

Ole Lund

List of Publications by Year in descending order

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Version: 2024-02-01

208
papers

40,082
citations

9428

76
h-index

3508

188
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221
all docs

221
docs citations

221
times ranked

38858
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | PlasmidHostFinder: Prediction of Plasmid Hosts Using Random Forest. <i>MSystems</i> , 2022, 7, e0118021. | 1.7 | 8 |
| 2 | Metagenomic DNA sequencing for semi-quantitative pathogen detection from urine: a prospective, laboratory-based, proof-of-concept study. <i>Lancet Microbe</i> , The, 2022, , . | 3.4 | 7 |
| 3 | Automated download and clean-up of family-specific databases for kmer-based virus identification. <i>Bioinformatics</i> , 2021, 37, 705-710. | 1.8 | 4 |
| 4 | MINTyper: an outbreak-detection method for accurate and rapid SNP typing of clonal clusters with noisy long reads. <i>Biology Methods and Protocols</i> , 2021, 6, bpab008. | 1.0 | 10 |
| 5 | Machine learning predicts and provides insights into milk acidification rates of <i>Lactococcus lactis</i> . <i>PLoS ONE</i> , 2021, 16, e0246287. | 1.1 | 7 |
| 6 | Rapid Open-Source SNP-Based Clustering Offers an Alternative to Core Genome MLST for Outbreak Tracing in a Hospital Setting. <i>Frontiers in Microbiology</i> , 2021, 12, 636608. | 1.5 | 3 |
| 7 | Predicting Antimicrobial Resistance Using Partial Genome Alignments. <i>MSystems</i> , 2021, 6, e0018521. | 1.7 | 11 |
| 8 | Identification of Single-Nucleotide Polymorphisms in the Mitochondrial Genome and Kelch 13 Gene of <i>Plasmodium falciparum</i> in Different Geographical Populations. <i>American Journal of Tropical Medicine and Hygiene</i> , 2021, , . | 0.6 | 1 |
| 9 | Understanding and predicting ciprofloxacin minimum inhibitory concentration in <i>Escherichia coli</i> with machine learning. <i>Scientific Reports</i> , 2020, 10, 15026. | 1.6 | 24 |
| 10 | <i>In Silico</i> Genotyping of <i>Escherichia coli</i> Isolates for Extraintestinal Virulence Genes by Use of Whole-Genome Sequencing Data. <i>Journal of Clinical Microbiology</i> , 2020, 58, . | 1.8 | 179 |
| 11 | ResFinder 4.0 for predictions of phenotypes from genotypes. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3491-3500. | 1.3 | 1,523 |
| 12 | AnOxPePred: using deep learning for the prediction of antioxidative properties of peptides. <i>Scientific Reports</i> , 2020, 10, 21471. | 1.6 | 71 |
| 13 | Large scale automated phylogenomic analysis of bacterial isolates and the Evergreen Online platform. <i>Communications Biology</i> , 2020, 3, 137. | 2.0 | 7 |
| 14 | An interactive database for the investigation of high-density peptide microarray guided interaction patterns and antivenom cross-reactivity. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008366. | 1.3 | 10 |
| 15 | Metaphylogenetic analysis of global sewage reveals that bacterial strains associated with human disease show less degree of geographic clustering. <i>Scientific Reports</i> , 2020, 10, 3033. | 1.6 | 7 |
| 16 | CCMetagen: comprehensive and accurate identification of eukaryotes and prokaryotes in metagenomic data. <i>Genome Biology</i> , 2020, 21, 103. | 3.8 | 91 |
| 17 | Prediction of Acquired Antimicrobial Resistance for Multiple Bacterial Species Using Neural Networks. <i>MSystems</i> , 2020, 5, . | 1.7 | 36 |
| 18 | Accelerating surveillance and research of antimicrobial resistance – an online repository for sharing of antimicrobial susceptibility data associated with whole-genome sequences. <i>Microbial Genomics</i> , 2020, 6, . | 1.0 | 5 |

