

Elizabeth E Fry

List of Publications by Year in descending order

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Version: 2024-02-01

74
papers

9,338
citations

81743

39
h-index

110170

64
g-index

79
all docs

79
docs citations

79
times ranked

11515
citing authors

#	ARTICLE	IF	CITATIONS
1	Structures and therapeutic potential of anti-RBD human monoclonal antibodies against SARS-CoV-2. <i>Theranostics</i> , 2022, 12, 1-17.	4.6	6
2	The antibody response to SARS-CoV-2 Beta underscores the antigenic distance to other variants. <i>Cell Host and Microbe</i> , 2022, 30, 53-68.e12.	5.1	52
3	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses. <i>Cell</i> , 2022, 185, 467-484.e15.	13.5	788
4	Purification of African Swine Fever Virus. <i>Methods in Molecular Biology</i> , 2022, 2503, 179-186.	0.4	0
5	Potent cross-reactive antibodies following Omicron breakthrough in vaccinees. <i>Cell</i> , 2022, 185, 2116-2131.e18.	13.5	105
6	Antibody escape of SARS-CoV-2 Omicron BA.4 and BA.5 from vaccine and BA.1 serum. <i>Cell</i> , 2022, 185, 2422-2433.e13.	13.5	532
7	Structures of Small Icosahedral Viruses. , 2021, , 278-289.		0
8	The antigenic anatomy of SARS-CoV-2 receptor binding domain. <i>Cell</i> , 2021, 184, 2183-2200.e22.	13.5	331
9	Evidence of escape of SARS-CoV-2 variant B.1.351 from natural and vaccine-induced sera. <i>Cell</i> , 2021, 184, 2348-2361.e6.	13.5	936
10	Reduced neutralization of SARS-CoV-2 B.1.1.7 variant by convalescent and vaccine sera. <i>Cell</i> , 2021, 184, 2201-2211.e7.	13.5	442
11	Antibody evasion by the P.1 strain of SARS-CoV-2. <i>Cell</i> , 2021, 184, 2939-2954.e9.	13.5	519
12	Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. <i>Cell</i> , 2021, 184, 4220-4236.e13.	13.5	630
13	Mammalian expression of virus-like particles as a proof of principle for next generation polio vaccines. <i>Npj Vaccines</i> , 2021, 6, 5.	2.9	23
14	Glutathione facilitates enterovirus assembly by binding at a druggable pocket. <i>Communications Biology</i> , 2020, 3, 9.	2.0	16
15	Hand-foot-and-mouth disease virus receptor KREMEN1 binds the canyon of Coxsackie Virus A10. <i>Nature Communications</i> , 2020, 11, 38.	5.8	28
16	Symmetrical arrangement of positively charged residues around the 5-fold axes of SAT type foot-and-mouth disease virus enhances cell culture of field viruses. <i>PLoS Pathogens</i> , 2020, 16, e1008828.	2.1	3
17	Structural basis for the neutralization of SARS-CoV-2 by an antibody from a convalescent patient. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 950-958.	3.6	268
18	Structural and functional analysis of protective antibodies targeting the threefold plateau of enterovirus 71. <i>Nature Communications</i> , 2020, 11, 5253.	5.8	11

