Morten Nielsen

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

232	19,983	65	139
papers	citations	h-index	g-index
247	26,464	7.3	7.19
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
232	Accurate MHC Motif Deconvolution of Immunopeptidomics Data Reveals a Significant Contribution of DRB3, 4 and 5 to the Total DR Immunopeptidome.. *Frontiers in Immunology*, **2022**, 13, 835454	8.4	0
231	Combined assessment of MHC binding and antigen abundance improves T cell epitope predictions.. *IScience*, **2022**, 103850	6.1	0
230	Tracking SARS-CoV-2 mutations and variants through the COG-UK-Mutation Explorer.. *Virus Evolution*, **2022**, 8, veac023	3.7	1
229	Neoantigen-specific CD8 T cell responses in the peripheral blood following PD-L1 blockade might predict therapy outcome in metastatic urothelial carcinoma.. *Nature Communications*, **2022**, 13, 1935	17.4	3
228	Neoantigen-reactive CD8+ T cells affect clinical outcome of adoptive transfer with tumor-infiltrating lymphocytes in melanoma. *Journal of Clinical Investigation*, **2021**,	15.9	5
227	Adoptive cell therapy with tumor-infiltrating lymphocytes supported by checkpoint inhibition across multiple solid cancer types **2021**, 9,		3
226	Rapid Identification of the Tumor-Specific Reactive TIL Repertoire Combined Detection of CD137, TNF, and IFN▯Following Recognition of Autologous Tumor-Antigens. *Frontiers in Immunology*, **2021**, 12, 705422	8.4	0
225	Integral Use of Immunopeptidomics and Immunoinformatics for the Characterization of Antigen Presentation and Rational Identification of BoLA-DR-Presented Peptides and Epitopes. *Journal of Immunology*, **2021**, 206, 2489-2497	5.3	2
224	TCRMatch: Predicting T-Cell Receptor Specificity Based on Sequence Similarity to Previously Characterized Receptors. *Frontiers in Immunology*, **2021**, 12, 640725	8.4	15
223	SARS-CoV-2 genome-wide T cell epitope mapping reveals immunodominance and substantial CD8 T cell activation in COVID-19 patients. *Science Immunology*, **2021**, 6,	28	65
222	Large-Scale Identification of T-Cell Epitopes Derived From Severe Acute Respiratory Syndrome Coronavirus 2 for the Development of Peptide Vaccines Against Coronavirus Disease 2019. *Journal of Infectious Diseases*, **2021**, 224, 956-966	7	1
221	Clinical efficacy of T-cell therapy after short-term BRAF-inhibitor priming in patients with checkpoint inhibitor-resistant metastatic melanoma **2021**, 9,		3
220	APRANK: Computational Prioritization of Antigenic Proteins and Peptides From Complete Pathogen Proteomes. *Frontiers in Immunology*, **2021**, 12, 702552	8.4	1
219	Improved prediction of HLA antigen presentation hotspots: Applications for immunogenicity risk assessment of therapeutic proteins. *Immunology*, **2021**, 162, 208-219	7.8	2
218	Utilizing Computational Machine Learning Tools to Understand Immunogenic Breadth in the Context of a CD8 T-Cell Mediated HIV Response. *Frontiers in Immunology*, **2021**, 12, 609884	8.4	3
217	Transcriptomic signatures of tumors undergoing T cell attack. *Cancer Immunology, Immunotherapy*, **2021**, 1	7.4	0
216	PopCover-2.0. Improved Selection of Peptide Sets With Optimal HLA and Pathogen Diversity Coverage. *Frontiers in Immunology*, **2021**, 12, 728936	8.4	1

215	Selective HLA restriction enables the evaluation and interpretation of immunogenic breadth at comparable levels to that observed with broader HLA distribution. *Proteomics*, **2021**, 21, e2100121	4.8	0
214	The Cancer Epitope Database and Analysis Resource: A Blueprint for the Establishment of a New Bioinformatics Resource for Use by the Cancer Immunology Community. *Frontiers in Immunology*, **2021**, 12, 735609	8.4	2
213	NetTCR-2.0 enables accurate prediction of TCR-peptide binding by using paired TCR▯and ▯ sequence data. *Communications Biology*, **2021**, 4, 1060	6.7	11
