

Yanay Ofran

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

3,218
citations

257450

24
h-index

345221

36
g-index

39
all docs

39
docs citations

39
times ranked

4268
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysing Six Types of Protein-Protein Interfaces. <i>Journal of Molecular Biology</i> , 2003, 325, 377-387.	4.2	378
2	The Structural Basis of Antibody-Antigen Recognition. <i>Frontiers in Immunology</i> , 2013, 4, 302.	4.8	361
3	ISIS: interaction sites identified from sequence. <i>Bioinformatics</i> , 2007, 23, e13-e16.	4.1	243
4	Protein-Protein Interaction Hotspots Carved into Sequences. <i>PLoS Computational Biology</i> , 2007, 3, e119.	3.2	229
5	Predicted protein-protein interaction sites from local sequence information. <i>FEBS Letters</i> , 2003, 544, 236-239.	2.8	222
6	Towards a consensus on datasets and evaluation metrics for developing B-cell epitope prediction tools. <i>Journal of Molecular Recognition</i> , 2007, 20, 75-82.	2.1	209
7	Prediction of DNA-binding residues from sequence. <i>Bioinformatics</i> , 2007, 23, i347-i353.	4.1	157
8	How far from the SNP may the causative genes be?. <i>Nucleic Acids Research</i> , 2016, 44, 6046-6054.	14.5	138
9	Paratome: an online tool for systematic identification of antigen-binding regions in antibodies based on sequence or structure. <i>Nucleic Acids Research</i> , 2012, 40, W521-W524.	14.5	126
10	Structural Consensus among Antibodies Defines the Antigen Binding Site. <i>PLoS Computational Biology</i> , 2012, 8, e1002388.	3.2	99
11	A Systematic Comparison of Free and Bound Antibodies Reveals Binding-Related Conformational Changes. <i>Journal of Immunology</i> , 2012, 189, 4890-4899.	0.8	96
12	Beyond annotation transfer by homology: novel protein-function prediction methods to assist drug discovery. <i>Drug Discovery Today</i> , 2005, 10, 1475-1482.	6.4	84
13	The Rough Guide to In Silico Function Prediction, or How To Use Sequence and Structure Information To Predict Protein Function. <i>PLoS Computational Biology</i> , 2008, 4, e1000160.	3.2	83
14	The indistinguishability of epitopes from protein surface is explained by the distinct binding preferences of each of the six antigen-binding loops. <i>Protein Engineering, Design and Selection</i> , 2013, 26, 599-609.	2.1	82
15	Epitome: database of structure-inferred antigenic epitopes. <i>Nucleic Acids Research</i> , 2006, 34, D777-D780.	14.5	78
16	Automated Identification of Complementarity Determining Regions (CDRs) Reveals Peculiar Characteristics of CDRs and B Cell Epitopes. <i>Journal of Immunology</i> , 2008, 181, 6230-6235.	0.8	73
17	Antibody specific epitope prediction—emergence of a new paradigm. <i>Current Opinion in Virology</i> , 2015, 11, 98-102.	5.4	64
18	Using a Combined Computational-Experimental Approach to Predict Antibody-Specific B Cell Epitopes. <i>Structure</i> , 2014, 22, 646-657.	3.3	63

#	ARTICLE	IF	CITATIONS
19	Computational Design of Epitope-Specific Functional Antibodies. <i>Cell Reports</i> , 2018, 25, 2121-2131.e5.	6.4	55
20	PEASE: predicting B-cell epitopes utilizing antibody sequence. <i>Bioinformatics</i> , 2015, 31, 1313-1315.	4.1	51
21	Computational design of antibodies. <i>Current Opinion in Structural Biology</i> , 2018, 51, 156-162.	5.7	48
22	Large-scale analysis of somatic hypermutations in antibodies reveals which structural regions, positions and amino acids are modified to improve affinity. <i>FEBS Journal</i> , 2014, 281, 306-319.	4.7	45
23	Potent Neutralization of Vaccinia Virus by Divergent Murine Antibodies Targeting a Common Site of Vulnerability in L1 Protein. <i>Journal of Virology</i> , 2014, 88, 11339-11355.	3.4	40
24	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2017, 38, 1182-1192.	2.5	39
25	Proteins of the same fold and unrelated sequences have similar amino acid composition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 275-279.	2.6	26
26	De-novo protein function prediction using DNA binding and RNA binding proteins as a test case. <i>Nature Communications</i> , 2016, 7, 13424.	12.8	22
27	Lateral acquisition of genes is affected by the friendliness of their products. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 343-348.	7.1	21
28	Computational Identification of Antigen-Binding Antibody Fragments. <i>Journal of Immunology</i> , 2013, 190, 2327-2334.	0.8	21
29	Understanding differences between synthetic and natural antibodies can help improve antibody engineering. <i>MABs</i> , 2016, 8, 278-287.	5.2	18
30	Unveiling Protein Functions through the Dynamics of the Interaction Network. <i>PLoS ONE</i> , 2011, 6, e17679.	2.5	14
31	Large Scale Analysis of Phenotype-Pathway Relationships Based on GWAS Results. <i>PLoS ONE</i> , 2014, 9, e100887.	2.5	14
32	Targeting the actin nucleation promoting factor WASp provides a therapeutic approach for hematopoietic malignancies. <i>Nature Communications</i> , 2021, 12, 5581.	12.8	8
33	Create and assess protein networks through molecular characteristics of individual proteins. <i>Bioinformatics</i> , 2006, 22, e402-e407.	4.1	6
34	The Two Cultures and Systems Biology: How Philosophy Starts Where Science Ends. <i>European Legacy</i> , 2008, 13, 589-604.	0.2	2
35	Integrating genomic data from high-throughput studies with computational modeling reveals differences in the molecular basis of hyposalivation between type 1 and type 2 diabetes. <i>Clinical Oral Investigations</i> , 2018, 22, 151-159.	3.0	2
36	Co-expression and co-localization of hub proteins and their partners are encoded in protein sequence. <i>Molecular BioSystems</i> , 2014, 10, 787.	2.9	1

#	ARTICLE	IF	CITATIONS
37	MOLECULAR BIOINFORMATICS FOR DISEASE “ SESSION INTRODUCTION. , 2008, , .		0
38	Antibody Modeling, Engineering, and Design. , 2018, , 1-8.		0
39	MOLECULAR BIOINFORMATICS FOR DISEASE: PROTEIN INTERACTIONS AND PHENOMICS “ Session Introduction. , 2007, , .		0