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19	Neutralization of SARS-CoV-2 by Destruction of the Prefusion Spike. <i>Cell Host and Microbe</i> , 2020, 28, 445-454.e6.	5.1	298
20	Title is missing!. , 2020, 16, e1008828.		0
21	Title is missing!. , 2020, 16, e1008828.		0
22	Title is missing!. , 2020, 16, e1008828.		0
23	Title is missing!. , 2020, 16, e1008828.		0
24	Title is missing!. , 2020, 16, e1008828.		0
25	Title is missing!. , 2020, 16, e1008828.		0
26	Hepatitis A Virus Capsid Structure. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a031807.	2.9	18
27	Structure-Based in Silico Screening Identifies a Potent Ebolavirus Inhibitor from a Traditional Chinese Medicine Library. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 2928-2937.	2.9	34
28	Unexpected mode of engagement between enterovirus 71 and its receptor SCARB2. <i>Nature Microbiology</i> , 2019, 4, 414-419.	5.9	73
29	Target Identification and Mode of Action of Four Chemically Divergent Drugs against Ebolavirus Infection. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 724-733.	2.9	66
30	Seneca Valley virus attachment and uncoating mediated by its receptor anthrax toxin receptor 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13087-13092.	3.3	30
31	Redundant Late Domain Functions of Tandem VP2 YPX ₃ L Motifs in Nonlytic Cellular Egress of Quasi-enveloped Hepatitis A Virus. <i>Journal of Virology</i> , 2018, 92, .	1.5	31
32	Chimeric O1K foot-and-mouth disease virus with SAT2 outer capsid as an FMD vaccine candidate. <i>Scientific Reports</i> , 2018, 8, 13654.	1.6	11
33	Neutralization Mechanisms of Two Highly Potent Antibodies against Human Enterovirus 71. <i>MBio</i> , 2018, 9, .	1.8	26
34	Structures of Ebola Virus Glycoprotein Complexes with Tricyclic Antidepressant and Antipsychotic Drugs. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 4938-4945.	2.9	38
35	Generation and characterisation of recombinant FMDV antibodies: Applications for advancing diagnostic and laboratory assays. <i>PLoS ONE</i> , 2018, 13, e0201853.	1.1	3
36	Potent neutralization of hepatitis A virus reveals a receptor mimic mechanism and the receptor recognition site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 770-775.	3.3	42

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37	Near-atomic structure of Japanese encephalitis virus reveals critical determinants of virulence and stability. <i>Nature Communications</i> , 2017, 8, 14.	5.8	117
38	High-speed fixed-target serial virus crystallography. <i>Nature Methods</i> , 2017, 14, 805-810.	9.0	106
39	Rules of engagement between β 2 integrin and foot-and-mouth disease virus. <i>Nature Communications</i> , 2017, 8, 15408.	5.8	75
40	SAT2 Foot-and-Mouth Disease Virus Structurally Modified for Increased Thermostability. <i>Journal of Virology</i> , 2017, 91, .	1.5	28
41	Plant-made polio type 3 stabilized VLPs as a candidate synthetic polio vaccine. <i>Nature Communications</i> , 2017, 8, 245.	5.8	91
42	Structures of foot and mouth disease virus pentamers: Insight into capsid dissociation and unexpected pentamer reassociation. <i>PLoS Pathogens</i> , 2017, 13, e1006607.	2.1	21
43	Structure of human Aichi virus and implications for receptor binding. <i>Nature Microbiology</i> , 2016, 1, 16150.	5.9	36
44	Toremifene interacts with and destabilizes the Ebola virus glycoprotein. <i>Nature</i> , 2016, 535, 169-172.	13.7	210
45	Application of the thermofluor PaSTRy technique for improving foot-and-mouth disease virus vaccine formulation. <i>Journal of General Virology</i> , 2016, 97, 1557-1565.	1.3	21
46	Tracking the Antigenic Evolution of Foot-and-Mouth Disease Virus. <i>PLoS ONE</i> , 2016, 11, e0159360.	1.1	32
47	Potent antiviral agents fail to elicit genetically-stable resistance mutations in either enterovirus 71 or Coxsackievirus A16. <i>Antiviral Research</i> , 2015, 124, 77-82.	1.9	22
48	Tandem Fusion of Hepatitis B Core Antigen Allows Assembly of Virus-Like Particles in Bacteria and Plants with Enhanced Capacity to Accommodate Foreign Proteins. <i>PLoS ONE</i> , 2015, 10, e0120751.	1.1	105
49	Structure of Ljungan virus provides insight into genome packaging of this picornavirus. <i>Nature Communications</i> , 2015, 6, 8316.	5.8	43
50	Structure-based energetics of protein interfaces guides foot-and-mouth disease virus vaccine design. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 788-794.	3.6	89
51	Structures of Coxsackievirus A16 Capsids with Native Antigenicity: Implications for Particle Expansion, Receptor Binding, and Immunogenicity. <i>Journal of Virology</i> , 2015, 89, 10500-10511.	1.5	58
52	Hepatitis A virus and the origins of picornaviruses. <i>Nature</i> , 2015, 517, 85-88.	13.7	158
53	Structure Elucidation of Coxsackievirus A16 in Complex with GPP3 Informs a Systematic Review of Highly Potent Capsid Binders to Enteroviruses. <i>PLoS Pathogens</i> , 2015, 11, e1005165.	2.1	20
54	Lysosome sorting of β -glucocerebrosidase by LIMP-2 is targeted by the mannose 6-phosphate receptor. <i>Nature Communications</i> , 2014, 5, 4321.	5.8	78