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|----|---|-----|-----------|
| 19 | Ceftriaxone use in a tertiary care hospital in Kilimanjaro, Tanzania: A need for a hospital antibiotic stewardship programme. PLoS ONE, 2019, 14, e0220261. | 1.1 | 27 |
| 20 | 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 2014–2017. Malaria Journal, 2019, 18, 252. | 0.8 | 17 |
| 21 | High-Throughput Sequencing-Based Investigation of Viruses in Human Cancers by Multienrichment Approach. Journal of Infectious Diseases, 2019, 220, 1312-1324. | 1.9 | 13 |
| 22 | Specific gut microbiome members are associated with distinct immune markers in pediatric allogeneic hematopoietic stem cell transplantation. Microbiome, 2019, 7, 131. | 4.9 | 65 |
| 23 | Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. Nature Communications, 2019, 10, 1124. | 5.8 | 612 |
| 24 | 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. | 1.3 | 46 |
| 25 | LRE-Finder, a Web tool for detection of the 23S rRNA mutations and the oprA, cfr, cfr(B) and poxtA genes encoding linezolid resistance in enterococci from whole-genome sequences. Journal of Antimicrobial Chemotherapy, 2019, 74, 1473-1476. | 1.3 | 58 |
| 26 | The COMPARE Data Hubs. Database: the Journal of Biological Databases and Curation, 2019, 2019, . | 1.4 | 28 |
| 27 | Improved Resistance Prediction in Mycobacterium tuberculosis by Better Handling of Insertions and Deletions, Premature Stop Codons, and Filtering of Non-informative Sites. Frontiers in Microbiology, 2019, 10, 2464. | 1.5 | 7 |
| 28 | 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. | 1.3 | 17 |
| 29 | SCC <i>mecA</i> Finder, a Web-Based Tool for Typing of Staphylococcal Cassette Chromosome <i>mecA</i> in Staphylococcus aureus Using Whole-Genome Sequence Data. MSphere, 2018, 3, . | 1.3 | 197 |
| 30 | 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, . | 1.8 | 42 |
| 31 | Antibody Cross-Reactivity in Antivenom Research. Toxins, 2018, 10, 393. | 1.5 | 33 |
| 32 | Rapid and precise alignment of raw reads against redundant databases with KMA. BMC Bioinformatics, 2018, 19, 307. | 1.2 | 433 |
| 33 | Hospital Epidemiology of Methicillin-Resistant <i>Staphylococcus aureus</i> in a Tertiary Care Hospital in Moshi, Tanzania, as Determined by Whole Genome Sequencing. BioMed Research International, 2018, 2018, 1-12. | 0.9 | 14 |
| 34 | Abundance and diversity of the faecal resistome in slaughter pigs and broilers in nine European countries. Nature Microbiology, 2018, 3, 898-908. | 5.9 | 230 |
| 35 | 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. | 1.5 | 22 |
| 36 | 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. | 1.3 | 19 |

