Monica L FernÃ¡ndez-Quintero

List of Publications by Year
in descending order

		567281	642732
36 papers	**698** citations	**15** h-index	**23** g-index
41 all docs	**41** docs citations	**41** times ranked	**481** citing authors

#	Article	IF	Citations
1	Broadly neutralizing antibodies target a haemagglutinin anchor epitope. Nature, 2022, 602, 314-320.	27.8	78
2	Characterizing the Diversity of the CDR-H3 Loop Conformational Ensembles in Relationship to Antibody Binding Properties. Frontiers in Immunology, 2018, 9, 3065.	4.8	73
3	Polyreactive Broadly Neutralizing B cells Are Selected to Provide Defense against Pandemic Threat Influenza Viruses. Immunity, 2020, 53, 1230-1244.e5.	14.3	61
4	CDR-H3 loop ensemble in solution – conformational selection upon antibody binding. MAbs, 2019, 11, 1077-1088.	5.2	49
5	Antibodies exhibit multiple paratope states influencing VH–VL domain orientations. Communications Biology, 2020, 3, 589.	4.4	38
6	Antibody CDR loops as ensembles in solution vs. canonical clusters from X-ray structures. MAbs, 2020, 12, 1744328.	5.2	34
7	Local and Global Rigidification Upon Antibody Affinity Maturation. Frontiers in Molecular Biosciences, 2020, 7, 182.	3.5	29
8	V_H–V_L interdomain dynamics observed by computer simulations and NMR. Proteins: Structure, Function and Bioinformatics, 2020, 88, 830-839.	2.6	28
9	*CACNA1I* gain-of-function mutations differentially affect channel gating and cause neurodevelopmental disorders. Brain, 2021, 144, 2092-2106.	7.6	26
10	Conformational Ensembles of Antibodies Determine Their Hydrophobicity. Biophysical Journal, 2021, 120, 143-157.	0.5	23
11	T-Cell Receptor Variable β Domains Rigidify During Affinity Maturation. Scientific Reports, 2020, 10, 4472.	3.3	20
12	Ensembles in solution as a new paradigm for antibody structure prediction and design. MAbs, 2021, 13, 1923122.	5.2	19
13	Transitions of CDR-L3 Loop Canonical Cluster Conformations on the Micro-to-Millisecond Timescale. Frontiers in Immunology, 2019, 10, 2652.	4.8	18
14	Structural determinants of voltage-gating properties in calcium channels. ELife, 2021, 10, .	6.0	18
15	Conformational selection of allergen-antibody complexes—surface plasticity of paratopes and epitopes. Protein Engineering, Design and Selection, 2019, 32, 513-523.	2.1	17
16	Antibody humanization—the Influence of the antibody framework on the CDR-H3 loop ensemble in solution. Protein Engineering, Design and Selection, 2019, 32, 411-422.	2.1	17
17	T-Cell Receptor CDR3 Loop Conformations in Solution Shift the Relative Vα-Vβ Domain Distributions. Frontiers in Immunology, 2020, 11, 1440.	4.8	17
18	Mutation of Framework Residue H71 Results in Different Antibody Paratope States in Solution. Frontiers in Immunology, 2021, 12, 630034.	4.8	17

#	Article	IF	Citations
19	Cav1.4 dysfunction and congenital stationary night blindness type 2. Pflugers Archiv European Journal of Physiology, 2021, 473, 1437-1454.	2.8	13
20	Surprisingly Fast Interface and Elbow Angle Dynamics of Antigen-Binding Fragments. Frontiers in Molecular Biosciences, 2020, 7, 609088.	3.5	11
21	Germline-Dependent Antibody Paratope States and Pairing Specific VH-VL Interface Dynamics. Frontiers in Immunology, 2021, 12, 675655.	4.8	11
22	STACKED â€" _S_olvation _T_heory of _A_romatic _C_omplexes as _K_ey for _E_stimating _D_rug Binding. Journal of Chemical Information and Modeling, 2020, 60, 2304-2313.	5.4	10
23	Shark Antibody Variable Domains Rigidify Upon Affinity Maturationâ€"Understanding the Potential of Shark Immunoglobulins as Therapeutics. Frontiers in Molecular Biosciences, 2021, 8, 639166.	3.5	9
24	Paratope states in solution improve structure prediction and docking. Structure, 2022, 30, 430-440.e3.	3.3	8
25	Explicit solvation thermodynamics in ionic solution: extending grid inhomogeneous solvation theory to solvation free energy of saltâ€"water mixtures. Journal of Computer-Aided Molecular Design, 2022, 36, 101-116.	2.9	8
26	Nanobody Paratope Ensembles in Solution Characterized by MD Simulations and NMR. International Journal of Molecular Sciences, 2022, 23, 5419.	4.1	6
27	pH-Induced Local Unfolding of the Phl p 6 Pollen Allergen From cpH-MD. Frontiers in Molecular Biosciences, 2020, 7, 603644.	3.5	5
28	Pore mutation N617D in the skeletal muscle DHPR blocks Ca2+ influx due to atypical high-affinity Ca2+ binding. ELife, 2021, 10, .	6.0	5
29	Implementation of the Freely Jointed Chain Model to Assess Kinetics and Thermodynamics of Thermosensitive Coilâ€"Globule Transition by Markov States. Journal of Physical Chemistry B, 2021, 125, 4898-4909.	2.6	4
30	CDR loop interactions can determine heavy and light chain pairing preferences in bispecific antibodies. MAbs, 2022, 14, 2024118.	5.2	4
31	Comparing Antibody Interfaces to Inform Rational Design of New Antibody Formats. Frontiers in Molecular Biosciences, 2022, 9, 812750.	3.5	4
32	Calcium current modulation by the γ1 subunit depends on alternative splicing of CaV1.1. Journal of General Physiology, 2022, 154, .	1.9	4
33	Ion-pair interactions between voltage-sensing domain IV and pore domain I regulate CaV1.1 gating. Biophysical Journal, 2021, 120, 4429-4441.	0.5	3
34	Grid inhomogeneous solvation theory for cross-solvation in rigid solvents. Journal of Chemical Physics, 2022, 156, .	3.0	3
35	Essential role of a conserved aspartate for the enzymatic activity of plasmanylethanolamine desaturase. Cellular and Molecular Life Sciences, 2022, 79, 214.	5.4	2
36	Conformational Shifts of Stacked Heteroaromatics: Vacuum vs. Water Studied by Machine Learning. Frontiers in Chemistry, 2021, 9, 641610.	3.6	1