212	CD4 T Cell Responses to in Immune Cattle Recognize a Diverse Set of Parasite Antigens Presented on the Surface of Infected Lymphoblasts. *Journal of Immunology*, **2021**, 207, 1965-1977	5.3	1
211	NetMHCphosPan - Pan-specific prediction of MHC class I antigen presentation of phosphorylated ligands. *ImmunoInformatics*, **2021**, 1-2, 100005		1
210	Immunoinformatics: Predicting Peptide▯MHC Binding. *Annual Review of Biomedical Data Science*, **2020**, 3, 191-215	5.6	18
209	HLA Class II Specificity Assessed by High-Density Peptide Microarray Interactions. *Journal of Immunology*, **2020**, 205, 290-299	5.3	7
208	In vitro 4-1BB stimulation promotes expansion of CD8 tumor-infiltrating lymphocytes from various sarcoma subtypes. *Cancer Immunology, Immunotherapy*, **2020**, 69, 2179-2191	7.4	11
207	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. *Nucleic Acids Research*, **2020**, 48, W449-W454	20.1	299
206	Benchmarking predictions of MHC class I restricted T cell epitopes in a comprehensively studied model system. *PLoS Computational Biology*, **2020**, 16, e1007757	5	29
205	Evaluation of T-Cell Responses Against Shared Melanoma Associated Antigens and Predicted Neoantigens in Cutaneous Melanoma Patients Treated With the CSF-470 Allogeneic Cell Vaccine Plus BCG and GM-CSF. *Frontiers in Immunology*, **2020**, 11, 1147	8.4	1
204	Immunopeptidomic Data Integration to Artificial Neural Networks Enhances Protein-Drug Immunogenicity Prediction. *Frontiers in Immunology*, **2020**, 11, 1304	8.4	6
203	In Silico Guided Discovery of Novel Class I and II Epitopes Recognized by T Cells from ChagasO Disease Patients. *Journal of Immunology*, **2020**, 204, 1571-1581	5.3	2
202	Factors Influencing the Prevalence of Resistance-Associated Substitutions in NS5A Protein in Treatment-Naive Patients with Chronic Hepatitis C. *Biomedicines*, **2020**, 8,	4.8	1
201	Improved Prediction of MHC II Antigen Presentation through Integration and Motif Deconvolution of Mass Spectrometry MHC Eluted Ligand Data. *Journal of Proteome Research*, **2020**, 19, 2304-2315	5.6	106
200	T Cell Epitope Predictions. *Annual Review of Immunology*, **2020**, 38, 123-145	34.7	69
199	Adoptive cell therapy in combination with checkpoint inhibitors in ovarian cancer. *Oncotarget*, **2020** , 11, 2092-2105	3.3	27
198	The Immune Epitope Database and Analysis Resource Program 2003-2018: reflections and outlook. *Immunogenetics*, **2020**, 72, 57-76	3.2	22

197	Qualitative Analysis of Tumor-Infiltrating Lymphocytes across Human Tumor Types Reveals a Higher Proportion of Bystander CD8 T Cells in Non-Melanoma Cancers Compared to Melanoma. *Cancers*, **2020**, 12,	6.6	6
196	Unbiased Characterization of Peptide-HLA Class II Interactions Based on Large-Scale Peptide Microarrays; Assessment of the Impact on HLA Class II Ligand and Epitope Prediction. *Frontiers in Immunology*, **2020**, 11, 1705	8.4	1
195	Robust T Cell Immunity in Convalescent Individuals with Asymptomatic or Mild COVID-19. *Cell*, **2020** , 183, 158-168.e14	56.2	955
194	A Systematic, Unbiased Mapping of CD8 and CD4 T Cell Epitopes in Yellow Fever Vaccinees. *Frontiers in Immunology*, **2020**, 11, 1836	8.4	6
193	TRAV1-2 CD8 T-cells including oligoconal expansions of MAIT cells are enriched in the airways in human tuberculosis. *Communications Biology*, **2019**, 2, 203	6.7	36
192	Improved peptide-MHC class II interaction prediction through integration of eluted ligand and peptide affinity data. *Immunogenetics*, **2019**, 71, 445-454	3.2	31
191	IEDB-AR: immune epitope database-analysis resource in 2019. *Nucleic Acids Research*, **2019**, 47, W502-W506	20.1	136
