Ole Lund

List of Publications by Year
in descending order

208 papers	40,082 citations	8181 76 h-index	3034 188 g-index
221 all docs	221 docs citations	221 times ranked	35545 citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of acquired antimicrobial resistance genes. Journal of Antimicrobial Chemotherapy, 2012, 67, 2640-2644.	3.0	4,515
2	<i>In Silico</i> Detection and Typing of Plasmids using PlasmidFinder and Plasmid Multilocus Sequence Typing. Antimicrobial Agents and Chemotherapy, 2014, 58, 3895-3903.	3.2	3,558
3	Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria. Journal of Clinical Microbiology, 2012, 50, 1355-1361.	3.9	1,925
4	ResFinder 4.0 for predictions of phenotypes from genotypes. Journal of Antimicrobial Chemotherapy, 2020, 75, 3491-3500.	3.0	1,523
5	Real-Time Whole-Genome Sequencing for Routine Typing, Surveillance, and Outbreak Detection of Verotoxigenic Escherichia coli. Journal of Clinical Microbiology, 2014, 52, 1501-1510.	3.9	1,142
6	Improved method for predicting linear B-cell epitopes. Immunome Research, 2006, 2, 2.	0.1	1,034
7	Reliable prediction of T-cell epitopes using neural networks with novel sequence representations. Protein Science, 2003, 12, 1007-1017.	7.6	1,013
8	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. Nature Biotechnology, 2014, 32, 822-828.	17.5	909
9	NetMHCpan, a method for MHC class I binding prediction beyond humans. Immunogenetics, 2009, 61, 1-13.	2.4	725
10	NetMHC-3.0: accurate web accessible predictions of human, mouse and monkey MHC class I affinities for peptides of length 8â€"11. Nucleic Acids Research, 2008, 36, W509-W512.	14.5	722
11	Solving the Problem of Comparing Whole Bacterial Genomes across Different Sequencing Platforms. PLoS ONE, 2014, 9, e104984.	2.5	696
12	Large-scale validation of methods for cytotoxic T-lymphocyte epitope prediction. BMC Bioinformatics, 2007, 8, 424.	2.6	687
13	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. Science, 2011, 334, 94-98.	12.6	675
14	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. Nature Communications, 2019, 10, 1124.	12.8	612
15	NetMHCpan, a Method for Quantitative Predictions of Peptide Binding to Any HLA-A and -B Locus Protein of Known Sequence. PLoS ONE, 2007, 2, e796.	2.5	598
16	Insights from 20 years of bacterial genome sequencing. Functional and Integrative Genomics, 2015, 15, 141-161.	3.5	580
17	Peptide binding predictions for HLA DR, DP and DQ molecules. BMC Bioinformatics, 2010, 11, 568.	2.6	570
18	Reliable B Cell Epitope Predictions: Impacts of Method Development and Improved Benchmarking. PLoS Computational Biology, 2012, 8, e1002829.	3.2	557

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19	Computational Immunology Meets Bioinformatics: The Use of Prediction Tools for Molecular Binding in the Simulation of the Immune System. PLoS ONE, 2010, 5, e9862.	2.5	535
20	PointFinder: a novel web tool for WGS-based detection of antimicrobial resistance associated with chromosomal point mutations in bacterial pathogens. Journal of Antimicrobial Chemotherapy, 2017, 72, 2764-2768.	3.0	534
21	Prediction of residues in discontinuous B‐cell epitopes using protein 3D structures. Protein Science, 2006, 15, 2558-2567.	7.6	525
22	Prediction of MHC class II binding affinity using SMM-align, a novel stabilization matrix alignment method. BMC Bioinformatics, 2007, 8, 238.	2.6	499
23	NetOglyc: prediction of mucin type O-glycosylation sites based on sequence context and surface accessibility. Glycoconjugate Journal, 1998, 15, 115-130.	2.7	493
24	NN-align. An artificial neural network-based alignment algorithm for MHC class II peptide binding prediction. BMC Bioinformatics, 2009, 10, 296.	2.6	451
25	Immune epitope database analysis resource. Nucleic Acids Research, 2012, 40, W525-W530.	14.5	446
26	Rapid and precise alignment of raw reads against redundant databases with KMA. BMC Bioinformatics, 2018, 19, 307.	2.6	433
