>2021</b> , 11, 4290	4.9	9
101	Broad sarbecovirus neutralization by a human monoclonal antibody. <i>Nature</i> , <b>2021</b> , 597, 103-108	50.4	94
100	Multivalent designed proteins protect against SARS-CoV-2 variants of concern <b>2021</b> ,		4
99	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. <i>Nature</i> , <b>2021</b> , 597, 97-102	50.4	118
98	Molecular basis of immune evasion by the delta and kappa SARS-CoV-2 variants <b>2021</b> ,		31
97	Discovery and Characterization of Spike N-Terminal Domain-Binding Aptamers for Rapid SARS-CoV-2 Detection. <i>Angewandte Chemie</i> , <b>2021</b> , 133, 21381-21385	3.6	1
96	Lectins enhance SARS-CoV-2 infection and influence neutralizing antibodies. <i>Nature</i> , <b>2021</b> , 598, 342-347	50.4	63
95	Discovery and Characterization of Spike N-Terminal Domain-Binding Aptamers for Rapid SARS-CoV-2 Detection. <i>Angewandte Chemie - International Edition</i> , <b>2021</b> , 60, 21211-21215	16.4	9
94	Elicitation of broadly protective sarbecovirus immunity by receptor-binding domain nanoparticle vaccines. <i>Cell</i> , <b>2021</b> , 184, 5432-5447.e16	56.2	34
93	Broad betacoronavirus neutralization by a stem helix-specific human antibody. <i>Science</i> , <b>2021</b> , 373, 1109-1116	33.3	80
92	SARS-CoV-2 B.1.1.7 sensitivity to mRNA vaccine-elicited, convalescent and monoclonal antibodies <b>2021</b> ,		69
91	Delta breakthrough infections elicit potent, broad and durable neutralizing antibody responses. <b>2021</b> ,		3

90	Protocol and Reagents for Pseudotyping Lentiviral Particles with SARS-CoV-2 Spike Protein for Neutralization Assays. <i>Viruses</i> , <b>2020</b> , 12,	6.2	360
89	Cross-neutralization of SARS-CoV-2 by a human monoclonal SARS-CoV antibody. <i>Nature</i> , <b>2020</b> , 583, 290-304	30.4	1028
88	Structure, Function, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein. <i>Cell</i> , <b>2020</b> , 181, 281-292.e6	56.2	4571
87	Tailored design of protein nanoparticle scaffolds for multivalent presentation of viral glycoprotein antigens. <i>ELife</i> , <b>2020</b> , 9,	8.9	51
86	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> , <b>2020</b> , 221, S471-S479	7	16
85	Structural and functional analysis of a potent sarbecovirus neutralizing antibody <b>2020</b> ,		42
84	Serological identification of SARS-CoV-2 infections among children visiting a hospital during the initial Seattle outbreak <b>2020</b> ,		9
83	Single-dose replicating RNA vaccine induces neutralizing antibodies against SARS-CoV-2 in nonhuman primates <b>2020</b> ,		17
82	Closing coronavirus spike glycoproteins by structure-guided design <b>2020</b> ,		7
81	Deep mutational scanning of SARS-CoV-2 receptor binding domain reveals constraints on folding and ACE2 binding <b>2020</b> ,		33
80	Elicitation of potent neutralizing antibody responses by designed protein nanoparticle vaccines for SARS-CoV-2 <b>2020</b> ,		10
79	Designed proteins assemble antibodies into modular nanocages <b>2020</b> ,		5
78	Mapping Neutralizing and Immunodominant Sites on the SARS-CoV-2 Spike Receptor-Binding Domain by Structure-Guided High-Resolution Serology. <i>Cell</i> , <b>2020</b> , 183, 1024-1042.e21	56.2	601
77	HIV-1 VRC01 Germline-Targeting Immunogens Select Distinct Epitope-Specific B Cell Receptors. <i>Immunity</i> , <b>2020</b> , 53, 840-851.e6	32.3	8
76	An -derived replicon RNA vaccine induces SARS-CoV-2 neutralizing antibody and T cell responses in mice and nonhuman primates. <i>Science Translational Medicine</i> , <b>2020</b> , 12,	17.5	96
