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List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	ZDOCK server: interactive docking prediction of protein–protein complexes and symmetric multimers. Bioinformatics, 2014, 30, 1771-1773.	4.1	1,313
2	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. Genome Research, 2012, 22, 1798-1812.	5.5	762
3	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
4	Accelerating Protein Docking in ZDOCK Using an Advanced 3D Convolution Library. PLoS ONE, 2011, 6, e24657.	2.5	490
5	ZRANK: Reranking protein docking predictions with an optimized energy function. Proteins: Structure, Function and Bioinformatics, 2007, 67, 1078-1086.	2.6	401
6	Updates to the Integrated Protein–Protein Interaction Benchmarks: Docking Benchmark Version 5 and Affinity Benchmark Version 2. Journal of Molecular Biology, 2015, 427, 3031-3041.	4.2	348
7	Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium. Nucleic Acids Research, 2013, 41, D171-D176.	14.5	274
8	Integrating statistical pair potentials into protein complex prediction. Proteins: Structure, Function and Bioinformatics, 2007, 69, 511-520.	2.6	273
9	Protein-protein docking benchmark 2.0: An update. Proteins: Structure, Function and Bioinformatics, 2005, 60, 214-216.	2.6	254
10	Protein–protein docking benchmark version 3.0. Proteins: Structure, Function and Bioinformatics, 2008, 73, 705-709.	2.6	224
11	M-ZDOCK: a grid-based approach for Cn symmetric multimer docking. Bioinformatics, 2005, 21, 1472-1478.	4.1	160
12	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	2.6	148
13	Benchmarking <scp>AlphaFold</scp> for protein complex modeling reveals accuracy determinants. Protein Science, 2022, 31, .	7.6	133
14	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
15	A combination of rescoring and refinement significantly improves protein docking performance. Proteins: Structure, Function and Bioinformatics, 2008, 72, 270-279.	2.6	126
16	ZDOCK and RDOCK performance in CAPRI rounds 3, 4, and 5. Proteins: Structure, Function and Bioinformatics, 2005, 60, 207-213.	2.6	102
17	Blind prediction of homo―and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	2.6	99
18	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	2.6	87

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19	Global mapping of antibody recognition of the hepatitis C virus E2 glycoprotein: Implications for vaccine design. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6946-E6954.	7.1	86
20	A flexible docking approach for prediction of T cell receptor–peptide–MHC complexes. Protein Science, 2013, 22, 35-46.	7.6	75
21	Prediction of protein–protein binding free energies. Protein Science, 2012, 21, 396-404.	7.6	74
22	Prediction of protein assemblies, the next frontier: The <scp>CASP14â€CAPRI</scp> experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1800-1823.	2.6	73
23	Performance of ZDOCK and ZRANK in CAPRI rounds 13–19. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3104-3110.	2.6	72
24	Structural Basis for Penetration of the Glycan Shield of Hepatitis C Virus E2 Glycoprotein by a Broadly Neutralizing Human Antibody. Journal of Biological Chemistry, 2015, 290, 10117-10125.	3.4	69
25	TCR3d: The T cell receptor structural repertoire database. Bioinformatics, 2019, 35, 5323-5325.	4.1	69
26	ATLAS: A database linking binding affinities with structures for wild-type and mutant TCR-pMHC complexes. Proteins: Structure, Function and Bioinformatics, 2017, 85, 908-916.	2.6	68
27	Computational Design of the Affinity and Specificity of a Therapeutic T Cell Receptor. PLoS Computational Biology, 2014, 10, e1003478.	3.2	67
28	Structureâ€based design of a Tâ€cell receptor leads to nearly 100â€fold improvement in binding affinity for pepMHC. Proteins: Structure, Function and Bioinformatics, 2009, 74, 948-960.	2.6	66
29	An expanded benchmark for antibody-antigen docking and affinity prediction reveals insights into antibody recognition determinants. Structure, 2021, 29, 606-621.e5.	3.3	65
30	Cutting Edge: Evidence for a Dynamically Driven T Cell Signaling Mechanism. Journal of Immunology, 2012, 188, 5819-5823.	0.8	63
31	TCRmodel: high resolution modeling of T cell receptors from sequence. Nucleic Acids Research, 2018, 46, W396-W401.	14.5	62
32	Cellular origins and genetic landscape of cutaneous gamma delta T cell lymphomas. Nature Communications, 2020, 11, 1806.	12.8	62
33	The performance of ZDOCK and ZRANK in rounds 6–11 of CAPRI. Proteins: Structure, Function and Bioinformatics, 2007, 69, 719-725.	2.6	61
