

Morten Nielsen

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232
papers

19,983
citations

65
h-index

139
g-index

247
ext. papers

26,464
ext. citations

7.3
avg, IF

7.19
L-index

#	Paper	IF	Citations
232	Robust T Cell Immunity in Convalescent Individuals with Asymptomatic or Mild COVID-19. <i>Cell</i> , 2020 , 183, 158-168.e14	56.2	955
231	Reliable prediction of T-cell epitopes using neural networks with novel sequence representations. <i>Protein Science</i> , 2003 , 12, 1007-17	6.3	783
230	Improved method for predicting linear B-cell epitopes. <i>Immunome Research</i> , 2006 , 2, 2		780
229	NetMHCpan-4.0: Improved Peptide-MHC Class I Interaction Predictions Integrating Eluted Ligand and Peptide Binding Affinity Data. <i>Journal of Immunology</i> , 2017 , 199, 3360-3368	5.3	645
228	Gapped sequence alignment using artificial neural networks: application to the MHC class I system. <i>Bioinformatics</i> , 2016 , 32, 511-7	7.2	570
227	BepiPred-2.0: improving sequence-based B-cell epitope prediction using conformational epitopes. <i>Nucleic Acids Research</i> , 2017 , 45, W24-W29	20.1	545
226	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, W509-12	20.1	545
225	NetMHCpan, a method for MHC class I binding prediction beyond humans. <i>Immunogenetics</i> , 2009 , 61, 1-13	3.2	522
224	A generic method for assignment of reliability scores applied to solvent accessibility predictions. <i>BMC Structural Biology</i> , 2009 , 9, 51	2.7	471
223	Large-scale validation of methods for cytotoxic T-lymphocyte epitope prediction. <i>BMC Bioinformatics</i> , 2007 , 8, 424	3.6	459
222	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	3.7	444
221	Prediction of residues in discontinuous B-cell epitopes using protein 3D structures. <i>Protein Science</i> , 2006 , 15, 2558-67	6.3	415
220	Peptide binding predictions for HLA DR, DP and DQ molecules. <i>BMC Bioinformatics</i> , 2010 , 11, 568	3.6	408
219	Reliable B cell epitope predictions: impacts of method development and improved benchmarking. <i>PLoS Computational Biology</i> , 2012 , 8, e1002829	5	367
218	Prediction of MHC class II binding affinity using SMM-align, a novel stabilization matrix alignment method. <i>BMC Bioinformatics</i> , 2007 , 8, 238	3.6	356
217	Improved methods for predicting peptide binding affinity to MHC class II molecules. <i>Immunology</i> , 2018 , 154, 394-406	7.8	343
216	NN-align. An artificial neural network-based alignment algorithm for MHC class II peptide binding prediction. <i>BMC Bioinformatics</i> , 2009 , 10, 296	3.6	336