75	Structure-guided covalent stabilization of coronavirus spike glycoprotein trimers in the closed conformation. <i>Nature Structural and Molecular Biology</i> , <b>2020</b> , 27, 942-949	17.6	89
74	Deep Mutational Scanning of SARS-CoV-2 Receptor Binding Domain Reveals Constraints on Folding and ACE2 Binding. <i>Cell</i> , <b>2020</b> , 182, 1295-1310.e20	56.2	935
73	Elicitation of Potent Neutralizing Antibody Responses by Designed Protein Nanoparticle Vaccines for SARS-CoV-2. <i>Cell</i> , <b>2020</b> , 183, 1367-1382.e17	56.2	217

72	Serological identification of SARS-CoV-2 infections among children visiting a hospital during the initial Seattle outbreak. <i>Nature Communications</i> , <b>2020</b> , 11, 4378	17.4	45
71	Ultrapotent human antibodies protect against SARS-CoV-2 challenge via multiple mechanisms. <i>Science</i> , <b>2020</b> , 370, 950-957	33.3	314
70	De novo design of picomolar SARS-CoV-2 miniprotein inhibitors. <i>Science</i> , <b>2020</b> , 370, 426-431	33.3	219
69	Unexpected Receptor Functional Mimicry Elucidates Activation of Coronavirus Fusion. <i>Cell</i> , <b>2019</b> , 176, 1026-1039.e15	56.2	416
68	Structural basis for human coronavirus attachment to sialic acid receptors. <i>Nature Structural and Molecular Biology</i> , <b>2019</b> , 26, 481-489	17.6	341
67	Induction of Potent Neutralizing Antibody Responses by a Designed Protein Nanoparticle Vaccine for Respiratory Syncytial Virus. <i>Cell</i> , <b>2019</b> , 176, 1420-1431.e17	56.2	190
66	Cryo-EM Structure of Nipah Virus Fusion Glycoprotein in Complex with a Monoclonal Antibody Reveals Mechanism of Neutralization. <i>Microscopy and Microanalysis</i> , <b>2019</b> , 25, 1328-1329	0.5	
65	Structural Studies of Coronavirus Fusion Proteins. <i>Microscopy and Microanalysis</i> , <b>2019</b> , 25, 1300-1301	0.5	3
64	Structural insights into coronavirus entry. <i>Advances in Virus Research</i> , <b>2019</b> , 105, 93-116	10.7	479
63	Overcoming Steric Restrictions of VRC01 HIV-1 Neutralizing Antibodies through Immunization. <i>Cell Reports</i> , <b>2019</b> , 29, 3060-3072.e7	10.6	11
62	Structures of MERS-CoV spike glycoprotein in complex with sialoside attachment receptors. <i>Nature Structural and Molecular Biology</i> , <b>2019</b> , 26, 1151-1157	17.6	161
61	An antibody against the F glycoprotein inhibits Nipah and Hendra virus infections. <i>Nature Structural and Molecular Biology</i> , <b>2019</b> , 26, 980-987	17.6	28
60	Automatically Fixing Errors in Glycoprotein Structures with Rosetta. <i>Structure</i> , <b>2019</b> , 27, 134-139.e3	5.2	59
59	An Antibody Targeting the Fusion Machinery Neutralizes Dual-Tropic Infection and Defines a Site of Vulnerability on Epstein-Barr Virus. <i>Immunity</i> , <b>2018</b> , 48, 799-811.e9	32.3	72
58	Allosteric effects in bacteriophage HK97 procapsids revealed directly from covariance analysis of cryo EM data. <i>Journal of Structural Biology</i> , <b>2018</b> , 202, 129-141	3.4	5
57	Germline VRC01 antibody recognition of a modified clade C HIV-1 envelope trimer and a glycosylated HIV-1 gp120 core. <i>ELife</i> , <b>2018</b> , 7,	8.9	19
56	Glycan Shield and Fusion Activation of a Deltacoronavirus Spike Glycoprotein Fine-Tuned for Enteric Infections. <i>Journal of Virology</i> , <b>2018</b> , 92,	6.6	92
55	Structure of the type VI secretion system TssK-TssF-TssG baseplate subcomplex revealed by cryo-electron microscopy. <i>Nature Communications</i> , <b>2018</b> , 9, 5385	17.4	20

54	Vitrification after multiple rounds of sample application and blotting improves particle density on cryo-electron microscopy grids. <i>Journal of Structural Biology</i> , <b>2017</b> , 198, 38-42	3.4	43