34	Affinity maturation of a broadly neutralizing human monoclonal antibody that prevents acute hepatitis C virus infection in mice. Hepatology, 2016, 64, 1922-1933.	7.3	60
35	CoV3D: a database of high resolution coronavirus protein structures. Nucleic Acids Research, 2021, 49, D282-D287.	14.5	58
36	Crystal structure of <i>Streptococcus pyogenes</i> EndoS, an immunomodulatory endoglycosidase specific for human IgG antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6714-6719.	7.1	56

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37	Hepatitis C virus vaccine candidates inducing protective neutralizing antibodies. Expert Review of Vaccines, 2016, 15, 1535-1544.	4.4	55
38	How structural adaptability exists alongside HLA-A2 bias in the human αβ TCR repertoire. Proceedings of the United States of America, 2016, 113, E1276-85.	7.1	55
39	Antigenicity and Immunogenicity of Differentially Glycosylated Hepatitis C Virus E2 Envelope Proteins Expressed in Mammalian and Insect Cells. Journal of Virology, 2019, 93, .	3.4	51
40	Blind prediction of interfacial water positions in CAPRI. Proteins: Structure, Function and Bioinformatics, 2014, 82, 620-632.	2.6	50
41	Structure-Based Design of Hepatitis C Virus Vaccines That Elicit Neutralizing Antibody Responses to a Conserved Epitope. Journal of Virology, 2017, 91, .	3.4	50
42	Vaccination with Cancer- and HIV Infection-Associated Endogenous Retrotransposable Elements Is Safe and Immunogenic. Journal of Immunology, 2012, 189, 1467-1479.	0.8	46
43	Peptide–MHC (pMHC) binding to a human antiviral T cell receptor induces long-range allosteric communication between pMHC- and CD3-binding sites. Journal of Biological Chemistry, 2018, 293, 15991-16005.	3.4	45
44	Broadly neutralizing antibodies from an individual that naturally cleared multiple hepatitis C virus infections uncover molecular determinants for E2 targeting and vaccine design. PLoS Pathogens, 2019, 15, e1007772.	4.7	45
45	Viral evasion and challenges of hepatitis C virus vaccine development. Current Opinion in Virology, 2016, 20, 55-63.	5.4	44
46	Designing a B Cell-Based Vaccine against a Highly Variable Hepatitis C Virus. Frontiers in Microbiology, 2017, 8, 2692.	3.5	43
47	Zika virus NS5 protein antagonizes type I interferon production via blocking TBK1 activation. Virology, 2019, 527, 180-187.	2.4	43
48	Structural Basis for Clonal Diversity of the Public T Cell Response to a Dominant Human Cytomegalovirus Epitope. Journal of Biological Chemistry, 2015, 290, 29106-29119.	3.4	41
49	Structural basis for oligoclonal T cell recognition of a shared p53 cancer neoantigen. Nature Communications, 2020, 11, 2908.	12.8	40
50	Evaluating template-based and template-free protein-protein complex structure prediction. Briefings in Bioinformatics, 2014, 15, 169-176.	6.5	35
51	Mapping Determinants of Virus Neutralization and Viral Escape for Rational Design of a Hepatitis C Virus Vaccine. Frontiers in Immunology, 2018, 9, 1194.	4.8	34
52	Exploring the DNA-recognition potential of homeodomains. Genome Research, 2012, 22, 1889-1898.	5.5	26
53	High-Throughput Sequencing Analysis of Post-Liver Transplantation HCV E2 Glycoprotein Evolution in the Presence and Absence of Neutralizing Monoclonal Antibody. PLoS ONE, 2014, 9, e100325.	2.5	23
54	Anti-CfaE nanobodies provide broad cross-protection against major pathogenic enterotoxigenic Escherichia coli strains, with implications for vaccine design. Scientific Reports, 2021, 11, 2751.	3.3	23

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55	Performance of ZDOCK in CAPRI rounds 20–26. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2175-2182.	2.6	22
56	Resolving self-association of a therapeutic antibody by formulation optimization and molecular approaches. MAbs, 2014, 6, 1533-1539.	5.2	20
57	An Antigenically Diverse, Representative Panel of Envelope Glycoproteins for Hepatitis C Virus Vaccine Development. Gastroenterology, 2022, 162, 562-574.	1.3	20
58	Structural assessment of HLA-A2-restricted SARS-CoV-2 spike epitopes recognized by public and private T-cell receptors. Nature Communications, 2022, 13, 19.	12.8	20
59	Protein–Protein Docking: Overview and Performance Analysis. , 2008, 413, 283-314.		19
60	Design of a native-like secreted form of the hepatitis C virus E1E2 heterodimer. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	19