27	Rapid Whole-Genome Sequencing for Detection and Characterization of Microorganisms Directly from Clinical Samples. Journal of Clinical Microbiology, 2014, 52, 139-146.	3.9	424
28	The role of the proteasome in generating cytotoxic T-cell epitopes: insights obtained from improved predictions of proteasomal cleavage. Immunogenetics, 2005, 57, 33-41.	2.4	416
29	PathogenFinder - Distinguishing Friend from Foe Using Bacterial Whole Genome Sequence Data. PLoS ONE, 2013, 8, e77302.	2.5	365
30	The Immune Epitope Database and Analysis Resource: From Vision to Blueprint. PLoS Biology, 2005, 3, e91.	5.6	342
31	NetMHCcons: a consensus method for the major histocompatibility complex class I predictions. Immunogenetics, 2012, 64, 177-186.	2.4	333
32	Genotyping using whole-genome sequencing is a realistic alternative to surveillance based on phenotypic antimicrobial susceptibility testing. Journal of Antimicrobial Chemotherapy, 2013, 68, 771-777.	3.0	307
33	CPHmodels-3.0—remote homology modeling using structure-guided sequence profiles. Nucleic Acids Research, 2010, 38, W576-W581.	14.5	305
34	Immune epitope database analysis resource (IEDB-AR). Nucleic Acids Research, 2008, 36, W513-W518.	14.5	304
35	An integrative approach to CTL epitope prediction: A combined algorithm integrating MHC class I binding, TAP transport efficiency, and proteasomal cleavage predictions. European Journal of Immunology, 2005, 35, 2295-2303.	2.9	290
36	T-bet and Eomes Are Differentially Linked to the Exhausted Phenotype of CD8+ T Cells in HIV Infection. PLoS Pathogens, 2014, 10, e1004251.	4.7	273

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37	Definition of supertypes for HLA molecules using clustering of specificity matrices. Immunogenetics, 2004, 55, 797-810.	2.4	269
38	Prediction of O-glycosylation of mammalian proteins: specificity patterns of UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase. Biochemical Journal, 1995, 308, 801-813.	3.7	260
39	Improved prediction of MHC class I and class II epitopes using a novel Gibbs sampling approach. Bioinformatics, 2004, 20, 1388-1397.	4.1	254
40	A Community Resource Benchmarking Predictions of Peptide Binding to MHC-I Molecules. PLoS Computational Biology, 2006, 2, e65.	3.2	254
41	Quantitative Predictions of Peptide Binding to Any HLA-DR Molecule of Known Sequence: NetMHCIIpan. PLoS Computational Biology, 2008, 4, e1000107.	3.2	254
42	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, 711-724.	2.4	254
43	Benchmarking of Methods for Genomic Taxonomy. Journal of Clinical Microbiology, 2014, 52, 1529-1539.	3.9	241
44	Structural analysis of B-cell epitopes in antibody:protein complexes. Molecular Immunology, 2013, 53, 24-34.	2.2	237
45	Abundance and diversity of the faecal resistome in slaughter pigs and broilers in nine European countries. Nature Microbiology, 2018, 3, 898-908.	13.3	230
46	The PickPocket method for predicting binding specificities for receptors based on receptor pocket similarities: application to MHC-peptide binding. Bioinformatics, 2009, 25, 1293-1299.	4.1	225
47	Accurate approximation method for prediction of class I MHC affinities for peptides of length 8, 10 and 11 using prediction tools trained on 9mers. Bioinformatics, 2008, 24, 1397-1398.	4.1	216
48	Evaluation of Whole Genome Sequencing for Outbreak Detection of Salmonella enterica. PLoS ONE, 2014, 9, e87991.	2.5	215
49	Towards a consensus on datasets and evaluation metrics for developing B-cell epitope prediction tools. Journal of Molecular Recognition, 2007, 20, 75-82.	2.1	209
50	MHC Class II epitope predictive algorithms. Immunology, 2010, 130, 319-328.	4.4	198
51	SCC <i>mec</i> Finder, a Web-Based Tool for Typing of Staphylococcal Cassette Chromosome <i>mec</i> in Staphylococcus aureus Using Whole-Genome Sequence Data. MSphere, 2018, 3, .	2.9	197