190	Antibody Specific B-Cell Epitope Predictions: Leveraging Information From Antibody-Antigen Protein Complexes. *Frontiers in Immunology*, **2019**, 10, 298	8.4	43
189	T-Cell Receptor Cognate Target Prediction Based on Paired □and □Chain Sequence and Structural CDR Loop Similarities. *Frontiers in Immunology*, **2019**, 10, 2080	8.4	21
188	TCRpMHCmodels: Structural modelling of TCR-pMHC class I complexes. *Scientific Reports*, **2019**, 9, 14530	4.9	17
187	Benchmark datasets of immune receptor-epitope structural complexes. *BMC Bioinformatics*, **2019**, 20, 490	3.6	6
186	NNAlign_MA; MHC Peptidome Deconvolution for Accurate MHC Binding Motif Characterization and Improved T-cell Epitope Predictions. *Molecular and Cellular Proteomics*, **2019**, 18, 2459-2477	7.6	36
185	Enhancing Mass Spectrometry-Based MHC-I Peptide Identification Through a Targeted Database Search Approach. *Methods in Molecular Biology*, **2019**, 2024, 301-307	1.4	1
184	NetSurfP-2.0: Improved prediction of protein structural features by integrated deep learning. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 520-527	4.2	214
183	Immunization With the CSF-470 Vaccine Plus BCG and rhGM-CSF Induced in a Cutaneous Melanoma Patient a TCR□Repertoire Found at Vaccination Site and Tumor Infiltrating Lymphocytes That Persisted in Blood. *Frontiers in Immunology*, **2019**, 10, 2213	8.4	2
182	Characterization of Antigenic MHC-Class-I-Restricted T Cell Epitopes in the Glycoprotein of Ebolavirus. *Cell Reports*, **2019**, 29, 2537-2545.e3	10.6	4
181	A generic deep convolutional neural network framework for prediction of receptor-ligand interactions-NetPhosPan: application to kinase phosphorylation prediction. *Bioinformatics*, **2019**, 35, 1098-1107	7.2	11
180	MS-Rescue: A Computational Pipeline to Increase the Quality and Yield of Immunopeptidomics Experiments. *Proteomics*, **2019**, 19, e1800357	4.8	17

179	Predicted MHC peptide binding promiscuity explains MHC class I ÒhotspotsÓ of antigen presentation defined by mass spectrometry eluted ligand data. *Immunology*, **2018**, 154, 407-417	7.8	8
178	NetH2pan: A Computational Tool to Guide MHC Peptide Prediction on Murine Tumors. *Cancer Immunology Research*, **2018**, 6, 636-644	12.5	9
177	Identification of the cognate peptide-MHC target of T cell receptors using molecular modeling and force field scoring. *Molecular Immunology*, **2018**, 94, 91-97	4.3	24
176	Computational Tools for the Identification and Interpretation of Sequence Motifs in Immunopeptidomes. *Proteomics*, **2018**, 18, e1700252	4.8	33
175	Improved methods for predicting peptide binding affinity to MHC class II molecules. *Immunology*, **2018**, 154, 394-406	7.8	343
174	An automated benchmarking platform for MHC class II binding prediction methods. *Bioinformatics*, **2018**, 34, 1522-1528	7.2	43
173	Bioinformatics Tools for the Prediction of T-Cell Epitopes. *Methods in Molecular Biology*, **2018**, 1785, 269-281	1.4	13
172	The SysteMHC Atlas project. *Nucleic Acids Research*, **2018**, 46, D1237-D1247	20.1	87
171	Determination of a Predictive Cleavage Motif for Eluted Major Histocompatibility Complex Class II Ligands. *Frontiers in Immunology*, **2018**, 9, 1795	8.4	31
170	Predicting HLA CD4 Immunogenicity in Human Populations. *Frontiers in Immunology*, **2018**, 9, 1369	8.4	48
169	Improved Prediction of Bovine Leucocyte Antigens (BoLA) Presented Ligands by Use of Mass-Spectrometry-Determined Ligand and in Vitro Binding Data. *Journal of Proteome Research*, **2018**, 17, 559-567	5.6	22
168	T cell receptor fingerprinting enables in-depth characterization of the interactions governing recognition of peptide-MHC complexes. *Nature Biotechnology*, **2018**,	44.5	57
167	Footprints of antigen processing boost MHC class II natural ligand predictions. *Genome Medicine*, **2018**, 10, 84	14.4	45
