

# Lindsay G Cowell

## List of Publications by Year in descending order

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Version: 2024-02-01

36  
papers

1,287  
citations

471509

17  
h-index

454955

30  
g-index

38  
all docs

38  
docs citations

38  
times ranked

1948  
citing authors

#	ARTICLE	IF	CITATIONS
1	Burden of Renal Cysts Imaging: A Survey of Patients among the Greater Plains Collaborative. <i>Urologia Internationalis</i> , 2022, 106, 693-699.	1.3	0
2	Prevalence of Select New Symptoms and Conditions Among Persons Aged Younger Than 20 Years and 20 Years or Older at 31 to 150 Days After Testing Positive or Negative for SARS-CoV-2. <i>JAMA Network Open</i> , 2022, 5, e2147053.	5.9	33
3	Data Sharing and Reuse: A Method by the AIRR Community. <i>Methods in Molecular Biology</i> , 2022, , 447-476.	0.9	2
4	Blood-based biomarkers of human papillomavirus-associated cancers: A systematic review and meta-analysis. <i>Cancer</i> , 2021, 127, 850-864.	4.1	24
5	TCRMatch: Predicting T-Cell Receptor Specificity Based on Sequence Similarity to Previously Characterized Receptors. <i>Frontiers in Immunology</i> , 2021, 12, 640725.	4.8	64
6	T Cell Receptor Repertoires Acquired via Routine Pap Testing May Help Refine Cervical Cancer and Precancer Risk Estimates. <i>Frontiers in Immunology</i> , 2021, 12, 624230.	4.8	3
7	Reconstituting T cell receptor selection in-silico. <i>Genes and Immunity</i> , 2021, 22, 187-193.	4.1	2
8	Outcome and Immune Correlates of a Phase II Trial of High-Dose Interleukin-2 and Stereotactic Ablative Radiotherapy for Metastatic Renal Cell Carcinoma. <i>Clinical Cancer Research</i> , 2021, 27, 6716-6725.	7.0	12
9	The immuneML ecosystem for machine learning analysis of adaptive immune receptor repertoires. <i>Nature Machine Intelligence</i> , 2021, 3, 936-944.	16.0	35
10	Mining adaptive immune receptor repertoires for biological and clinical information using machine learning. <i>Current Opinion in Systems Biology</i> , 2020, 24, 109-119.	2.6	58
11	Biophysicochemical motifs in T cell receptor sequences as a potential biomarker for high-grade serous ovarian carcinoma. <i>PLoS ONE</i> , 2020, 15, e0229569.	2.5	16
12	The ADC API: A Web API for the Programmatic Query of the AIRR Data Commons. <i>Frontiers in Big Data</i> , 2020, 3, 22.	2.9	24
13	The Diagnostic, Prognostic, and Therapeutic Potential of Adaptive Immune Receptor Repertoire Profiling in Cancer. <i>Cancer Research</i> , 2020, 80, 643-654.	0.9	28
14	Developing and validating an approach for diagnosing and prognosticating cancer from biochemical motifs in T-cell receptors.. <i>Journal of Clinical Oncology</i> , 2020, 38, e15260-e15260.	1.6	1
15	Title is missing!. , 2020, 15, e0229569.		0
16	Title is missing!. , 2020, 15, e0229569.		0
17	Title is missing!. , 2020, 15, e0229569.		0
18	Title is missing!. , 2020, 15, e0229569.		0

#	ARTICLE	IF	CITATIONS
19	Machine learning on sequential data using a recurrent weighted average. <i>Neurocomputing</i> , 2019, 331, 281-288.	5.9	16
20	Biophysicochemical Motifs in T-cell Receptor Sequences Distinguish Repertoires from Tumor-Infiltrating Lymphocyte and Adjacent Healthy Tissue. <i>Cancer Research</i> , 2019, 79, 1671-1680.	0.9	79
21	iReceptor: A platform for querying and analyzing antibody/Bâ€cell and Tâ€cell receptor repertoire data across federated repositories. <i>Immunological Reviews</i> , 2018, 284, 24-41.	6.0	132
22	VDJServer: A Cloud-Based Analysis Portal and Data Commons for Immune Repertoire Sequences and Rearrangements. <i>Frontiers in Immunology</i> , 2018, 9, 976.	4.8	68
23	Adaptive Immune Receptor Repertoire Community recommendations for sharing immune-repertoire sequencing data. <i>Nature Immunology</i> , 2017, 18, 1274-1278.	14.5	163
24	Reproducibility and Reuse of Adaptive Immune Receptor Repertoire Data. <i>Frontiers in Immunology</i> , 2017, 8, 1418.	4.8	102
25	Statistical classifiers for diagnosing disease from immune repertoires: a case study using multiple sclerosis. <i>BMC Bioinformatics</i> , 2017, 18, 401.	2.6	57
26	VDJPipe: a pipelined tool for pre-processing immune repertoire sequencing data. <i>BMC Bioinformatics</i> , 2017, 18, 448.	2.6	18
27	Cell type discovery and representation in the era of high-content single cell phenotyping. <i>BMC Bioinformatics</i> , 2017, 18, 559.	2.6	51
28	VDJML: a file format with tools for capturing the results of inferring immune receptor rearrangements. <i>BMC Bioinformatics</i> , 2016, 17, 333.	2.6	16
29	iWAS â€“ A novel approach to analyzing Next Generation Sequence data for immunology. <i>Cellular Immunology</i> , 2016, 299, 6-13.	3.0	8
30	Individual heritable differences result in unique cell lymphocyte receptor repertoires of naÃve and antigen-experienced cells. <i>Nature Communications</i> , 2016, 7, 11112.	12.8	123
31	owlcpp: a C++ library for working with OWL ontologies. <i>Journal of Biomedical Semantics</i> , 2015, 6, 35.	1.6	5
32	RAG Represents a Widespread Threat to the Lymphocyte Genome. <i>Cell</i> , 2015, 162, 751-765.	28.9	98
33	MSPrecise: A molecular diagnostic test for multiple sclerosis using next generation sequencing. <i>Gene</i> , 2015, 572, 191-197.	2.2	17
34	The Antibody Genetics of Multiple Sclerosis: Comparing Next-Generation Sequencing to Sanger Sequencing. <i>Frontiers in Neurology</i> , 2014, 5, 166.	2.4	10
35	Design and evaluation of a bacterial clinical infectious diseases ontology. <i>AMIA ... Annual Symposium proceedings</i> , 2013, 2013, 502-11.	0.2	7
36	Data Availability of Open T-Cell Receptor Repertoire Data, a Systematic Assessment. <i>Frontiers in Systems Biology</i> , 0, 2, .	0.7	5