52	MR1-restricted MAIT cells display ligand discrimination and pathogen selectivity through distinct T cell receptor usage. Journal of Experimental Medicine, 2014, 211, 1601-1610.	8.5	196
53	<i>In Silico</i> Genotyping of Escherichia coli Isolates for Extraintestinal Virulence Genes by Use of Whole-Genome Sequencing Data. Journal of Clinical Microbiology, 2020, 58, .	3.9	179
54	Benchmarking of methods for identification of antimicrobial resistance genes in bacterial whole genome data. Journal of Antimicrobial Chemotherapy, 2016, 71, 2484-2488.	3.0	166

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55	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. Nature Communications, 2015, 6, 5969.	12.8	164
56	A Bacterial Analysis Platform: An Integrated System for Analysing Bacterial Whole Genome Sequencing Data for Clinical Diagnostics and Surveillance. PLoS ONE, 2016, 11, e0157718.	2.5	161
57	Ten years of bacterial genome sequencing: comparative-genomics-based discoveries. Functional and Integrative Genomics, 2006, 6, 165-185.	3.5	156
58	Development of a Web Tool for Escherichia coli Subtyping Based on <i>fimH</i> Alleles. Journal of Clinical Microbiology, 2017, 55, 2538-2543.	3.9	136
59	Simultaneous alignment and clustering of peptide data using a Gibbs sampling approach. Bioinformatics, 2013, 29, 8-14.	4.1	134
60	Protein distance constraints predicted by neural networks and probability density functions. Protein Engineering, Design and Selection, 1997, 10, 1241-1248.	2.1	132
61	NetMHCIIpan-2.0 - Improved pan-specific HLA-DR predictions using a novel concurrent alignment and weight optimization training procedure. Immunome Research, 2010, 6, 9.	0.1	132
62	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. Nature, 2017, 548, 87-91.	27.8	130
63	Automated benchmarking of peptide-MHC class I binding predictions. Bioinformatics, 2015, 31, 2174-2181.	4.1	127
64	MHCcluster, a method for functional clustering of MHC molecules. Immunogenetics, 2013, 65, 655-665.	2.4	116
65	Modeling the adaptive immune system: predictions and simulations. Bioinformatics, 2007, 23, 3265-3275.	4.1	115
66	Prediction of protein secondary structure at 80% accuracy. Proteins: Structure, Function and Bioinformatics, 2000, 41, 17-20.	2.6	112
67	HostPhinder: A Phage Host Prediction Tool. Viruses, 2016, 8, 116.	3.3	112
68	O-GLYCBASE version 2.0: a revised database of O-glycosylated proteins. Nucleic Acids Research, 1997, 25, 278-282.	14.5	109
69	Major histocompatibility complex class I binding predictions as a tool in epitope discovery. Immunology, 2010, 130, 309-318.	4.4	109
70	Amino Acid Similarity Accounts for T Cell Cross-Reactivity and for â€œHolesâ€•in the T Cell Repertoire. PLoS ONE, 2008, 3, e1831.	2.5	106
71	The design and implementation of the immune epitope database and analysis resource. Immunogenetics, 2005, 57, 326-336.	2.4	105
72	Global Genomic Epidemiology of Salmonella enterica Serovar Typhimurium DT104. Applied and Environmental Microbiology, 2016, 82, 2516-2526.	3.1	105

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73	CTL epitopes for influenza A including the H5N1 bird flu; genome-, pathogen-, and HLA-wide screening. Vaccine, 2007, 25, 2823-2831.	3.8	94
74	CCMetagen: comprehensive and accurate identification of eukaryotes and prokaryotes in metagenomic data. Genome Biology, 2020, 21, 103.	8.8	91
75	Coronavirus 3CLpro proteinase cleavage sites: possible relevance to SARS virus pathology. BMC Bioinformatics, 2004, 5, 72.	2.6	88
76	Prediction of epitopes using neural network based methods. Journal of Immunological Methods, 2011, 374, 26-34.	1.4	88
77	Propionibacterium acnes: Disease-Causing Agent or Common Contaminant? Detection in Diverse Patient Samples by Next-Generation Sequencing. Journal of Clinical Microbiology, 2016, 54, 980-987.	3.9	87