166	Epitope Specific Antibodies and T Cell Receptors in the Immune Epitope Database. *Frontiers in Immunology*, **2018**, 9, 2688	8.4	20
165	Use of a Regression Model to Study Host-Genomic Determinants of Phage Susceptibility in MRSA. *Antibiotics*, **2018**, 7,	4.9	4
164	Adoptive cell therapy with tumor-infiltrating lymphocytes in patients with metastatic ovarian cancer: a pilot study. *OncoImmunology*, **2018**, 7, e1502905	7.2	50
163	Unconventional Peptide Presentation by Major Histocompatibility Complex (MHC) Class I Allele HLA-A*02:01: BREAKING CONFINEMENT. *Journal of Biological Chemistry*, **2017**, 292, 5262-5270	5.4	36
162	MuPeXI: prediction of neo-epitopes from tumor sequencing data. *Cancer Immunology, Immunotherapy*, **2017**, 66, 1123-1130	7.4	95

161	Prediction and in vitro verification of potential CTL epitopes conserved among PRRSV-2 strains. *Immunogenetics*, **2017**, 69, 689-702	3.2	7
160	The Intergenic Recombinant HLA-B*46:01 Has a Distinctive Peptidome that Includes KIR2DL3 Ligands. *Cell Reports*, **2017**, 19, 1394-1405	10.6	26
159	BepiPred-2.0: improving sequence-based B-cell epitope prediction using conformational epitopes. *Nucleic Acids Research*, **2017**, 45, W24-W29	20.1	545
158	Machine learning reveals a non-canonical mode of peptide binding to MHC class II molecules. *Immunology*, **2017**, 152, 255-264	7.8	18
157	MHC-I Ligand Discovery Using Targeted Database Searches of Mass Spectrometry Data: Implications for T-Cell Immunotherapies. *Journal of Proteome Research*, **2017**, 16, 1806-1816	5.6	42
156	NetMHCpan-4.0: Improved Peptide-MHC Class I Interaction Predictions Integrating Eluted Ligand and Peptide Binding Affinity Data. *Journal of Immunology*, **2017**, 199, 3360-3368	5.3	645
155	GibbsCluster: unsupervised clustering and alignment of peptide sequences. *Nucleic Acids Research*, **2017**, 45, W458-W463	20.1	94
154	MIToS.jl: mutual information tools for protein sequence analysis in the Julia language. *Bioinformatics*, **2017**, 33, 564-565	7.2	5
153	An introduction to deep learning on biological sequence data: examples and solutions. *Bioinformatics*, **2017**, 33, 3685-3690	7.2	81
152	Protein features as determinants of wild-type glycoside hydrolase thermostability. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 2036-2044	4.2	4
151	NNAlign: a platform to construct and evaluate artificial neural network models of receptor-ligand interactions. *Nucleic Acids Research*, **2017**, 45, W344-W349	20.1	38
150	Metagenomic Analysis of Therapeutic PYO Phage Cocktails from 1997 to 2014. *Viruses*, **2017**, 9,	6.2	36
149	An Analysis of Natural T Cell Responses to Predicted Tumor Neoepitopes. *Frontiers in Immunology*, **2017**, 8, 1566	8.4	51
148	Next-generation ELISA diagnostic assay for Chagas Disease based on the combination of short peptidic epitopes. *PLoS Neglected Tropical Diseases*, **2017**, 11, e0005972	4.8	19
147	ArrayPitope: Automated Analysis of Amino Acid Substitutions for Peptide Microarray-Based Antibody Epitope Mapping. *PLoS ONE*, **2017**, 12, e0168453	3.7	8
146	Citrullination only infrequently impacts peptide binding to HLA class II MHC. *PLoS ONE*, **2017**, 12, e0177140	3.7	27
145	Identification of immediate early gene products of bovine herpes virus 1 (BHV-1) as dominant antigens recognized by CD8 T cells in immune cattle. *Journal of General Virology*, **2017**, 98, 1843-1854	4.9	8
144	Linear epitope mapping of peanut allergens demonstrates individualized and persistent antibody-binding patterns. *Journal of Allergy and Clinical Immunology*, **2016**, 138, 1728-1730	11.5	13

143	A novel approach to probe host-pathogen interactions of bovine digital dermatitis, a model of a complex polymicrobial infection. *BMC Genomics*, **2016**, 17, 987	4.5	11
