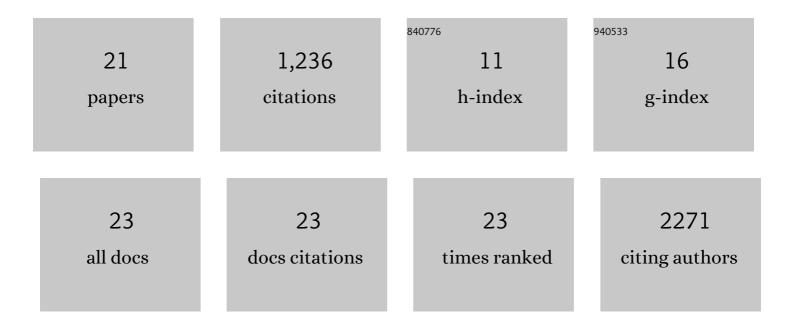
Alexander M Sevy

List of Publications by Year in descending order

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

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#	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