78	Application of Whole-Genome Sequencing Data for O-Specific Antigen Analysis and *In Silico* Serotyping of Pseudomonas aeruginosa Isolates. Journal of Clinical Microbiology, 2016, 54, 1782-1788.	3.9	85
79	Epitope Mapping and Topographic Analysis of VAR2CSA DBL3X Involved in P. falciparum Placental Sequestration. PLoS Pathogens, 2006, 2, e124.	4.7	83
80	Multidrug-resistant Neisseria gonorrhoeae infection with ceftriaxone resistance and intermediate resistance to azithromycin, Denmark, 2017. Eurosurveillance, 2017, 22, .	7.0	83
81	Immune system simulation online. Bioinformatics, 2011, 27, 2013-2014.	4.1	82
82	ChemProt-3.0: a global chemical biology diseases mapping. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav123.	3.0	75
83	Structural Insight into Epitopes in the Pregnancy-Associated Malaria Protein VAR2CSA. PLoS Pathogens, 2008, 4, e42.	4.7	74
84	Meta-genomic analysis of toilet waste from long distance flights; a step towards global surveillance of infectious diseases and antimicrobial resistance. Scientific Reports, 2015, 5, 11444.	3.3	74
85	AnOxPePred: using deep learning for the prediction of antioxidative properties of peptides. Scientific Reports, 2020, 10, 21471.	3.3	71
86	Meta-analysis of proportion estimates of Extended-Spectrum-Beta-Lactamase-producing Enterobacteriaceae in East Africa hospitals. Antimicrobial Resistance and Infection Control, 2016, 5, 18.	4.1	70
87	Multiparametric Bioinformatics Distinguish the CD4/CD8 Ratio as a Suitable Laboratory Predictor of Combined T Cell Pathogenesis in HIV Infection. Journal of Immunology, 2014, 192, 2099-2108.	0.8	69
88	New Genome-Wide Algorithm Identifies Novel In-Vivo Expressed Mycobacterium Tuberculosis Antigens Inducing Human T-Cell Responses with Classical and Unconventional Cytokine Profiles. Scientific Reports, 2016, 6, 37793.	3.3	69
89	MGmapper: Reference based mapping and taxonomy annotation of metagenomics sequence reads. PLoS ONE, 2017, 12, e0176469.	2.5	66
90	Perturbed CD8+ T cell TIGIT/CD226/PVR axis despite early initiation of antiretroviral treatment in HIV infected individuals. Scientific Reports, 2017, 7, 40354.	3.3	65

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91	Specific gut microbiome members are associated with distinct immune markers in pediatric allogeneic hematopoietic stem cell transplantation. Microbiome, 2019, 7, 131.	11.1	65
92	Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. Emerging Infectious Diseases, 2012, 18, e1-e1.	4.3	64
93	High-throughput sequencing enhanced phage display enables the identification of patient-specific epitope motifs in serum. Scientific Reports, 2015, 5, 12913.	3.3	62
94	Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. Emerging Infectious Diseases, 2012, 18, e1-e1.	4.3	61
95	SARS CTL vaccine candidates; HLA supertype-, genome-wide scanning and biochemical validation. Tissue Antigens, 2004, 63, 395-400.	1.0	60
96	MHC motif viewer. Immunogenetics, 2008, 60, 759-765.	2.4	60
97	NNAlign: A Web-Based Prediction Method Allowing Non-Expert End-User Discovery of Sequence Motifs in Quantitative Peptide Data. PLoS ONE, 2011, 6, e26781.	2.5	60
98	The validity of predicted T-cell epitopes. Trends in Biotechnology, 2006, 24, 537-538.	9.3	59
99	MetaPhinderâ€"Identifying Bacteriophage Sequences in Metagenomic Data Sets. PLoS ONE, 2016, 11, e0163111.	2.5	59
100	LRE-Finder, a Web tool for detection of the 23S rRNA mutations and the optrA, cfr, cfr(B) and poxtA genes encoding linezolid resistance in enterococci from whole-genome sequences. Journal of Antimicrobial Chemotherapy, 2019, 74, 1473-1476.	3.0	58
101	High throughput resistance profiling of Plasmodium falciparum infections based on custom dual indexing and Illumina next generation sequencing-technology. Scientific Reports, 2017, 7, 2398.	3.3	57
102	MULTIPRED2: A computational system for large-scale identification of peptides predicted to bind to HLA supertypes and alleles. Journal of Immunological Methods, 2011, 374, 53-61.	1.4	55