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|----|---|------|-----------|
| 37 | Direct whole-genome sequencing of Plasmodium falciparum specimens from dried erythrocyte spots. <i>Malaria Journal</i> , 2018, 17, 91. | 0.8 | 12 |
| 38 | Bacterial whole genome-based phylogeny: construction of a new benchmarking dataset and assessment of some existing methods. <i>BMC Genomics</i> , 2017, 18, 19. | 1.2 | 40 |
| 39 | The CGE Tool Box. , 2017, , 65-90. | | 3 |
| 40 | Norwegian patients and retail chicken meat share cephalosporin-resistant <i>Escherichia coli</i> and IncK/bla CMY-2 resistance plasmids. <i>Clinical Microbiology and Infection</i> , 2017, 23, 407.e9-407.e15. | 2.8 | 48 |
| 41 | Patterns of infections, aetiological agents and antimicrobial resistance at a tertiary care hospital in northern Tanzania. <i>Tropical Medicine and International Health</i> , 2017, 22, 454-464. | 1.0 | 43 |
| 42 | Perturbed CD8+ T cell TIGIT/CD226/PVR axis despite early initiation of antiretroviral treatment in HIV infected individuals. <i>Scientific Reports</i> , 2017, 7, 40354. | 1.6 | 65 |
| 43 | Development of a Web Tool for <i>Escherichia coli</i> Subtyping Based on <i>fimH</i> Alleles. <i>Journal of Clinical Microbiology</i> , 2017, 55, 2538-2543. | 1.8 | 136 |
| 44 | High throughput resistance profiling of <i>Plasmodium falciparum</i> infections based on custom dual indexing and Illumina next generation sequencing-technology. <i>Scientific Reports</i> , 2017, 7, 2398. | 1.6 | 57 |
| 45 | Evaluating next-generation sequencing for direct clinical diagnostics in diarrhoeal disease. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2017, 36, 1325-1338. | 1.3 | 36 |
| 46 | High-density peptide microarray exploration of the antibody response in a rabbit immunized with a neurotoxic venom fraction. <i>Toxicon</i> , 2017, 138, 151-158. | 0.8 | 12 |
| 47 | PointFinder: a novel web tool for WGS-based detection of antimicrobial resistance associated with chromosomal point mutations in bacterial pathogens. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2764-2768. | 1.3 | 534 |
| 48 | Assembly and analysis of 100 full MHC haplotypes from the Danish population. <i>Genome Research</i> , 2017, 27, 1597-1607. | 2.4 | 15 |
| 49 | RUCS: rapid identification of PCR primers for unique core sequences. <i>Bioinformatics</i> , 2017, 33, 3917-3921. | 1.8 | 28 |
| 50 | MGmapper: Reference based mapping and taxonomy annotation of metagenomics sequence reads. <i>PLoS ONE</i> , 2017, 12, e0176469. | 1.1 | 66 |
| 51 | Global Microbial Identifier. , 2017, , 13-31. | | 13 |
| 52 | Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017, 548, 87-91. | 13.7 | 130 |
| 53 | Cross-recognition of a pit viper (<i>Crotalinae</i>) polyspecific antivenom explored through high-density peptide microarray epitope mapping. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005768. | 1.3 | 17 |
| 54 | ArrayPitope: Automated Analysis of Amino Acid Substitutions for Peptide Microarray-Based Antibody Epitope Mapping. <i>PLoS ONE</i> , 2017, 12, e0168453. | 1.1 | 11 |