142	NetMHCpan-3.0; improved prediction of binding to MHC class I molecules integrating information from multiple receptor and peptide length datasets. *Genome Medicine*, **2016**, 8, 33	14.4	315
141	The Length Distribution of Class I-Restricted T Cell Epitopes Is Determined by Both Peptide Supply and MHC Allele-Specific Binding Preference. *Journal of Immunology*, **2016**, 196, 1480-7	5.3	106
140	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. *Immunogenetics*, **2016**, 68, 157-65	3.2	11
139	Gapped sequence alignment using artificial neural networks: application to the MHC class I system. *Bioinformatics*, **2016**, 32, 511-7	7.2	570
138	Immunogenicity of HLA Class I and II Double Restricted Influenza A-Derived Peptides. *PLoS ONE*, **2016**, 11, e0145629	3.7	8
137	MetaPhinder-Identifying Bacteriophage Sequences in Metagenomic Data Sets. *PLoS ONE*, **2016**, 11, e0163111	3.7	32
136	Toxoplasma gondii peptide ligands open the gate of the HLA class I binding groove. *ELife*, **2016**, 5,	8.9	55
135	HostPhinder: A Phage Host Prediction Tool. *Viruses*, **2016**, 8,	6.2	63
134	The Gly16 Allele of the Gly16Arg Single-Nucleotide Polymorphism in the Adrenergic Receptor Gene Augments Perioperative Use of Vasopressors: A Retrospective Cohort Study. *Anesthesia and Analgesia*, **2016**, 122, 1385-93	3.9	6
133	Pan-Specific Prediction of Peptide-MHC Class I Complex Stability, a Correlate of T Cell Immunogenicity. *Journal of Immunology*, **2016**, 197, 1517-24	5.3	103
132	T-cell recognition is shaped by epitope sequence conservation in the host proteome and microbiome. *Immunology*, **2016**, 148, 34-9	7.8	22
131	Sequence diversity between class I MHC loci of African native and introduced Bos taurus cattle in Theileria parva endemic regions: in silico peptide binding prediction identifies distinct functional clusters. *Immunogenetics*, **2016**, 68, 339-52	3.2	4
130	Expanding specificity of class I restricted CD8 T cells for viral epitopes following multiple inoculations of swine with a human adenovirus vectored foot-and-mouth disease virus (FMDV) vaccine. *Veterinary Immunology and Immunopathology*, **2016**, 181, 59-67	2	7
129	Defining the HLA class I-associated viral antigen repertoire from HIV-1-infected human cells. *European Journal of Immunology*, **2016**, 46, 60-9	6.1	45
128	Automated benchmarking of peptide-MHC class I binding predictions. *Bioinformatics*, **2015**, 31, 2174-81	7.2	100
127	High-throughput sequencing enhanced phage display enables the identification of patient-specific epitope motifs in serum. *Scientific Reports*, **2015**, 5, 12913	4.9	46
126	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. *Immunogenetics*, **2015**, 67, 73-84	3.2	63

125	LYRA, a webserver for lymphocyte receptor structural modeling. *Nucleic Acids Research*, **2015**, 43, W349-55	20.1	41
124	A modern approach for epitope prediction: identification of foot-and-mouth disease virus peptides binding bovine leukocyte antigen (BoLA) class I molecules. *Immunogenetics*, **2015**, 67, 691-703	3.2	12
123	Towards High-throughput Immunomics for Infectious Diseases: Use of Next-generation Peptide Microarrays for Rapid Discovery and Mapping of Antigenic Determinants. *Molecular and Cellular Proteomics*, **2015**, 14, 1871-84	7.6	61
122	Accurate pan-specific prediction of peptide-MHC class II binding affinity with improved binding core identification. *Immunogenetics*, **2015**, 67, 641-50	3.2	200
121	Ebolavirus comparative genomics. *FEMS Microbiology Reviews*, **2015**, 39, 764-78	15.1	34
120	Unmasking determinants of specificity in the human kinome. *Cell*, **2015**, 163, 187-201	56.2	58
119	Prediction of Antibody Epitopes. *Methods in Molecular Biology*, **2015**, 1348, 23-32	1.4	6