103	<i>Ebolavirus</i> comparative genomics. FEMS Microbiology Reviews, 2015, 39, 764-778.	8.6	54
104	Machine learning competition in immunology â€" Prediction of HLA class I binding peptides. Journal of Immunological Methods, 2011, 374, 1-4.	1.4	53
105	State of the art and challenges in sequence based T-cell epitope prediction. Immunome Research, 2010, 6, S3.	0.1	52
106	Broadly Immunogenic HLA Class I Supertype-Restricted Elite CTL Epitopes Recognized in a Diverse Population Infected with Different HIV-1 Subtypes. Journal of Immunology, 2008, 180, 5092-5100.	0.8	51
107	Genome-Based In Silico Identification of New <i>Mycobacterium tuberculosis</i> Antigens Activating Polyfunctional CD8+ T Cells in Human Tuberculosis. Journal of Immunology, 2011, 186, 1068-1080.	0.8	50
108	ChemProt-2.0: visual navigation in a disease chemical biology database. Nucleic Acids Research, 2012, 41, D464-D469.	14.5	50

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109	Immunological Bioinformatics. , 2005, , .		49
110	Norwegian patients and retail chicken meat share cephalosporin-resistant Escherichia coli and IncK/bla CMY-2 resistance plasmids. Clinical Microbiology and Infection, 2017, 23, 407.e9-407.e15.	6.0	48
111	Using WGS to identify antibiotic resistance genes and predict antimicrobial resistance phenotypes in MDR Acinetobacter baumannii in Tanzania. Journal of Antimicrobial Chemotherapy, 2019, 74, 1484-1493.	3.0	46
112	Stoichiometry of Monoclonal Antibody Neutralization of T-Cell Line-Adapted Human Immunodeficiency Virus Type 1. Journal of Virology, 1999, 73, 8364-8370.	3.4	46
113	Limitations of Ab Initio Predictions of Peptide Binding to MHC Class II Molecules. PLoS ONE, 2010, 5, e9272.	2.5	45
114	Patterns of infections, aetiological agents and antimicrobial resistance at a tertiary care hospital in northern Tanzania. Tropical Medicine and International Health, 2017, 22, 454-464.	2.3	43
115	CHTyper, a Web Tool for Subtyping of Extraintestinal Pathogenic Escherichia coli Based on the <i>fumC</i> and <i>fimH</i> Alleles. Journal of Clinical Microbiology, 2018, 56, .	3.9	42
116	Identification of CD8+ T Cell Epitopes in the West Nile Virus Polyprotein by Reverse-Immunology Using NetCTL. PLoS ONE, 2010, 5, e12697.	2.5	41
117	Bacterial whole genome-based phylogeny: construction of a new benchmarking dataset and assessment of some existing methods. BMC Genomics, 2017, 18, 19.	2.8	40
118	Increased adhesion as a mechanism of antibody-dependent and antibody-independent complement-mediated enhancement of human immunodeficiency virus infection. Journal of Virology, 1995, 69, 2393-2400.	3.4	40
119	ImmunoGrid: towards agent-based simulations of the human immune system at a natural scale <sup /> . Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2010, 368, 2799-2815.	3.4	39
120	Predictions versus high-throughput experiments in T-cell epitope discovery: competition or synergy?. Expert Review of Vaccines, 2012, 11, 43-54.	4.4	39
121	What Can We Learn from a Metagenomic Analysis of a Georgian Bacteriophage Cocktail?. Viruses, 2015, 7, 6570-6589.	3.3	38
122	O-GLYCBASE: a revised database of O-glycosylated proteins. Nucleic Acids Research, 1996, 24, 248-252.	14.5	37
123	Porcine major histocompatibility complex (MHC) class I molecules and analysis of their peptide-binding specificities. Immunogenetics, 2011, 63, 821-834.	2.4	37
124	Evaluating next-generation sequencing for direct clinical diagnostics in diarrhoeal disease. European Journal of Clinical Microbiology and Infectious Diseases, 2017, 36, 1325-1338.	2.9	36
125	Prediction of Acquired Antimicrobial Resistance for Multiple Bacterial Species Using Neural Networks. MSystems, 2020, 5, .	3.8	36
126	Prediction of the secondary structure of HIV-1 gp120. , 1996, 25, 1-11.		35

