

Alexander M Sevy

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

1,236
citations

840776

11
h-index

940533

16
g-index

23
all docs

23
docs citations

23
times ranked

2271
citing authors

#	ARTICLE	IF	CITATIONS
1	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	19.0	513
2	High frequency of shared clonotypes in human B cell receptor repertoires. <i>Nature</i> , 2019, 566, 398-402.	27.8	262
3	Protocols for Molecular Modeling with Rosetta3 and RosettaScripts. <i>Biochemistry</i> , 2016, 55, 4748-4763.	2.5	182
4	Multifunctional Pan-ebolavirus Antibody Recognizes a Site of Broad Vulnerability on the Ebolavirus Glycoprotein. <i>Immunity</i> , 2018, 49, 363-374.e10.	14.3	61
5	Structural basis for nonneutralizing antibody competition at antigenic site II of the respiratory syncytial virus fusion protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6849-E6858.	7.1	38
6	Design of Protein Multi-specificity Using an Independent Sequence Search Reduces the Barrier to Low Energy Sequences. <i>PLoS Computational Biology</i> , 2015, 11, e1004300.	3.2	33
7	Modeling Immunity with Rosetta: Methods for Antibody and Antigen Design. <i>Biochemistry</i> , 2021, 60, 825-846.	2.5	24
8	Multistate design of influenza antibodies improves affinity and breadth against seasonal viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1597-1602.	7.1	23
9	Computationally Designed Cyclic Peptides Derived from an Antibody Loop Increase Breadth of Binding for Influenza Variants. <i>Structure</i> , 2020, 28, 1114-1123.e4.	3.3	21
10	Antibodies: Computer-Aided Prediction of Structure and Design of Function. <i>Microbiology Spectrum</i> , 2014, 2, .	3.0	17
11	Multi-state design of flexible proteins predicts sequences optimal for conformational change. <i>PLoS Computational Biology</i> , 2020, 16, e1007339.	3.2	17
12	Identification of Structurally Related Antibodies in Antibody Sequence Databases Using Rosetta-Derived Position-Specific Scoring. <i>Structure</i> , 2020, 28, 1124-1130.e5.	3.3	11
13	Discovery of Marburg virus neutralizing antibodies from virus-naïve human antibody repertoires using large-scale structural predictions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31142-31148.	7.1	10
14	Structure- and sequence-based design of synthetic single-domain antibody libraries. <i>Protein Engineering, Design and Selection</i> , 2020, 33, .	2.1	10
15	Integrating linear optimization with structural modeling to increase HIV neutralization breadth. <i>PLoS Computational Biology</i> , 2018, 14, e1005999.	3.2	8
16	Immune repertoire fingerprinting by principal component analysis reveals shared features in subject groups with common exposures. <i>BMC Bioinformatics</i> , 2019, 20, 629.	2.6	5
17	Antibodies: Computer-Aided Prediction of Structure and Design of Function. , 0, , 173-190.		0
18	Multi-state design of flexible proteins predicts sequences optimal for conformational change. , 2020, 16, e1007339.		0

#	ARTICLE	IF	CITATIONS
19	Multi-state design of flexible proteins predicts sequences optimal for conformational change. , 2020, 16, e1007339.		0
20	Multi-state design of flexible proteins predicts sequences optimal for conformational change. , 2020, 16, e1007339.		0
21	Multi-state design of flexible proteins predicts sequences optimal for conformational change. , 2020, 16, e1007339.		0