118	Improved pan-specific MHC class I peptide-binding predictions using a novel representation of the MHC-binding cleft environment. *Tissue Antigens*, **2014**, 83, 94-100		9
117	Characterization of binding specificities of bovine leucocyte class I molecules: impacts for rational epitope discovery. *Immunogenetics*, **2014**, 66, 705-18	3.2	14
116	Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions. *BMC Bioinformatics*, **2014**, 15, 241	3.6	63
115	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. *Veterinary Research*, **2014**, 45, 50	3.8	25
114	NetTepi: an integrated method for the prediction of T cell epitopes. *Immunogenetics*, **2014**, 66, 449-56	3.2	36
113	Identification and HLA-tetramer-validation of human CD4+ and CD8+ T cell responses against HCMV proteins IE1 and IE2. *PLoS ONE*, **2014**, 9, e94892	3.7	17
112	The interplay of sequence conservation and T cell immune recognition **2014**,		1
111	Uncovering the peptide-binding specificities of HLA-C: a general strategy to determine the specificity of any MHC class I molecule. *Journal of Immunology*, **2014**, 193, 4790-802	5.3	51
110	MR1-restricted MAIT cells display ligand discrimination and pathogen selectivity through distinct T cell receptor usage. *Journal of Experimental Medicine*, **2014**, 211, 1601-10	16.6	144
109	NetMHCstab - predicting stability of peptide-MHC-I complexes; impacts for cytotoxic T lymphocyte epitope discovery. *Immunology*, **2014**, 141, 18-26	7.8	83
108	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. *Immunogenetics*, **2013**, 65, 711-24	3.2	192

107	MHCcluster, a method for functional clustering of MHC molecules. *Immunogenetics*, **2013**, 65, 655-65	3.2	77
106	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	3.2	10
105	Evaluation of peptide selection approaches for epitope-based vaccine design. *Tissue Antigens*, **2013** , 82, 243-51		24
104	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. *Animal Genetics*, **2013**, 44, 251-8	2.5	17
103	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	1.4	2
102	Structural analysis of B-cell epitopes in antibody:protein complexes. *Molecular Immunology*, **2013**, 53, 24-34	4.3	173
101	SigniSite: Identification of residue-level genotype-phenotype correlations in protein multiple sequence alignments. *Nucleic Acids Research*, **2013**, 41, W286-91	20.1	14
100	Simultaneous alignment and clustering of peptide data using a Gibbs sampling approach. *Bioinformatics*, **2013**, 29, 8-14	7.2	81
99	MISTIC: Mutual information server to infer coevolution. *Nucleic Acids Research*, **2013**, 41, W8-14	20.1	113
98	Characterizing the binding motifs of 11 common human HLA-DP and HLA-DQ molecules using NNAlign. *Immunology*, **2012**, 136, 306-11	7.8	22
97	NetMHCcons: a consensus method for the major histocompatibility complex class I predictions. *Immunogenetics*, **2012**, 64, 177-86	3.2	233
96	Designing bovine T cell vaccines via reverse immunology. *Ticks and Tick-borne Diseases*, **2012**, 3, 188-92	3.6	27
95	Predictions versus high-throughput experiments in T-cell epitope discovery: competition or synergy?. *Expert Review of Vaccines*, **2012**, 11, 43-54	5.2	33
94	Immune epitope database analysis resource. *Nucleic Acids Research*, **2012**, 40, W525-30	20.1	322
93	Disentangling evolutionary signals: conservation, specificity determining positions and coevolution. Implication for catalytic residue prediction. *BMC Bioinformatics*, **2012**, 13, 235	3.6	31
92	Peptide-MHC class I stability is a better predictor than peptide affinity of CTL immunogenicity. *European Journal of Immunology*, **2012**, 42, 1405-16	6.1	140
91	Reliable B cell epitope predictions: impacts of method development and improved benchmarking. *PLoS Computational Biology*, **2012**, 8, e1002829	5	367