61	Mutational analysis of the latency-associated nuclear antigen DNA-binding domain of Kaposi's sarcoma-associated herpesvirus reveals structural conservation among gammaherpesvirus origin-binding proteins. Journal of General Virology, 2010, 91, 2203-2215.	2.9	19
62	Structure-Based Design of Hepatitis C Virus E2 Glycoprotein Improves Serum Binding and Cross-Neutralization. Journal of Virology, 2020, 94, .	3.4	17
63	Backbone Flexibility of CDR3 and Immune Recognition of Antigens. Journal of Molecular Biology, 2014, 426, 1583-1599.	4.2	16
64	A generalized framework for computational design and mutational scanning of T-cell receptor binding interfaces. Protein Engineering, Design and Selection, 2016, 29, 595-606.	2.1	16
65	<i>In Vivo</i> and <i>In Vitro</i> Potency of Polyphosphazene Immunoadjuvants with Hepatitis C Virus Antigen and the Role of Their Supramolecular Assembly. Molecular Pharmaceutics, 2021, 18, 726-734.	4.6	16
66	Geometrical characterization of T cell receptor binding modes reveals classâ€specific binding to maximize access to antigen. Proteins: Structure, Function and Bioinformatics, 2020, 88, 503-513.	2.6	15
67	Bioinformatic Requirements for Protein Database Searching Using Predicted Epitopes from Disease-associated Antibodies. Molecular and Cellular Proteomics, 2008, 7, 247-256.	3.8	13
68	Performance of ZDOCK and IRAD in CAPRI rounds 28–34. Proteins: Structure, Function and Bioinformatics, 2017, 85, 408-416.	2.6	13
69	High-throughput modeling and scoring of TCR-pMHC complexes to predict cross-reactive peptides. Bioinformatics, 2021, 36, 5377-5385.	4.1	13
70	Structural and energetic profiling of SARS-CoV-2 receptor binding domain antibody recognition and the impact of circulating variants. PLoS Computational Biology, 2021, 17, e1009380.	3.2	13
71	Computational Modeling of Hepatitis C Virus Envelope Glycoprotein Structure and Recognition. Frontiers in Immunology, 2018, 9, 1117.	4.8	12
72	Computational Modeling of T Cell Receptor Complexes. Methods in Molecular Biology, 2016, 1414, 319-340.	0.9	11

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73	Combinations of Affinity-Enhancing Mutations in a T Cell Receptor Reveal Highly Nonadditive Effects within and between Complementarity Determining Regions and Chains. Biochemistry, 2010, 49, 7050-7059.	2.5	10
74	The Missing Heritability in T1D and Potential New Targets for Prevention. Journal of Diabetes Research, 2013, 2013, 1-10.	2.3	9
75	An extended motif in the SARS-CoV-2 spike modulates binding and release of host coatomer in retrograde trafficking. Communications Biology, 2022, 5, 115.	4.4	9
76	T cell receptors employ diverse strategies to target a p53 cancer neoantigen. Journal of Biological Chemistry, 2022, 298, 101684.	3.4	9
77	Molecular Basis of a Million-Fold Affinity Maturation Process in a Protein–Protein Interaction. Journal of Molecular Biology, 2011, 411, 321-328.	4.2	7
78	Structure-Based and Rational Design of a Hepatitis C Virus Vaccine. Viruses, 2021, 13, 837.	3.3	7
79	Molecular Determinants of Filament Capping Proteins Required for the Formation of Functional Flagella in Gram-Negative Bacteria. Biomolecules, 2021, 11, 1397.	4.0	7
80	Induction of broadly neutralizing antibodies using a secreted form of the hepatitis C virus E1E2 heterodimer as a vaccine candidate. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2112008119.	7.1	7
81	Structural Features of Antibody-Peptide Recognition. Frontiers in Immunology, 0, 13, .	4.8	7
82	Newcastle disease virus vectors expressing consensus sequence of the H7 HA protein protect broiler chickens and turkeys against highly pathogenic H7N8 virus. Vaccine, 2019, 37, 4956-4962.	3.8	6
83	Modeling T cell receptor recognition of CD1-lipid and MR1-metabolite complexes. BMC Bioinformatics, 2014, 15, 319.	2.6	5
84	Structural and Biophysical Characterization of the HCV E1E2 Heterodimer for Vaccine Development. Viruses, 2021, 13, 1027.	3.3	5
85	Structure Prediction of Protein Complexes. Biological and Medical Physics Series, 2007, , 109-134.	0.4	5
86	Modeling and Viewing T Cell Receptors Using TCRmodel and TCR3d. Methods in Molecular Biology, 2020, 2120, 197-212.	0.9	4
87	T Cell Receptor Genotype and Ubash3a Determine Susceptibility to Rat Autoimmune Diabetes. Genes, 2021, 12, 852.	2.4	3
88	Computational Reprogramming of T Cell Antigen Receptor Binding Properties. Methods in Molecular Biology, 2016, 1414, 305-318.	0.9	2
89	Biophysical Characterization of TCR Variants with Reengineered Specificity and Affinity. FASEB Journal, 2015, 29, 571.30.	0.5	0