

Claus Lundegaard

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

9,826
citations

145106

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299063

42
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43
all docs

43
docs citations

43
times ranked

12092
citing authors

#	ARTICLE	IF	CITATIONS
1	MHCcluster, a method for functional clustering of MHC molecules. Immunogenetics, 2013, 65, 655-665.	1.2	116
2	In silico peptide-binding predictions of passerine MHC class I reveal similarities across distantly related species, suggesting convergence on the level of protein function. Immunogenetics, 2013, 65, 299-311.	1.2	14
3	Bioinformatics Identification of Antigenic Peptide: Predicting the Specificity of Major MHC Class I and II Pathway Players. Methods in Molecular Biology, 2013, 960, 247-260.	0.4	2
4	Reliable B Cell Epitope Predictions: Impacts of Method Development and Improved Benchmarking. PLoS Computational Biology, 2012, 8, e1002829.	1.5	557
5	Predictions versus high-throughput experiments in T-cell epitope discovery: competition or synergy?. Expert Review of Vaccines, 2012, 11, 43-54.	2.0	39
6	Immune epitope database analysis resource. Nucleic Acids Research, 2012, 40, W525-W530.	6.5	446
7	NetMHCcons: a consensus method for the major histocompatibility complex class I predictions. Immunogenetics, 2012, 64, 177-186.	1.2	333
8	Characterization of HIV-Specific CD4+ T Cell Responses against Peptides Selected with Broad Population and Pathogen Coverage. PLoS ONE, 2012, 7, e39874.	1.1	22
9	Human Leukocyte Antigen (HLA) Class I Restricted Epitope Discovery in Yellow Fever and Dengue Viruses: Importance of HLA Binding Strength. PLoS ONE, 2011, 6, e26494.	1.1	30
10	Prediction of epitopes using neural network based methods. Journal of Immunological Methods, 2011, 374, 26-34.	0.6	88
11	Machine learning competition in immunology – Prediction of HLA class I binding peptides. Journal of Immunological Methods, 2011, 374, 1-4.	0.6	53
12	NetCTLpan: pan-specific MHC class I pathway epitope predictions. Immunogenetics, 2010, 62, 357-368.	1.2	329
13	State of the art and challenges in sequence based T-cell epitope prediction. Immunome Research, 2010, 6, S3.	0.1	52
14	MHC Class II epitope predictive algorithms. Immunology, 2010, 130, 319-328.	2.0	198
15	Major histocompatibility complex class I binding predictions as a tool in epitope discovery. Immunology, 2010, 130, 309-318.	2.0	109
16	NetTurnP – Neural Network Prediction of Beta-turns by Use of Evolutionary Information and Predicted Protein Sequence Features. PLoS ONE, 2010, 5, e15079.	1.1	83
17	Mice, men and MHC supertypes. Expert Review of Vaccines, 2010, 9, 713-718.	2.0	2
18	CPHmodels-3.0 – remote homology modeling using structure-guided sequence profiles. Nucleic Acids Research, 2010, 38, W576-W581.	6.5	305

#	ARTICLE	IF	CITATIONS
19	NetMHCIIpan-2.0 - Improved pan-specific HLA-DR predictions using a novel concurrent alignment and weight optimization training procedure. <i>Immunome Research</i> , 2010, 6, 9.	0.1	132
20	Pan-specific MHC class I predictors: a benchmark of HLA class I pan-specific prediction methods. <i>Bioinformatics</i> , 2009, 25, 83-89.	1.8	100
21	A generic method for assignment of reliability scores applied to solvent accessibility predictions. <i>BMC Structural Biology</i> , 2009, 9, 51.	2.3	555
22	The peptide-binding specificity of HLA-A*3001 demonstrates membership of the HLA-A3 supertype. <i>Immunogenetics</i> , 2008, 60, 633-643.	1.2	21
23	Immune epitope database analysis resource (IEDB-AR). <i>Nucleic Acids Research</i> , 2008, 36, W513-W518.	6.5	304
24	Quantitative Predictions of Peptide Binding to Any HLA-DR Molecule of Known Sequence: NetMHCIIpan. <i>PLoS Computational Biology</i> , 2008, 4, e1000107.	1.5	254
25	Accurate approximation method for prediction of class I MHC affinities for peptides of length 8, 10 and 11 using prediction tools trained on 9mers. <i>Bioinformatics</i> , 2008, 24, 1397-1398.	1.8	216
26	NetMHC-3.0: accurate web accessible predictions of human, mouse and monkey MHC class I affinities for peptides of length 8-11. <i>Nucleic Acids Research</i> , 2008, 36, W509-W512.	6.5	722
27	Modeling the adaptive immune system: predictions and simulations. <i>Bioinformatics</i> , 2007, 23, 3265-3275.	1.8	115
28	CTL epitopes for influenza A including the H5N1 bird flu; genome-, pathogen-, and HLA-wide screening. <i>Vaccine</i> , 2007, 25, 2823-2831.	1.7	94
29	Prediction of MHC class II binding affinity using SMM-align, a novel stabilization matrix alignment method. <i>BMC Bioinformatics</i> , 2007, 8, 238.	1.2	499
30	Large-scale validation of methods for cytotoxic T-lymphocyte epitope prediction. <i>BMC Bioinformatics</i> , 2007, 8, 424.	1.2	687
31	NetMHCpan, a Method for Quantitative Predictions of Peptide Binding to Any HLA-A and -B Locus Protein of Known Sequence. <i>PLoS ONE</i> , 2007, 2, e796.	1.1	598
32	Modelling the Human Immune System by Combining Bioinformatics and Systems Biology Approaches. <i>Journal of Biological Physics</i> , 2006, 32, 335-353.	0.7	19
33	The validity of predicted T-cell epitopes. <i>Trends in Biotechnology</i> , 2006, 24, 537-538.	4.9	59
34	A Community Resource Benchmarking Predictions of Peptide Binding to MHC-I Molecules. <i>PLoS Computational Biology</i> , 2006, 2, e65.	1.5	254
35	An integrative approach to CTL epitope prediction: A combined algorithm integrating MHC class I binding, TAP transport efficiency, and proteasomal cleavage predictions. <i>European Journal of Immunology</i> , 2005, 35, 2295-2303.	1.6	290
36	The role of the proteasome in generating cytotoxic T-cell epitopes: insights obtained from improved predictions of proteasomal cleavage. <i>Immunogenetics</i> , 2005, 57, 33-41.	1.2	416

#	ARTICLE	IF	CITATIONS
37	Immunological Bioinformatics. , 2005, , .		49
38	Improved prediction of MHC class I and class II epitopes using a novel Gibbs sampling approach. Bioinformatics, 2004, 20, 1388-1397.	1.8	254
39	Definition of supertypes for HLA molecules using clustering of specificity matrices. Immunogenetics, 2004, 55, 797-810.	1.2	269
40	MHC Class I Epitope Binding Prediction Trained on Small Data Sets. Lecture Notes in Computer Science, 2004, , 217-225.	1.0	2
41	Reliable prediction of T-cell epitopes using neural networks with novel sequence representations. Protein Science, 2003, 12, 1007-1017.	3.1	1,013
42	Selecting Informative Data for Developing Peptide-MHC Binding Predictors Using a Query by Committee Approach. Neural Computation, 2003, 15, 2931-2942.	1.3	14
43	Prediction of protein secondary structure at 80% accuracy. Proteins: Structure, Function and Bioinformatics, 2000, 41, 17-20.	1.5	112