Rationalization and Design of the Complementarity Det Antibody-Antigen Recognition Interface

Citation Report

#	Article	IF	Citations
1	Protein-Protein Interaction Site Predictions with Three-Dimensional Probability Distributions of Interacting Atoms on Protein Surfaces. PLoS ONE, 2012, 7, e37706.	1.1	25
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3	MAPs: a database of modular antibody parts for predicting tertiary structures and designing affinity matured antibodies. BMC Bioinformatics, 2013, 14, 168.	1.2	24
4	Computational design of protein–protein interactions. Current Opinion in Structural Biology, 2013, 23, 903-910.	2.6	53
5	Minireview: Applied Structural Bioinformatics in Proteomics. Protein Journal, 2013, 32, 505-511.	0.7	9
6	Residue-Level Prediction of HIV-1 Antibody Epitopes Based on Neutralization of Diverse Viral Strains. Journal of Virology, 2013, 87, 10047-10058.	1.5	64
7	Isolation, Characterization, and Molecular Modeling of a Rheumatoid Factor from a Hepatitis C Virus Infected Patient with Sjögren's Syndrome. Scientific World Journal, The, 2013, 2013, 1-11.	0.8	6
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9	NEP: web server for epitope prediction based on antibody neutralization of viral strains with diverse sequences. Nucleic Acids Research, 2014, 42, W64-W71.	6.5	16
10	Loop-Sequence Features and Stability Determinants in Antibody Variable Domains by High-Throughput Experiments. Structure, 2014, 22, 9-21.	1.6	26
11	Antibody Variable Domain Interface and Framework Sequence Requirements for Stability and Function by High-Throughput Experiments. Structure, 2014, 22, 22-34.	1.6	22
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16	Rational design of antibodies targeting specific epitopes within intrinsically disordered proteins. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9902-9907.	3.3	113
17	Algorithmic approaches to protein-protein interaction site prediction. Algorithms for Molecular Biology, 2015, 10, 7.	0.3	62
18	Predominant structural configuration of natural antibody repertoires enables potent antibody responses against protein antigens. Scientific Reports, 2015, 5, 12411.	1.6	17

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19	CCharPPI web server: computational characterization of protein–protein interactions from structure. Bioinformatics, 2015, 31, 123-125.	1.8	61
20	Predicting Ligand Binding Sites on Protein Surfaces by 3-Dimensional Probability Density Distributions of Interacting Atoms. PLoS ONE, 2016, 11, e0160315.	1.1	17
21	High throughput cytotoxicity screening of anti-HER2 immunotoxins conjugated with antibody fragments from phage-displayed synthetic antibody libraries. Scientific Reports, 2016, 6, 31878.	1.6	19
22	Antibodyomics: bioinformatics technologies for understanding B‑cell immunity to <scp>HIV</scp>‑1. Immunological Reviews, 2017, 275, 108-128.	2.8	32
23	Structural Analysis of Recent Allergen-Antibody Complexes and Future Directions. Current Allergy and Asthma Reports, 2019, 19, 17.	2.4	6
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31	Crystal structures of human Fabs targeting the Bexsero meningococcal vaccine antigen NHBA. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 305-314.	0.4	5
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33	Anti-ROR1 scFv-EndoG as a Novel Anti-Cancer Therapeutic Drug. Asian Pacific Journal of Cancer Prevention, 2018, 19, 97-102.	0.5	5
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