215	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	3.2	336
214	Immune epitope database analysis resource. <i>Nucleic Acids Research</i> , 2012 , 40, W525-30	20.1	322
213	NetMHCpan-3.0; improved prediction of binding to MHC class I molecules integrating information from multiple receptor and peptide length datasets. <i>Genome Medicine</i> , 2016 , 8, 33	14.4	315
212	NetMHCpan-4.1 and NetMHCIIpan-4.0: improved predictions of MHC antigen presentation by concurrent motif deconvolution and integration of MS MHC eluted ligand data. <i>Nucleic Acids Research</i> , 2020 , 48, W449-W454	20.1	299
211	Seq2Logo: a method for construction and visualization of amino acid binding motifs and sequence profiles including sequence weighting, pseudo counts and two-sided representation of amino acid enrichment and depletion. <i>Nucleic Acids Research</i> , 2012 , 40, W281-7	20.1	259
210	CPHmodels-3.0--remote homology modeling using structure-guided sequence profiles. <i>Nucleic Acids Research</i> , 2010 , 38, W576-81	20.1	258
209	Immune epitope database analysis resource (IEDB-AR). <i>Nucleic Acids Research</i> , 2008 , 36, W513-8	20.1	240
208	NetMHCcons: a consensus method for the major histocompatibility complex class I predictions. <i>Immunogenetics</i> , 2012 , 64, 177-86	3.2	233
207	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, 2295-303	6.1	229
206	A community resource benchmarking predictions of peptide binding to MHC-I molecules. <i>PLoS Computational Biology</i> , 2006 , 2, e65	5	224
205	Definition of supertypes for HLA molecules using clustering of specificity matrices. <i>Immunogenetics</i> , 2004 , 55, 797-810	3.2	224
204	Improved prediction of MHC class I and class II epitopes using a novel Gibbs sampling approach. <i>Bioinformatics</i> , 2004 , 20, 1388-97	7.2	223
203	NetSurfP-2.0: Improved prediction of protein structural features by integrated deep learning. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 520-527	4.2	214
202	From lanosterol to cholesterol: structural evolution and differential effects on lipid bilayers. <i>Biophysical Journal</i> , 2002 , 82, 1429-44	2.9	208
201	Quantitative predictions of peptide binding to any HLA-DR molecule of known sequence: NetMHCIIpan. <i>PLoS Computational Biology</i> , 2008 , 4, e1000107	5	207
200	NetCTLpan: pan-specific MHC class I pathway epitope predictions. <i>Immunogenetics</i> , 2010 , 62, 357-68	3.2	205
199	Accurate pan-specific prediction of peptide-MHC class II binding affinity with improved binding core identification. <i>Immunogenetics</i> , 2015 , 67, 641-50	3.2	200
198	NetMHCIIpan-3.0, a common pan-specific MHC class II prediction method including all three human MHC class II isotypes, HLA-DR, HLA-DP and HLA-DQ. <i>Immunogenetics</i> , 2013 , 65, 711-24	3.2	192

197	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, 1397-8	7.2	177
196	Structural analysis of B-cell epitopes in antibody:protein complexes. <i>Molecular Immunology</i> , 2013 , 53, 24-34	4.3	173
195	MHC class II epitope predictive algorithms. <i>Immunology</i> , 2010 , 130, 319-28	7.8	157
194	MR1-restricted MAIT cells display ligand discrimination and pathogen selectivity through distinct T cell receptor usage. <i>Journal of Experimental Medicine</i> , 2014 , 211, 1601-10	16.6	144
193	Peptide-MHC class I stability is a better predictor than peptide affinity of CTL immunogenicity. <i>European Journal of Immunology</i> , 2012 , 42, 1405-16	6.1	140
192	The PickPocket method for predicting binding specificities for receptors based on receptor pocket similarities: application to MHC-peptide binding. <i>Bioinformatics</i> , 2009 , 25, 1293-9	7.2	139
191	IEDB-AR: immune epitope database-analysis resource in 2019. <i>Nucleic Acids Research</i> , 2019 , 47, W502-W506	50.1	136
190	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		117
189	MISTIC: Mutual information server to infer coevolution. <i>Nucleic Acids Research</i> , 2013 , 41, W8-14	20.1	113
188	Improved Prediction of MHC II Antigen Presentation through Integration and Motif Deconvolution of Mass Spectrometry MHC Eluted Ligand Data. <i>Journal of Proteome Research</i> , 2020 , 19, 2304-2315	5.6	106
187	The Length Distribution of Class I-Restricted T Cell Epitopes Is Determined by Both Peptide Supply and MHC Allele-Specific Binding Preference. <i>Journal of Immunology</i> , 2016 , 196, 1480-7	5.3	106
186	Pan-Specific Prediction of Peptide-MHC Class I Complex Stability, a Correlate of T Cell Immunogenicity. <i>Journal of Immunology</i> , 2016 , 197, 1517-24	5.3	103
185	Modeling the adaptive immune system: predictions and simulations. <i>Bioinformatics</i> , 2007 , 23, 3265-75	7.2	101
184	Automated benchmarking of peptide-MHC class I binding predictions. <i>Bioinformatics</i> , 2015 , 31, 2174-81	7.2	100
183	Prediction of protein secondary structure at 80% accuracy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 41, 17-20	4.2	96
182	MuPeXI: prediction of neo-epitopes from tumor sequencing data. <i>Cancer Immunology, Immunotherapy</i> , 2017 , 66, 1123-1130	7.4	95
181	GibbsCluster: unsupervised clustering and alignment of peptide sequences. <i>Nucleic Acids Research</i> , 2017 , 45, W458-W463	20.1	94
180	Major histocompatibility complex class I binding predictions as a tool in epitope discovery. <i>Immunology</i> , 2010 , 130, 309-18	7.8	91