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55	Exploiting fast detectors to enter a new dimension in room-temperature crystallography. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1248-1256.	2.5	72
56	More-powerful virus inhibitors from structure-based analysis of HEV71 capsid-binding molecules. Nature Structural and Molecular Biology, 2014, 21, 282-288.	3.6	88
57	Efficient production of foot-and-mouth disease virus empty capsids in insect cells following down regulation of 3C protease activity. Journal of Virological Methods, 2013, 187, 406-412.	1.0	51
58	Picornavirus uncoating intermediate captured in atomic detail. Nature Communications, 2013, 4, 1929.	5.8	148
59	Rational Engineering of Recombinant Picornavirus Capsids to Produce Safe, Protective Vaccine Antigen. PLoS Pathogens, 2013, 9, e1003255.	2.1	126
60	Structure determination from a single high-pressure-frozen virus crystal. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 308-312.	2.5	8
61	Characterization of epitope-tagged foot-and-mouth disease virus. Journal of General Virology, 2012, 93, 2371-2381.	1.3	30
62	A plate-based high-throughput assay for virus stability and vaccine formulation. Journal of Virological Methods, 2012, 185, 166-170.	1.0	94
63	A sensor-adaptor mechanism for enterovirus uncoating from structures of EV71. Nature Structural and Molecular Biology, 2012, 19, 424-429.	3.6	347
64	<i>In situ</i> macromolecular crystallography using microbeams. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 592-600.	2.5	113
65	Outrunning free radicals in room-temperature macromolecular crystallography. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 810-818.	2.5	83
66	What Does it Take to Make a Virus: The Concept of the Viral 'Self'. , 2010, , 35-58.		17
67	Equine Rhinitis A Virus and Its Low pH Empty Particle: Clues Towards an Aphthovirus Entry Mechanism?. PLoS Pathogens, 2009, 5, e1000620.	2.1	64
68	Structure of Foot-and-mouth disease virus serotype A1061 alone and complexed with oligosaccharide receptor: receptor conservation in the face of antigenic variation. Journal of General Virology, 2005, 86, 1909-1920.	1.3	95
69	Structure and receptor binding. Virus Research, 2003, 91, 33-46.	1.1	129
70	Virus Crystallography. Molecular Biotechnology, 1999, 12, 13-24.	1.3	22
71	Perturbations in the surface structure of A22 Iraq foot-and-mouth disease virus accompanying coupled changes in host cell specificity and antigenicity. Structure, 1996, 4, 135-145.	1.6	100
72	Structural comparison of two strains of foot-and-mouth disease virus subtype O1 and a laboratory antigenic variant, G67. Structure, 1995, 3, 571-580.	1.6	77

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73	The three-dimensional structure of foot-and-mouth disease virus at 2.9 Å... resolution. Nature, 1989, 337, 709-716.	13.7	887
74	Universal detection of foot and mouth disease virus based on the conserved VP0 protein. Wellcome Open Research, 0, 3, 88.	0.9	2