53	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> , <b>2017</b> , 114, 4430-4435	11.5	35
52	Cryo-EM structure of human adenovirus D26 reveals the conservation of structural organization among human adenoviruses. <i>Science Advances</i> , <b>2017</b> , 3, e1602670	14.3	48
51	RosettaES: a sampling strategy enabling automated interpretation of difficult cryo-EM maps. <i>Nature Methods</i> , <b>2017</b> , 14, 797-800	21.6	84
50	Local protein kinase A action proceeds through intact holoenzymes. <i>Science</i> , <b>2017</b> , 356, 1288-1293	33.3	104
49	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> , <b>2017</b> , 114, 11157-11162	11.5	351
48	The Therapeutic Antibody LM609 Selectively Inhibits Ligand Binding to Human $\alpha$ Integrin via Steric Hindrance. <i>Structure</i> , <b>2017</b> , 25, 1732-1739.e5	5.2	20
47	Crucial steps in the structure determination of a coronavirus spike glycoprotein using cryo-electron microscopy. <i>Protein Science</i> , <b>2017</b> , 26, 113-121	6.3	28
46	Intrinsic disorder within AKAP79 fine-tunes anchored phosphatase activity toward substrates and drug sensitivity. <i>ELife</i> , <b>2017</b> , 6,	8.9	14
45	Glycan shield and epitope masking of a coronavirus spike protein observed by cryo-electron microscopy. <i>Nature Structural and Molecular Biology</i> , <b>2016</b> , 23, 899-905	17.6	252
44	Secreted Effectors Encoded within and outside of the Francisella Pathogenicity Island Promote Intramacrophage Growth. <i>Cell Host and Microbe</i> , <b>2016</b> , 20, 573-583	23.4	45
43	Cryo-electron microscopy structure of a coronavirus spike glycoprotein trimer. <i>Nature</i> , <b>2016</b> , 531, 114-115	56.4	354
42	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> , <b>2016</b> , 193, 188-195	3.4	5
41	Integration of X-ray crystallography and electron cryo-microscopy in the analysis of virus structure and function. <i>Crystallography Reviews</i> , <b>2016</b> , 22, 102-127	1.3	2
40	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> , <b>2016</b> , 113, 2654-9	11.5	44
39	2.8 Å resolution reconstruction of the <i>Thermoplasma acidophilum</i> 20S proteasome using cryo-electron microscopy. <i>ELife</i> , <b>2015</b> , 4,	8.9	121
38	Architecture of a dsDNA viral capsid in complex with its maturation protease. <i>Structure</i> , <b>2014</b> , 22, 230-7	5.2	30
37	Structures and host-adhesion mechanisms of lactococcal siphophages. <i>Frontiers in Microbiology</i> , <b>2014</b> , 5, 3	5.7	53

36	Single-particle EM reveals plasticity of interactions between the adenovirus penton base and integrin $\alpha 5 \beta 1$ . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 8815-9	11.5	23
35	Studying 18 MDa virus assemblies with native mass spectrometry. <i>Angewandte Chemie - International Edition</i> , <b>2013</b> , 52, 4020-3	16.4	140
34	Cystovirus maturation at atomic resolution. <i>Structure</i> , <b>2013</b> , 21, 1266-8	5.2	2
33	Maximizing the potential of electron cryomicroscopy data collected using direct detectors. <i>Journal of Structural Biology</i> , <b>2013</b> , 184, 193-202	3.4	27
32	Visualizing a complete Siphoviridae member by single-particle electron microscopy: the structure of lactococcal phage TP901-1. <i>Journal of Virology</i> , <b>2013</b> , 87, 1061-8	6.6	48
31	Viral infection modulation and neutralization by camelid nanobodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, E1371-9	11.5	41
30	Structure, adsorption to host, and infection mechanism of virulent lactococcal phage p2. <i>Journal of Virology</i> , <b>2013</b> , 87, 12302-12	6.6	70