179	The SysteMHC Atlas project. <i>Nucleic Acids Research</i> , 2018 , 46, D1237-D1247	20.1	87
178	Pan-specific MHC class I predictors: a benchmark of HLA class I pan-specific prediction methods. <i>Bioinformatics</i> , 2009 , 25, 83-9	7.2	86
177	Robust T cell immunity in convalescent individuals with asymptomatic or mild COVID-19		85
176	NetMHCstab - predicting stability of peptide-MHC-I complexes; impacts for cytotoxic T lymphocyte epitope discovery. <i>Immunology</i> , 2014 , 141, 18-26	7.8	83
175	CTL epitopes for influenza A including the H5N1 bird flu; genome-, pathogen-, and HLA-wide screening. <i>Vaccine</i> , 2007 , 25, 2823-31	4.1	83
174	Prediction of epitopes using neural network based methods. <i>Journal of Immunological Methods</i> , 2011 , 374, 26-34	2.5	82
173	An introduction to deep learning on biological sequence data: examples and solutions. <i>Bioinformatics</i> , 2017 , 33, 3685-3690	7.2	81
172	Simultaneous alignment and clustering of peptide data using a Gibbs sampling approach. <i>Bioinformatics</i> , 2013 , 29, 8-14	7.2	81
171	Amino acid similarity accounts for T cell cross-reactivity and for "holes" in the T cell repertoire. <i>PLoS ONE</i> , 2008 , 3, e1831	3.7	81
170	MHCcluster, a method for functional clustering of MHC molecules. <i>Immunogenetics</i> , 2013 , 65, 655-65	3.2	77
169	Peptide binding to HLA class I molecules: homogenous, high-throughput screening, and affinity assays. <i>Journal of Biomolecular Screening</i> , 2009 , 14, 173-80		71
168	T Cell Epitope Predictions. <i>Annual Review of Immunology</i> , 2020 , 38, 123-145	34.7	69
167	SARS-CoV-2 genome-wide T cell epitope mapping reveals immunodominance and substantial CD8 T cell activation in COVID-19 patients. <i>Science Immunology</i> , 2021 , 6,	28	65
166	Different binding motifs of the celiac disease-associated HLA molecules DQ2.5, DQ2.2, and DQ7.5 revealed by relative quantitative proteomics of endogenous peptide repertoires. <i>Immunogenetics</i> , 2015 , 67, 73-84	3.2	63
165	Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions. <i>BMC Bioinformatics</i> , 2014 , 15, 241	3.6	63
164	Correction for phylogeny, small number of observations and data redundancy improves the identification of coevolving amino acid pairs using mutual information. <i>Bioinformatics</i> , 2009 , 25, 1125-31	7.2	63
163	HostPhinder: A Phage Host Prediction Tool. <i>Viruses</i> , 2016 , 8,	6.2	63
162	Off-lattice model for the phase behavior of lipid-cholesterol bilayers. <i>Physical Review E</i> , 1999 , 59, 5790-803	3.3	62