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|----|---|-----|-----------|
| 55 | Multidrug-resistant <i>Neisseria gonorrhoeae</i> infection with ceftriaxone resistance and intermediate resistance to azithromycin, Denmark, 2017. <i>Eurosurveillance</i> , 2017, 22, . | 3.9 | 83 |
| 56 | Identification of Known and Novel Recurrent Viral Sequences in Data from Multiple Patients and Multiple Cancers. <i>Viruses</i> , 2016, 8, 53. | 1.5 | 11 |
| 57 | HostPhinder: A Phage Host Prediction Tool. <i>Viruses</i> , 2016, 8, 116. | 1.5 | 112 |
| 58 | A Bacterial Analysis Platform: An Integrated System for Analysing Bacterial Whole Genome Sequencing Data for Clinical Diagnostics and Surveillance. <i>PLoS ONE</i> , 2016, 11, e0157718. | 1.1 | 161 |
| 59 | ChemProt-3.0: a global chemical biology diseases mapping. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav123. | 1.4 | 75 |
| 60 | New Genome-Wide Algorithm Identifies Novel In-Vivo Expressed Mycobacterium Tuberculosis Antigens Inducing Human T-Cell Responses with Classical and Unconventional Cytokine Profiles. <i>Scientific Reports</i> , 2016, 6, 37793. | 1.6 | 69 |
| 61 | Benchtop Whole-Genome Sequencing for Identification of Nosocomial Outbreaks in Tanzania. <i>Infection Control and Hospital Epidemiology</i> , 2016, 37, 622-623. | 1.0 | 2 |
| 62 | Global Genomic Epidemiology of <i>Salmonella enterica</i> Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2516-2526. | 1.4 | 105 |
| 63 | Application of Whole-Genome Sequencing Data for O-Specific Antigen Analysis and <i>In Silico</i> Serotyping of <i>Pseudomonas aeruginosa</i> Isolates. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1782-1788. | 1.8 | 85 |
| 64 | High-throughput immuno-profiling of mamba (<i>Dendroaspis</i>) venom toxin epitopes using high-density peptide microarrays. <i>Scientific Reports</i> , 2016, 6, 36629. | 1.6 | 33 |
| 65 | CD4+ T cells with an activated and exhausted phenotype distinguish immunodeficiency during aviremic HIV-2 infection. <i>Aids</i> , 2016, 30, 2415-2426. | 1.0 | 30 |
| 66 | Meta-analysis of proportion estimates of Extended-Spectrum-Beta-Lactamase-producing Enterobacteriaceae in East Africa hospitals. <i>Antimicrobial Resistance and Infection Control</i> , 2016, 5, 18. | 1.5 | 70 |
| 67 | Benchmarking of methods for identification of antimicrobial resistance genes in bacterial whole genome data. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2484-2488. | 1.3 | 166 |
| 68 | <i>Propionibacterium acnes</i> : Disease-Causing Agent or Common Contaminant? Detection in Diverse Patient Samples by Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2016, 54, 980-987. | 1.8 | 87 |
| 69 | MetaPhinder—Identifying Bacteriophage Sequences in Metagenomic Data Sets. <i>PLoS ONE</i> , 2016, 11, e0163111. | 1.1 | 59 |
| 70 | Meta-genomic analysis of toilet waste from long distance flights; a step towards global surveillance of infectious diseases and antimicrobial resistance. <i>Scientific Reports</i> , 2015, 5, 11444. | 1.6 | 74 |
| 71 | Reads2Type: a web application for rapid microbial taxonomy identification. <i>BMC Bioinformatics</i> , 2015, 16, 398. | 1.2 | 5 |
| 72 | What Can We Learn from a Metagenomic Analysis of a Georgian Bacteriophage Cocktail?. <i>Viruses</i> , 2015, 7, 6570-6589. | 1.5 | 38 |

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|----|--|-----|-----------|
| 73 | Multidimensional Clusters of CD4+ T Cell Dysfunction Are Primarily Associated with the CD4/CD8 Ratio in Chronic HIV Infection. PLoS ONE, 2015, 10, e0137635. | 1.1 | 14 |
| 74 | Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. Nature Communications, 2015, 6, 5969. | 5.8 | 164 |
| 75 | Insights from 20 years of bacterial genome sequencing. Functional and Integrative Genomics, 2015, 15, 141-161. | 1.4 | 580 |
| 76 | Automated benchmarking of peptide-MHC class I binding predictions. Bioinformatics, 2015, 31, 2174-2181. | 1.8 | 127 |
| 77 | High-throughput sequencing enhanced phage display enables the identification of patient-specific epitope motifs in serum. Scientific Reports, 2015, 5, 12913. | 1.6 | 62 |
| 78 | <i>Ebolavirus</i> comparative genomics. FEMS Microbiology Reviews, 2015, 39, 764-778. | 3.9 | 54 |
| 79 | T-bet and Eomes Are Differentially Linked to the Exhausted Phenotype of CD8+ T Cells in HIV Infection. PLoS Pathogens, 2014, 10, e1004251. | 2.1 | 273 |
| 80 | MR1-restricted MAIT cells display ligand discrimination and pathogen selectivity through distinct T cell receptor usage. Journal of Experimental Medicine, 2014, 211, 1601-1610. | 4.2 | 196 |
| 81 | Rapid Whole-Genome Sequencing for Detection and Characterization of Microorganisms Directly from Clinical Samples. Journal of Clinical Microbiology, 2014, 52, 3136-3136. | 1.8 | 9 |
| 82 | <i>In Silico</i> Detection and Typing of Plasmids using PlasmidFinder and Plasmid Multilocus Sequence Typing. Antimicrobial Agents and Chemotherapy, 2014, 58, 3895-3903. | 1.4 | 3,558 |
| 83 | Rapid Whole-Genome Sequencing for Detection and Characterization of Microorganisms Directly from Clinical Samples. Journal of Clinical Microbiology, 2014, 52, 139-146. | 1.8 | 424 |
| 84 | Benchmarking of Methods for Genomic Taxonomy. Journal of Clinical Microbiology, 2014, 52, 1529-1539. | 1.8 | 241 |
| 85 | Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. Nature Biotechnology, 2014, 32, 822-828. | 9.4 | 909 |
| 86 | Real-Time Whole-Genome Sequencing for Routine Typing, Surveillance, and Outbreak Detection of Verotoxigenic Escherichia coli. Journal of Clinical Microbiology, 2014, 52, 1501-1510. | 1.8 | 1,142 |
| 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. | 0.4 | 69 |
| 88 | NetFCM: A semi-automated web-based method for flow cytometry data analysis. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2014, 85, 969-977. | 1.1 | 5 |
| 89 | Evaluation of Whole Genome Sequencing for Outbreak Detection of Salmonella enterica. PLoS ONE, 2014, 9, e87991. | 1.1 | 215 |
| 90 | Solving the Problem of Comparing Whole Bacterial Genomes across Different Sequencing Platforms. PLoS ONE, 2014, 9, e104984. | 1.1 | 696 |