29	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> , <b>2013</b> , 110, 5504-9	11.5	61
28	Structure and functional analysis of the host recognition device of lactococcal phage tuc2009. <i>Journal of Virology</i> , <b>2013</b> , 87, 8429-40	6.6	42
27	Maturation in action: CryoEM study of a viral capsid caught during expansion. <i>Structure</i> , <b>2012</b> , 20, 1384-90	5.2	19
26	Virus maturation. <i>Annual Review of Biophysics</i> , <b>2012</b> , 41, 473-96	21.1	64
25	Movies of ice-embedded particles enhance resolution in electron cryo-microscopy. <i>Structure</i> , <b>2012</b> , 20, 1823-8	5.2	230
24	Structure of the phage TP901-1 1.8 MDa baseplate suggests an alternative host adhesion mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 8954-8	11.5	100
23	A common evolutionary origin for tailed-bacteriophage functional modules and bacterial machineries. <i>Microbiology and Molecular Biology Reviews</i> , <b>2011</b> , 75, 423-33, first page of table of contents	13.2	188
22	The opening of the SPP1 bacteriophage tail, a prevalent mechanism in Gram-positive-infecting siphophages. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 25397-405	5.4	39
21	Structure and molecular assignment of lactococcal phage TP901-1 baseplate. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 39079-86	5.4	53
20	Crystal structure of bacteriophage SPP1 distal tail protein (gp19.1): a baseplate hub paradigm in gram-positive infecting phages. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 36666-73	5.4	62
19	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> , <b>2010</b> , 19, 1439-43	6.3	12



18	Crystal structure and function of a DARPin neutralizing inhibitor of lactococcal phage TP901-1: comparison of DARPin and camelid VHH binding mode. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 30718-26	54	51
17	Production and biophysical characterization of the CorA transporter from <i>Methanosarcina mazei</i> . <i>Analytical Biochemistry</i> , <b>2009</b> , 388, 115-21	31	17
16	Broadly neutralizing antibodies overcome SARS-CoV-2 Omicron antigenic shift. <i>Nature</i> ,	504	44
15	SARS-CoV-2 Omicron spike mediated immune escape and tropism shift		23
14	Structural basis of SARS-CoV-2 Omicron immune evasion and receptor engagement		11
13	Structure, receptor recognition and antigenicity of the human coronavirus CCoV-HuPn-2018 spike glycoprotein		2
12	Tailored Design of Protein Nanoparticle Scaffolds for Multivalent Presentation of Viral Glycoprotein Antigens		7
11	Structure, function and antigenicity of the SARS-CoV-2 spike glycoprotein		126
10	Protocol and reagents for pseudotyping lentiviral particles with SARS-CoV-2 Spike protein for neutralization assays		45
9	Elicitation of broadly protective immunity to influenza by multivalent hemagglutinin nanoparticle vaccines		15
8	Generation of ordered protein assemblies using rigid three-body fusion		4
7	Hierarchical design of multi-scale protein complexes by combinatorial assembly of oligomeric helical bundle and repeat protein building blocks		4
6	Membrane lectins enhance SARS-CoV-2 infection and influence the neutralizing activity of different classes of antibodies		18
5	A human antibody that broadly neutralizes betacoronaviruses protects against SARS-CoV-2 by blocking the fusion machinery		13
4	ACE2 binding is an ancestral and evolvable trait of sarbecoviruses		10
3	Shifting mutational constraints in the SARS-CoV-2 receptor-binding domain during viral evolution		6
2	ACE2 engagement exposes the fusion peptide to pan-coronavirus neutralizing antibodies		3
1	Imprinted antibody responses against SARS-CoV-2 Omicron sublineages		5