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127	Interdisciplinary Analysis of HIV-Specific CD8+ T Cell Responses against Variant Epitopes Reveals Restricted TCR Promiscuity. Journal of Immunology, 2010, 184, 5383-5391.	0.8	34
128	Relationship between protein structure and geometrical constraints. Protein Science, 1996, 5, 2217-2225.	7.6	33
129	MatrixPlot: visualizing sequence constraints. Bioinformatics, 1999, 15, 769-770.	4.1	33
130	High-throughput immuno-profiling of mamba (Dendroaspis) venom toxin epitopes using high-density peptide microarrays. Scientific Reports, 2016, 6, 36629.	3.3	33
131	Antibody Cross-Reactivity in Antivenom Research. Toxins, 2018, 10, 393.	3.4	33
132	Systematic Characterisation of Cellular Localisation and Expression Profiles of Proteins Containing MHC Ligands. PLoS ONE, 2009, 4, e7448.	2.5	33
133	The MHC Motif Viewer: A Visualization Tool for MHC Binding Motifs. Current Protocols in Immunology, 2010, 88, Unit 18.17.	3.6	32
134	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.	2.5	30
135	CD4+ T cells with an activated and exhausted phenotype distinguish immunodeficiency during aviremic HIV-2 infection. Aids, 2016, 30, 2415-2426.	2.2	30
136	Identification of MHC class II restricted T-cell-mediated reactivity against MHC class I binding Mycobacterium tuberculosis peptides. Immunology, 2011, 132, 482-491.	4.4	28
137	RUCS: rapid identification of PCR primers for unique core sequences. Bioinformatics, 2017, 33, 3917-3921.	4.1	28
138	The COMPARE Data Hubs. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	28
139	Evaluation of peptide selection approaches for epitope‐based vaccine design. Tissue Antigens, 2013, 82, 243-251.	1.0	27
140	Ceftriaxone use in a tertiary care hospital in Kilimanjaro, Tanzania: A need for a hospital antibiotic stewardship programme. PLoS ONE, 2019, 14, e0220261.	2.5	27
141	Gene therapy of T helper cells in HIV infection: Mathematical model of the criteria for clinical effect. Bulletin of Mathematical Biology, 1997, 59, 725-745.	1.9	25
142	Induction of Antibodies against Epitopes Inaccessible on the HIV Type 1 Envelope Oligomer by Immunization with Recombinant Monomeric Glycoprotein 120. AIDS Research and Human Retroviruses, 1998, 14, 1451-1456.	1.1	24
143	Critical role of glycosylation in determining the length and structure of T cell epitopes. Immunome Research, 2009, 5, 4.	0.1	24
144	Understanding and predicting ciprofloxacin minimum inhibitory concentration in Escherichia coli with machine learning. Scientific Reports, 2020, 10, 15026.	3.3	24

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145	HLA Class I Binding 9mer Peptides from Influenza A Virus Induce CD4+ T Cell Responses. PLoS ONE, 2010, 5, e10533.	2.5	24
146	Whole genome sequencing reveals high clonal diversity of Escherichia coli isolated from patients in a tertiary care hospital in Moshi, Tanzania. Antimicrobial Resistance and Infection Control, 2018, 7, 72.	4.1	22
147	Characterization of HIV-Specific CD4+ T Cell Responses against Peptides Selected with Broad Population and Pathogen Coverage. PLoS ONE, 2012, 7, e39874.	2.5	22
148	The peptide-binding specificity of HLA-A*3001 demonstrates membership of the HLA-A3 supertype. Immunogenetics, 2008, 60, 633-643.	2.4	21
149	TheN-linked glycan of the V3 region of HIV-1 gp120 and CXCR4-dependent multiplication of a human immunodeficiency virus type 1 lymphocyte-tropic variant. FEBS Letters, 1999, 454, 47-52.	2.8	19
150	Modelling the Human Immune System by Combining Bioinformatics and Systems Biology Approaches. Journal of Biological Physics, 2006, 32, 335-353.	1.5	19
151	TAP-Independent MHC Class I Presentation. Current Immunology Reviews, 2006, 2, 233-245.	1.2	19
152	Molecular epidemiology of virulence and antimicrobial resistance determinants in Klebsiella pneumoniae from hospitalised patients in Kilimanjaro, Tanzania. European Journal of Clinical Microbiology and Infectious Diseases, 2018, 37, 1901-1914.	2.9	19