161	Towards High-throughput Immunomics for Infectious Diseases: Use of Next-generation Peptide Microarrays for Rapid Discovery and Mapping of Antigenic Determinants. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1871-84	7.6	61
160	Networks of high mutual information define the structural proximity of catalytic sites: implications for catalytic residue identification. <i>PLoS Computational Biology</i> , 2010 , 6, e1000978	5	61
159	Unmasking determinants of specificity in the human kinome. <i>Cell</i> , 2015 , 163, 187-201	56.2	58
158	T cell receptor fingerprinting enables in-depth characterization of the interactions governing recognition of peptide-MHC complexes. <i>Nature Biotechnology</i> , 2018 ,	44.5	57
157	Toxoplasma gondii peptide ligands open the gate of the HLA class I binding groove. <i>ELife</i> , 2016 , 5,	8.9	55
156	SARS CTL vaccine candidates; HLA supertype-, genome-wide scanning and biochemical validation. <i>Tissue Antigens</i> , 2004 , 63, 395-400		54
155	NNAlign: a web-based prediction method allowing non-expert end-user discovery of sequence motifs in quantitative peptide data. <i>PLoS ONE</i> , 2011 , 6, e26781	3.7	52
154	An Analysis of Natural T Cell Responses to Predicted Tumor Neoepitopes. <i>Frontiers in Immunology</i> , 2017 , 8, 1566	8.4	51
153	Uncovering the peptide-binding specificities of HLA-C: a general strategy to determine the specificity of any MHC class I molecule. <i>Journal of Immunology</i> , 2014 , 193, 4790-802	5.3	51
152	Adoptive cell therapy with tumor-infiltrating lymphocytes in patients with metastatic ovarian cancer: a pilot study. <i>Oncot Immunology</i> , 2018 , 7, e1502905	7.2	50
151	HLArestrictor--a tool for patient-specific predictions of HLA restriction elements and optimal epitopes within peptides. <i>Immunogenetics</i> , 2011 , 63, 43-55	3.2	49
150	Broadly immunogenic HLA class I supertype-restricted elite CTL epitopes recognized in a diverse population infected with different HIV-1 subtypes. <i>Journal of Immunology</i> , 2008 , 180, 5092-100	5.3	49
149	Predicting HLA CD4 Immunogenicity in Human Populations. <i>Frontiers in Immunology</i> , 2018 , 9, 1369	8.4	48
148	High-throughput sequencing enhanced phage display enables the identification of patient-specific epitope motifs in serum. <i>Scientific Reports</i> , 2015 , 5, 12913	4.9	46
147	Induction of foot-and-mouth disease virus-specific cytotoxic T cell killing by vaccination. <i>Vaccine Journal</i> , 2011 , 18, 280-8		45
146	MHC motif viewer. <i>Immunogenetics</i> , 2008 , 60, 759-65	3.2	45
145	The validity of predicted T-cell epitopes. <i>Trends in Biotechnology</i> , 2006 , 24, 537-8	15.1	45
144	No evidence for the use of DIR, D-D fusions, chromosome 15 open reading frames or VH replacement in the peripheral repertoire was found on application of an improved algorithm, JointML, to 6329 human immunoglobulin H rearrangements. <i>Immunology</i> , 2006 , 119, 265-77	7.8	45