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| 91 | 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. | 1.2 | 254 |
| 92 | MHCcluster, a method for functional clustering of MHC molecules. Immunogenetics, 2013, 65, 655-665. | 1.2 | 116 |
| 93 | Evaluation of peptide selection approaches for epitope-based vaccine design. Tissue Antigens, 2013, 82, 243-251. | 1.0 | 27 |
| 94 | 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. | 1.3 | 307 |
| 95 | Identification of Y-Chromosomally Encoded Minor Histocompatibility Antigens Using a Reverse Immunology Approach. Biology of Blood and Marrow Transplantation, 2013, 19, S335. | 2.0 | 0 |
| 96 | 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 |
| 97 | Structural analysis of B-cell epitopes in antibody:protein complexes. Molecular Immunology, 2013, 53, 24-34. | 1.0 | 237 |
| 98 | SigniSite: Identification of residue-level genotype-phenotype correlations in protein multiple sequence alignments. Nucleic Acids Research, 2013, 41, W286-W291. | 6.5 | 18 |
| 99 | Low-Bandwidth and Non-Compute Intensive Remote Identification of Microbes from Raw Sequencing Reads. PLoS ONE, 2013, 8, e83784. | 1.1 | 5 |
| 100 | Simultaneous alignment and clustering of peptide data using a Gibbs sampling approach. Bioinformatics, 2013, 29, 8-14. | 1.8 | 134 |
| 101 | Targeting of Conserved Gag-Epitopes in Early HIV Infection Is Associated with Lower Plasma Viral Load and Slower CD4 ⁺ T Cell Depletion. AIDS Research and Human Retroviruses, 2013, 29, 602-612. | 0.5 | 11 |
| 102 | PathogenFinder - Distinguishing Friend from Foe Using Bacterial Whole Genome Sequence Data. PLoS ONE, 2013, 8, e77302. | 1.1 | 365 |
| 103 | Reliable B Cell Epitope Predictions: Impacts of Method Development and Improved Benchmarking. PLoS Computational Biology, 2012, 8, e1002829. | 1.5 | 557 |
| 104 | ChemProt-2.0: visual navigation in a disease chemical biology database. Nucleic Acids Research, 2012, 41, D464-D469. | 6.5 | 50 |
| 105 | Identification of acquired antimicrobial resistance genes. Journal of Antimicrobial Chemotherapy, 2012, 67, 2640-2644. | 1.3 | 4,515 |
| 106 | Predictions versus high-throughput experiments in T-cell epitope discovery: competition or synergy?. Expert Review of Vaccines, 2012, 11, 43-54. | 2.0 | 39 |
| 107 | Immune epitope database analysis resource. Nucleic Acids Research, 2012, 40, W525-W530. | 6.5 | 446 |
| 108 | Multilocus Sequence Typing of Total-Genome-Sequenced Bacteria. Journal of Clinical Microbiology, 2012, 50, 1355-1361. | 1.8 | 1,925 |