90	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. *Nucleic Acids Research*, **2012**, 40, W281-7	20.1	259

89	The cancer exome generated by alternative mRNA splicing dilutes predicted HLA class I epitope density. *PLoS ONE*, **2012**, 7, e38670	3.7	13
88	Characterization of HIV-specific CD4+ T cell responses against peptides selected with broad population and pathogen coverage. *PLoS ONE*, **2012**, 7, e39874	3.7	19
87	NNAlign: a web-based prediction method allowing non-expert end-user discovery of sequence motifs in quantitative peptide data. *PLoS ONE*, **2011**, 6, e26781	3.7	52
86	Human leukocyte antigen (HLA) class I restricted epitope discovery in yellow fewer and dengue viruses: importance of HLA binding strength. *PLoS ONE*, **2011**, 6, e26494	3.7	26
85	Prediction of epitopes using neural network based methods. *Journal of Immunological Methods*, **2011**, 374, 26-34	2.5	82
84	HLArestrictor--a tool for patient-specific predictions of HLA restriction elements and optimal epitopes within peptides. *Immunogenetics*, **2011**, 63, 43-55	3.2	49
83	Porcine major histocompatibility complex (MHC) class I molecules and analysis of their peptide-binding specificities. *Immunogenetics*, **2011**, 63, 821-34	3.2	35
82	Induction of foot-and-mouth disease virus-specific cytotoxic T cell killing by vaccination. *Vaccine Journal*, **2011**, 18, 280-8		45
81	MHC class II epitope predictive algorithms. *Immunology*, **2010**, 130, 319-28	7.8	157
80	Major histocompatibility complex class I binding predictions as a tool in epitope discovery. *Immunology*, **2010**, 130, 309-18	7.8	91
79	Identification of CD8+ T cell epitopes in the West Nile virus polyprotein by reverse-immunology using NetCTL. *PLoS ONE*, **2010**, 5, e12697	3.7	29
78	In silico prediction of human pathogenicity in the □proteobacteria. *PLoS ONE*, **2010**, 5, e13680	3.7	13
77	Structural properties of MHC class II ligands, implications for the prediction of MHC class II epitopes. *PLoS ONE*, **2010**, 5, e15877	3.7	17
76	Interdisciplinary analysis of HIV-specific CD8+ T cell responses against variant epitopes reveals restricted TCR promiscuity. *Journal of Immunology*, **2010**, 184, 5383-91	5.3	29
75	The MHC motif viewer: a visualization tool for MHC binding motifs. *Current Protocols in Immunology* , **2010**, Chapter 18, Unit 18.17	4	30
74	Networks of high mutual information define the structural proximity of catalytic sites: implications for catalytic residue identification. *PLoS Computational Biology*, **2010**, 6, e1000978	5	61
73	CPHmodels-3.0--remote homology modeling using structure-guided sequence profiles. *Nucleic Acids Research*, **2010**, 38, W576-81	20.1	258
72	NetMHCIIpan-2.0 - Improved pan-specific HLA-DR predictions using a novel concurrent alignment and weight optimization training procedure. *Immunome Research*, **2010**, 6, 9		117

71	Degree of predicted minor histocompatibility antigen mismatch correlates with poorer clinical outcomes in nonmyeloablative allogeneic hematopoietic cell transplantation. *Biology of Blood and Marrow Transplantation*, **2010**, 16, 1370-81	4.7	10
70	NetCTLpan: pan-specific MHC class I pathway epitope predictions. *Immunogenetics*, **2010**, 62, 357-68	3.2	205
69	Peptide binding predictions for HLA DR, DP and DQ molecules. *BMC Bioinformatics*, **2010**, 11, 568	3.6	408
68	State of the art and challenges in sequence based T-cell epitope prediction. *Immunome Research*, **2010**, 6 Suppl 2, S3		43
67	Limitations of Ab initio predictions of peptide binding to MHC class II molecules. *PLoS ONE*, **2010**, 5, e9272	3.7	39
66	HLA class I binding 9mer peptides from influenza A virus induce CD4 T cell responses. *PLoS ONE*, **2010**, 5, e10533	3.7	20
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