143	Defining the HLA class I-associated viral antigen repertoire from HIV-1-infected human cells. <i>European Journal of Immunology</i> , 2016 , 46, 60-9	6.1	45
142	Footprints of antigen processing boost MHC class II natural ligand predictions. <i>Genome Medicine</i> , 2018 , 10, 84	14.4	45
141	Immunological Bioinformatics 2005 ,		44
140	Antibody Specific B-Cell Epitope Predictions: Leveraging Information From Antibody-Antigen Protein Complexes. <i>Frontiers in Immunology</i> , 2019 , 10, 298	8.4	43
139	An automated benchmarking platform for MHC class II binding prediction methods. <i>Bioinformatics</i> , 2018 , 34, 1522-1528	7.2	43
138	State of the art and challenges in sequence based T-cell epitope prediction. <i>Immunome Research</i> , 2010 , 6 Suppl 2, S3		43
137	MHC-I Ligand Discovery Using Targeted Database Searches of Mass Spectrometry Data: Implications for T-Cell Immunotherapies. <i>Journal of Proteome Research</i> , 2017 , 16, 1806-1816	5.6	42
136	LYRA, a webserver for lymphocyte receptor structural modeling. <i>Nucleic Acids Research</i> , 2015 , 43, W349-55.1		41
135	Limitations of Ab initio predictions of peptide binding to MHC class II molecules. <i>PLoS ONE</i> , 2010 , 5, e9237		39
134	NNAlign: a platform to construct and evaluate artificial neural network models of receptor-ligand interactions. <i>Nucleic Acids Research</i> , 2017 , 45, W344-W349	20.1	38
133	NetTCR: sequence-based prediction of TCR binding to peptide-MHC complexes using convolutional neural networks		37
132	Unconventional Peptide Presentation by Major Histocompatibility Complex (MHC) Class I Allele HLA-A*02:01: BREAKING CONFINEMENT. <i>Journal of Biological Chemistry</i> , 2017 , 292, 5262-5270	5.4	36
131	TRAV1-2 CD8 T-cells including oligoconal expansions of MAIT cells are enriched in the airways in human tuberculosis. <i>Communications Biology</i> , 2019 , 2, 203	6.7	36
130	NNAlign_MA; MHC Peptidome Deconvolution for Accurate MHC Binding Motif Characterization and Improved T-cell Epitope Predictions. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 2459-2477	7.6	36
129	NetTepi: an integrated method for the prediction of T cell epitopes. <i>Immunogenetics</i> , 2014 , 66, 449-56	3.2	36
128	Metagenomic Analysis of Therapeutic PYO Phage Cocktails from 1997 to 2014. <i>Viruses</i> , 2017 , 9,	6.2	36
127	Porcine major histocompatibility complex (MHC) class I molecules and analysis of their peptide-binding specificities. <i>Immunogenetics</i> , 2011 , 63, 821-34	3.2	35
126	Ebolavirus comparative genomics. <i>FEMS Microbiology Reviews</i> , 2015 , 39, 764-78	15.1	34

125	Computational Tools for the Identification and Interpretation of Sequence Motifs in Immunopeptidomes. <i>Proteomics</i> , 2018 , 18, e1700252	4.8	33
124	Predictions versus high-throughput experiments in T-cell epitope discovery: competition or synergy?. <i>Expert Review of Vaccines</i> , 2012 , 11, 43-54	5.2	33
123	MetaPhinder-Identifying Bacteriophage Sequences in Metagenomic Data Sets. <i>PLoS ONE</i> , 2016 , 11, e0163111	3.1	32
122	Improved peptide-MHC class II interaction prediction through integration of eluted ligand and peptide affinity data. <i>Immunogenetics</i> , 2019 , 71, 445-454	3.2	31
121	Determination of a Predictive Cleavage Motif for Eluted Major Histocompatibility Complex Class II Ligands. <i>Frontiers in Immunology</i> , 2018 , 9, 1795	8.4	31
120	Disentangling evolutionary signals: conservation, specificity determining positions and coevolution. Implication for catalytic residue prediction. <i>BMC Bioinformatics</i> , 2012 , 13, 235	3.6	31
119	The MHC motif viewer: a visualization tool for MHC binding motifs. <i>Current Protocols in Immunology</i> , 2010 , Chapter 18, Unit 18.17	4	30
118	Random-lattice models and simulation algorithms for the phase equilibria in two-dimensional condensed systems of particles with coupled internal and translational degrees of freedom. <i>Physical Review E</i> , 1996 , 54, 6889-6905	2.4	30
117	Benchmarking predictions of MHC class I restricted T cell epitopes in a comprehensively studied model system. <i>PLoS Computational Biology</i> , 2020 , 16, e1007757	5	29
116	Identification of CD8+ T cell epitopes in the West Nile virus polyprotein by reverse-immunology using NetCTL. <i>PLoS ONE</i> , 2010 , 5, e12697	3.7	29
115	Interdisciplinary analysis of HIV-specific CD8+ T cell responses against variant epitopes reveals restricted TCR promiscuity. <i>Journal of Immunology</i> , 2010 , 184, 5383-91	5.3	29
114	Designing bovine T cell vaccines via reverse immunology. <i>Ticks and Tick-borne Diseases</i> , 2012 , 3, 188-92	3.6	27
113	Citrullination only infrequently impacts peptide binding to HLA class II MHC. <i>PLoS ONE</i> , 2017 , 12, e0177140	3.9	27
112	Adoptive cell therapy in combination with checkpoint inhibitors in ovarian cancer. <i>Oncotarget</i> , 2020 , 11, 2092-2105	3.3	27
111	The Intergenic Recombinant HLA-B*46:01 Has a Distinctive Peptidome that Includes KIR2DL3 Ligands. <i>Cell Reports</i> , 2017 , 19, 1394-1405	10.6	26
110	Human leukocyte antigen (HLA) class I restricted epitope discovery in yellow fever and dengue viruses: importance of HLA binding strength. <i>PLoS ONE</i> , 2011 , 6, e26494	3.7	26
109	Use of "one-pot, mix-and-read" peptide-MHC class I tetramers and predictive algorithms to improve detection of cytotoxic T lymphocyte responses in cattle. <i>Veterinary Research</i> , 2014 , 45, 50	3.8	25
108	Systematic characterisation of cellular localisation and expression profiles of proteins containing MHC ligands. <i>PLoS ONE</i> , 2009 , 4, e7448	3.7	25