153	High-affinity human leucocyte antigen class I binding variola-derived peptides induce CD4+ T cell responses more than 30 years post-vaccinia virus vaccination. Clinical and Experimental Immunology, 2009, 155, 441-446.	2.6	18
154	SigniSite: Identification of residue-level genotype-phenotype correlations in protein multiple sequence alignments. Nucleic Acids Research, 2013, 41, W286-W291.	14.5	18
155	Mycobacterium leprae virulence-associated peptides are indicators of exposure to M. leprae in Brazil, Ethiopia and Nepal. Memorias Do Instituto Oswaldo Cruz, 2012, 107, 112-123.	1.6	17
156	Prevalence and risk factors for CTX-M gram-negative bacteria in hospitalized patients at a tertiary care hospital in Kilimanjaro, Tanzania. European Journal of Clinical Microbiology and Infectious Diseases, 2018, 37, 897-906.	2.9	17
157	Proof of concept: used malaria rapid diagnostic tests applied for parallel sequencing for surveillance of molecular markers of anti-malarial resistance in Bissau, Guinea-Bissau during 2014â€"2017. Malaria Journal, 2019, 18, 252.	2.3	17
158	Cross-recognition of a pit viper (Crotalinae) polyspecific antivenom explored through high-density peptide microarray epitope mapping. PLoS Neglected Tropical Diseases, 2017, 11, e0005768.	3.0	17
159	O-GLYCBASE Version 3.0: a revised database of O-glycosylated proteins. Nucleic Acids Research, 1998, 26, 387-389.	14.5	16
160	MHC-I-restricted epitopes conserved among variola and other related orthopoxviruses are recognized by T cells 30Âyears after vaccination. Archives of Virology, 2008, 153, 1833-1844.	2.1	16
161	Assembly and analysis of 100 full MHC haplotypes from the Danish population. Genome Research, 2017, 27, 1597-1607.	5.5	15
162	Selecting Informative Data for Developing Peptide-MHC Binding Predictors Using a Query by Committee Approach. Neural Computation, 2003, 15, 2931-2942.	2.2	14

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163	In Silico Prediction of Human Pathogenicity in the Î³-Proteobacteria. PLoS ONE, 2010, 5, e13680.	2.5	14
164	Plasmodium falciparum population dynamics in a cohort of pregnant women in Senegal. Malaria Journal, 2010, 9, 165.	2.3	14
165	Multidimensional Clusters of CD4+ T Cell Dysfunction Are Primarily Associated with the CD4/CD8 Ratio in Chronic HIV Infection. PLoS ONE, 2015, 10, e0137635.	2.5	14
166	Hospital Epidemiology of Methicillin-Resistant *Staphylococcus aureus* in a Tertiary Care Hospital in Moshi, Tanzania, as Determined by Whole Genome Sequencing. BioMed Research International, 2018, 2018, 1-12.	1.9	14
167	Insight into Antigenic Diversity of VAR2CSA-DBL5Îµ Domain from Multiple Plasmodium falciparum Placental Isolates. PLoS ONE, 2010, 5, e13105.	2.5	14
168	The Cancer Exome Generated by Alternative mRNA Splicing Dilutes Predicted HLA Class I Epitope Density. PLoS ONE, 2012, 7, e38670.	2.5	14
169	Complement-Mediated Enhancement of HIV-1 Infection in Peripheral Blood Mononuclear Cells. Scandinavian Journal of Infectious Diseases, 1997, 29, 447-452.	1.5	13
170	High-Throughput Sequencing-Based Investigation of Viruses in Human Cancers by Multienrichment Approach. Journal of Infectious Diseases, 2019, 220, 1312-1324.	4.0	13
171	Global Microbial Identifier. , 2017, , 13-31.		13
172	A model of enhancement and inhibition of HIV infection of monocytes by antibodies against HIV. Journal of Biological Physics, 1993, 19, 133-145.	1.5	12
173	Bistability in autoimmune diseases. Autoimmunity, 2011, 44, 256-260.	2.6	12
174	High-density peptide microarray exploration of the antibody response in a rabbit immunized with a neurotoxic venom fraction. Toxicon, 2017, 138, 151-158.	1.6	12
175	Direct whole-genome sequencing of Plasmodium falciparum specimens from dried erythrocyte spots. Malaria Journal, 2018, 17, 91.	2.3	12
176	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, 1370-1381.	2.0	11
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