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|-----|--|-----|-----------|
| 109 | Mycobacterium leprae virulence-associated peptides are indicators of exposure to M. leprae in Brazil, Ethiopia and Nepal. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2012, 107, 112-123. | 0.8 | 17 |
| 110 | Identification of a Novel UTY-Encoded Minor Histocompatibility Antigen. <i>Scandinavian Journal of Immunology</i> , 2012, 76, 141-150. | 1.3 | 6 |
| 111 | NetMHCcons: a consensus method for the major histocompatibility complex class I predictions. <i>Immunogenetics</i> , 2012, 64, 177-186. | 1.2 | 333 |
| 112 | The Cancer Exome Generated by Alternative mRNA Splicing Dilutes Predicted HLA Class I Epitope Density. <i>PLoS ONE</i> , 2012, 7, e38670. | 1.1 | 14 |
| 113 | Characterization of HIV-Specific CD4+ T Cell Responses against Peptides Selected with Broad Population and Pathogen Coverage. <i>PLoS ONE</i> , 2012, 7, e39874. | 1.1 | 22 |
| 114 | Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. <i>Emerging Infectious Diseases</i> , 2012, 18, e1-e1. | 2.0 | 64 |
| 115 | Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. <i>Emerging Infectious Diseases</i> , 2012, 18, e1-e1. | 2.0 | 61 |
| 116 | Bistability in autoimmune diseases. <i>Autoimmunity</i> , 2011, 44, 256-260. | 1.2 | 12 |
| 117 | Genome-Based In Silico Identification of New <i>Mycobacterium tuberculosis</i> Antigens Activating Polyfunctional CD8+ T Cells in Human Tuberculosis. <i>Journal of Immunology</i> , 2011, 186, 1068-1080. | 0.4 | 50 |
| 118 | NAlign: 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. | 1.1 | 60 |
| 119 | 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. | 1.1 | 30 |
| 120 | Identification of MHC class II restricted T-cell-mediated reactivity against MHC class I binding <i>Mycobacterium tuberculosis</i> peptides. <i>Immunology</i> , 2011, 132, 482-491. | 2.0 | 28 |
| 121 | Prediction of epitopes using neural network based methods. <i>Journal of Immunological Methods</i> , 2011, 374, 26-34. | 0.6 | 88 |
| 122 | MULTIPRED2: A computational system for large-scale identification of peptides predicted to bind to HLA supertypes and alleles. <i>Journal of Immunological Methods</i> , 2011, 374, 53-61. | 0.6 | 55 |
| 123 | Machine learning competition in immunology – Prediction of HLA class I binding peptides. <i>Journal of Immunological Methods</i> , 2011, 374, 1-4. | 0.6 | 53 |
| 124 | Concepts in Mechanism Based Modeling. , 2011, , 19-41. | | 0 |
| 125 | An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98. | 6.0 | 675 |
| 126 | Porcine major histocompatibility complex (MHC) class I molecules and analysis of their peptide-binding specificities. <i>Immunogenetics</i> , 2011, 63, 821-834. | 1.2 | 37 |

