

Robert J Pantazes

List of Publications by Year in descending order

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Version: 2024-02-01

13
papers

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citations

933447

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692
citing authors

#	ARTICLE	IF	CITATIONS
1	Nanobody-based CTLA4 inhibitors for immune checkpoint blockade therapy of canine cancer patients. <i>Scientific Reports</i> , 2021, 11, 20763.	3.3	10
2	Antibody epitope repertoire analysis enables rapid antigen discovery and multiplex serology. <i>Scientific Reports</i> , 2020, 10, 5294.	3.3	31
3	Development and Analyses of a Database of Antibody – Antigen Complexes. <i>Computer Aided Chemical Engineering</i> , 2018, 44, 2113-2118.	0.5	3
4	De novo design of antibody complementarity determining regions binding a FLAG tetra-peptide. <i>Scientific Reports</i> , 2017, 7, 10295.	3.3	27
5	Identification of disease-specific motifs in the antibody specificity repertoire via next-generation sequencing. <i>Scientific Reports</i> , 2016, 6, 30312.	3.3	35
6	Engineering pH responsive fibronectin domains for biomedical applications. <i>Journal of Biological Engineering</i> , 2015, 9, 6.	4.7	9
7	The Iterative Protein Redesign and Optimization (IPRO) suite of programs. <i>Journal of Computational Chemistry</i> , 2015, 36, 251-263.	3.3	34
8	OptMAVEEn – A New Framework for the de novo Design of Antibody Variable Region Models Targeting Specific Antigen Epitopes. <i>PLoS ONE</i> , 2014, 9, e105954.	2.5	59
9	MAPs: a database of modular antibody parts for predicting tertiary structures and designing affinity matured antibodies. <i>BMC Bioinformatics</i> , 2013, 14, 168.	2.6	24
10	OptZyme: Computational Enzyme Redesign Using Transition State Analogues. <i>PLoS ONE</i> , 2013, 8, e75358.	2.5	22
11	Recent advances in computational protein design. <i>Current Opinion in Structural Biology</i> , 2011, 21, 467-472.	5.7	78
12	Computational design of <i>Candida boidinii</i> xylose reductase for altered cofactor specificity. <i>Protein Science</i> , 2009, 18, 2125-2138.	7.6	84
13	Optimal protein library design using recombination or point mutations based on sequence-based scoring functions. <i>Protein Engineering, Design and Selection</i> , 2007, 20, 361-373.	2.1	37