107	Identification of the cognate peptide-MHC target of T cell receptors using molecular modeling and force field scoring. <i>Molecular Immunology</i> , 2018 , 94, 91-97	4.3	24
106	Evaluation of peptide selection approaches for epitope-based vaccine design. <i>Tissue Antigens</i> , 2013 , 82, 243-51		24
105	Modeling lipid-sterol bilayers: applications to structural evolution, lateral diffusion, and rafts. <i>Methods in Enzymology</i> , 2004 , 383, 198-229	1.7	24
104	Characterizing the binding motifs of 11 common human HLA-DP and HLA-DQ molecules using NNAlign. <i>Immunology</i> , 2012 , 136, 306-11	7.8	22
103	The Immune Epitope Database and Analysis Resource Program 2003-2018: reflections and outlook. <i>Immunogenetics</i> , 2020 , 72, 57-76	3.2	22
102	T-cell recognition is shaped by epitope sequence conservation in the host proteome and microbiome. <i>Immunology</i> , 2016 , 148, 34-9	7.8	22
101	Improved Prediction of Bovine Leucocyte Antigens (BoLA) Presented Ligands by Use of Mass-Spectrometry-Determined Ligand and in Vitro Binding Data. <i>Journal of Proteome Research</i> , 2018 , 17, 559-567	5.6	22
100	T-Cell Receptor Cognate Target Prediction Based on Paired H ₂ and I ₂ Chain Sequence and Structural CDR Loop Similarities. <i>Frontiers in Immunology</i> , 2019 , 10, 2080	8.4	21
99	HLA class I binding 9mer peptides from influenza A virus induce CD4 T cell responses. <i>PLoS ONE</i> , 2010 , 5, e10533	3.7	20
98	Epitope Specific Antibodies and T Cell Receptors in the Immune Epitope Database. <i>Frontiers in Immunology</i> , 2018 , 9, 2688	8.4	20
97	Magnetic ordering in the three-dimensional site-disordered Heisenberg model. <i>Physical Review B</i> , 1996 , 53, 343-349	3.3	19
96	Next-generation ELISA diagnostic assay for Chagas Disease based on the combination of short peptidic epitopes. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005972	4.8	19
95	Characterization of HIV-specific CD4+ T cell responses against peptides selected with broad population and pathogen coverage. <i>PLoS ONE</i> , 2012 , 7, e39874	3.7	19
94	Machine learning reveals a non-canonical mode of peptide binding to MHC class II molecules. <i>Immunology</i> , 2017 , 152, 255-264	7.8	18
93	Immunoinformatics: Predicting Peptide-MHC Binding. <i>Annual Review of Biomedical Data Science</i> , 2020 , 3, 191-215	5.6	18
92	TAP-Independent MHC Class I Presentation. <i>Current Immunology Reviews</i> , 2006 , 2, 233-245	1.3	18
91	Insecticide-treated bed nets reduce plasma antibody levels and limit the repertoire of antibodies to Plasmodium falciparum variant surface antigens. <i>Vaccine Journal</i> , 2001 , 8, 1289-91		18
90	TCR-pMHC models: Structural modelling of TCR-pMHC class I complexes. <i>Scientific Reports</i> , 2019 , 9, 14530	4.9	17