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|-----|---|-----|-----------|
| 127 | Immune system simulation online. <i>Bioinformatics</i> , 2011, 27, 2013-2014. | 1.8 | 82 |
| 128 | ImmunoGrid: towards agent-based simulations of the human immune system at a natural scale <sup />. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2010, 368, 2799-2815. | 1.6 | 39 |
| 129 | Peptide binding predictions for HLA DR, DP and DQ molecules. <i>BMC Bioinformatics</i> , 2010, 11, 568. | 1.2 | 570 |
| 130 | State of the art and challenges in sequence based T-cell epitope prediction. <i>Immunome Research</i> , 2010, 6, S3. | 0.1 | 52 |
| 131 | MHC Class II epitope predictive algorithms. <i>Immunology</i> , 2010, 130, 319-328. | 2.0 | 198 |
| 132 | Major histocompatibility complex class I binding predictions as a tool in epitope discovery. <i>Immunology</i> , 2010, 130, 309-318. | 2.0 | 109 |
| 133 | Computational Immunology Meets Bioinformatics: The Use of Prediction Tools for Molecular Binding in the Simulation of the Immune System. <i>PLoS ONE</i> , 2010, 5, e9862. | 1.1 | 535 |
| 134 | Identification of CD8+ T Cell Epitopes in the West Nile Virus Polyprotein by Reverse-Immunology Using NetCTL. <i>PLoS ONE</i> , 2010, 5, e12697. | 1.1 | 41 |
| 135 | In Silico Prediction of Human Pathogenicity in the $\hat{1}^3$ -Proteobacteria. <i>PLoS ONE</i> , 2010, 5, e13680. | 1.1 | 14 |
| 136 | Critical role of protein glycosylation in T cell immunity/autoimmunity. <i>Annals of the Rheumatic Diseases</i> , 2010, 69, A71-A72. | 0.5 | 1 |
| 137 | Interdisciplinary Analysis of HIV-Specific CD8+ T Cell Responses against Variant Epitopes Reveals Restricted TCR Promiscuity. <i>Journal of Immunology</i> , 2010, 184, 5383-5391. | 0.4 | 34 |
| 138 | The MHC Motif Viewer: A Visualization Tool for MHC Binding Motifs. <i>Current Protocols in Immunology</i> , 2010, 88, Unit 18.17. | 3.6 | 32 |
| 139 | CPHmodels-3.0â€™remote homology modeling using structure-guided sequence profiles. <i>Nucleic Acids Research</i> , 2010, 38, W576-W581. | 6.5 | 305 |
| 140 | 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 |
| 141 | Degree of Predicted Minor Histocompatibility Antigen Mismatch Correlates with Poorer Clinical Outcomes in Nonmyeloablative Allogeneic Hematopoietic Cell Transplantation. <i>Biology of Blood and Marrow Transplantation</i> , 2010, 16, 1370-1381. | 2.0 | 11 |
| 142 | Plasmodium falciparum population dynamics in a cohort of pregnant women in Senegal. <i>Malaria Journal</i> , 2010, 9, 165. | 0.8 | 14 |
| 143 | Limitations of Ab Initio Predictions of Peptide Binding to MHC Class II Molecules. <i>PLoS ONE</i> , 2010, 5, e9272. | 1.1 | 45 |
| 144 | HLA Class I Binding 9mer Peptides from Influenza A Virus Induce CD4+ T Cell Responses. <i>PLoS ONE</i> , 2010, 5, e10533. | 1.1 | 24 |

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|-----|---|-----|-----------|
| 145 | Insight into Antigenic Diversity of VAR2CSA-DBL5 μ Domain from Multiple Plasmodium falciparum Placental Isolates. PLoS ONE, 2010, 5, e13105. | 1.1 | 14 |
| 146 | The PickPocket method for predicting binding specificities for receptors based on receptor pocket similarities: application to MHC-peptide binding. Bioinformatics, 2009, 25, 1293-1299. | 1.8 | 225 |
| 147 | NN-align. An artificial neural network-based alignment algorithm for MHC class II peptide binding prediction. BMC Bioinformatics, 2009, 10, 296. | 1.2 | 451 |
| 148 | NetMHCpan, a method for MHC class I binding prediction beyond humans. Immunogenetics, 2009, 61, 1-13. | 1.2 | 725 |
| 149 | Critical role of glycosylation in determining the length and structure of T cell epitopes. Immunome Research, 2009, 5, 4. | 0.1 | 24 |
| 150 | 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. | 1.1 | 18 |
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