89	Identification of peptides from foot-and-mouth disease virus structural proteins bound by class I swine leukocyte antigen (SLA) alleles, SLA-1*0401 and SLA-2*0401. <i>Animal Genetics</i> , 2013 , 44, 251-8	2.5	17
88	Identification and HLA-tetramer-validation of human CD4+ and CD8+ T cell responses against HCMV proteins IE1 and IE2. <i>PLoS ONE</i> , 2014 , 9, e94892	3.7	17
87	Structural properties of MHC class II ligands, implications for the prediction of MHC class II epitopes. <i>PLoS ONE</i> , 2010 , 5, e15877	3.7	17
86	The peptide-binding specificity of HLA-A*3001 demonstrates membership of the HLA-A3 supertype. <i>Immunogenetics</i> , 2008 , 60, 633-43	3.2	17
85	Model of a sub-main transition in phospholipid bilayers. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1996 , 1283, 170-6	3.8	17
84	MS-Rescue: A Computational Pipeline to Increase the Quality and Yield of Immunopeptidomics Experiments. <i>Proteomics</i> , 2019 , 19, e1800357	4.8	17
83	NetMHCpan 4.0: Improved peptide-MHC class I interaction predictions integrating eluted ligand and peptide binding affinity data		16
82	Modelling the human immune system by combining bioinformatics and systems biology approaches. <i>Journal of Biological Physics</i> , 2006 , 32, 335-53	1.6	15
81	TCRMatch: Predicting T-Cell Receptor Specificity Based on Sequence Similarity to Previously Characterized Receptors. <i>Frontiers in Immunology</i> , 2021 , 12, 640725	8.4	15
80	Characterization of binding specificities of bovine leucocyte class I molecules: impacts for rational epitope discovery. <i>Immunogenetics</i> , 2014 , 66, 705-18	3.2	14
79	SigniSite: Identification of residue-level genotype-phenotype correlations in protein multiple sequence alignments. <i>Nucleic Acids Research</i> , 2013 , 41, W286-91	20.1	14
78	Bioinformatics Tools for the Prediction of T-Cell Epitopes. <i>Methods in Molecular Biology</i> , 2018 , 1785, 269-281	1.4	13
77	Linear epitope mapping of peanut allergens demonstrates individualized and persistent antibody-binding patterns. <i>Journal of Allergy and Clinical Immunology</i> , 2016 , 138, 1728-1730	11.5	13
76	In silico prediction of human pathogenicity in the ϵ proteobacteria. <i>PLoS ONE</i> , 2010 , 5, e13680	3.7	13
75	Selecting informative data for developing peptide-MHC binding predictors using a query by committee approach. <i>Neural Computation</i> , 2003 , 15, 2931-42	2.9	13
74	The cancer exome generated by alternative mRNA splicing dilutes predicted HLA class I epitope density. <i>PLoS ONE</i> , 2012 , 7, e38670	3.7	13
73	A modern approach for epitope prediction: identification of foot-and-mouth disease virus peptides binding bovine leukocyte antigen (BoLA) class I molecules. <i>Immunogenetics</i> , 2015 , 67, 691-703	3.2	12
72	In vitro 4-1BB stimulation promotes expansion of CD8 tumor-infiltrating lymphocytes from various sarcoma subtypes. <i>Cancer Immunology, Immunotherapy</i> , 2020 , 69, 2179-2191	7.4	11

71	A novel approach to probe host-pathogen interactions of bovine digital dermatitis, a model of a complex polymicrobial infection. <i>BMC Genomics</i> , 2016 , 17, 987	4.5	11
70	A combined prediction strategy increases identification of peptides bound with high affinity and stability to porcine MHC class I molecules SLA-1*04:01, SLA-2*04:01, and SLA-3*04:01. <i>Immunogenetics</i> , 2016 , 68, 157-65	3.2	11
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