Nir Hacohen

List of Publications by Year
in descending order

120 papers	30,594 citations	21215 62 h-index	27587 110 g-index
144 all docs	144 docs citations	144 times ranked	53685 citing authors

#	Article	IF	Citations
1	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. Nature Biotechnology, 2022, 40, 209-217.	9.4	127
2	Urine Proteomics and Renal <scp>Single‐Cell</scp> Transcriptomics Implicate Interleukin‐16 in Lupus Nephritis. Arthritis and Rheumatology, 2022, 74, 829-839.	2.9	38
3	Alveolar, Endothelial, and Organ Injury Marker Dynamics in Severe COVID-19. American Journal of Respiratory and Critical Care Medicine, 2022, 205, 507-519.	2.5	56
4	Reply To: High Renin Levels in Severe COVID-19 are Indicative for a Hypo-Renin-Angiotensin-System State. American Journal of Respiratory and Critical Care Medicine, 2022, , .	2.5	0
5	Systematic identification of genomic elements that regulate <i>FCGR2A</i> expression and harbor variants linked with autoimmune disease. Human Molecular Genetics, 2022, 31, 1946-1961.	1.4	7
6	Landscape of helper and regulatory antitumour CD4+ T cells in melanoma. Nature, 2022, 605, 532-538.	13.7	70
7	Prioritization of autoimmune disease-associated genetic variants that perturb regulatory element activity in T cells. Nature Genetics, 2022, 54, 603-612.	9.4	15
8	Abstract 2030: A single-cell spatially resolved map of colorectal cancer identifies novel spatial relationships between cancer cells and the microenvironment. Cancer Research, 2022, 82, 2030-2030.	0.4	3
9	Abstract 3610: In vivo CRISPR screens reveal the landscape of immune evasion pathways across cancer. Cancer Research, 2022, 82, 3610-3610.	0.4	0
10	Clinical characteristics and molecular features of non-small cell lung cancers (NSCLCs) following disease progression on immune checkpoint inhibitors (ICIs).. Journal of Clinical Oncology, 2022, 40, e21178-e21178.	0.8	0
11	The Kinetics of SARS-CoV-2 Antibody Development Is Associated with Clearance of RNAemia. MBio, 2022, 13, .	1.8	10
12	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. Nature Biotechnology, 2021, 39, 451-461.	9.4	150
13	Optimized Liquid and Gas Phase Fractionation Increases HLA-Peptidome Coverage for Primary Cell and Tissue Samples. Molecular and Cellular Proteomics, 2021, 20, 100133.	2.5	32
14	Personal neoantigen vaccines induce persistent memory T cell responses and epitope spreading in patients with melanoma. Nature Medicine, 2021, 27, 515-525.	15.2	248
15	A unique subset of glycolytic tumour-propagating cells drives squamous cell carcinoma. Nature Metabolism, 2021, 3, 182-195.	5.1	17
16	Epitope spreading toward wild-type melanocyte-lineage antigens rescues suboptimal immune checkpoint blockade responses. Science Translational Medicine, 2021, 13, .	5.8	54
17	Some antibodies can dampen antiviral defences in people with severe COVID. Nature, 2021, 591, 37-39.	13.7	1
18	Viral Load Kinetics of Severe Acute Respiratory Syndrome Coronavirus 2 in Hospitalized Individuals With Coronavirus Disease 2019. Open Forum Infectious Diseases, 2021, 8, ofab153.	0.4	20

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19	Genome-wide enhancer maps link risk variants to disease genes. Nature, 2021, 593, 238-243.	13.7	332
20	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. Nature, 2021, 595, 107-113.	13.7	537
21	Longitudinal proteomic analysis of severe COVID-19 reveals survival-associated signatures, tissue-specific cell death, and cell-cell interactions. Cell Reports Medicine, 2021, 2, 100287.	3.3	183
22	Characterizing the tumor and immune landscape of melanoma patients treated with combined checkpoint blockade and MAPK targeted therapy.. Journal of Clinical Oncology, 2021, 39, 9522-9522.	0.8	1
23	Plasma from patients with bacterial sepsis or severe COVID-19 induces suppressive myeloid cell production from hematopoietic progenitors in vitro. Science Translational Medicine, 2021, 13, .	5.8	64
24	Profiling SARS-CoV-2 HLA-I peptidome reveals TÂcell epitopes from out-of-frame ORFs. Cell, 2021, 184, 3962-3980.e17.	13.5	98
25	SARS-CoV-2 viremia is associated with distinct proteomic pathways and predicts COVID-19 outcomes. Journal of Clinical Investigation, 2021, 131, .	3.9	94
26	Differentiation of exhausted CD8+ T cells after termination of chronic antigen stimulation stops short of achieving functional T cell memory. Nature Immunology, 2021, 22, 1030-1041.	7.0	63
27	Phenotype, specificity and avidity of antitumour CD8+ T cells in melanoma. Nature, 2021, 596, 119-125.	13.7	239
28	Harnessing the Potential of Multiomics Studies for Precision Medicine in Infectious Disease. Open Forum Infectious Diseases, 2021, 8, ofab483.	0.4	13
29	Early cross-coronavirus reactive signatures of humoral immunity against COVID-19. Science Immunology, 2021, 6, eabj2901.	5.6	67
30	Spatially organized multicellular immune hubs in human colorectal cancer. Cell, 2021, 184, 4734-4752.e20.	13.5	256
31	Increased T-cell receptor repertoire diversity to predict better overall survival in gastrointestinal malignancies.. Journal of Clinical Oncology, 2021, 39, 474-474.	0.8	0
32	Plasma <scp>P</scp>‐selectin is an early marker of thromboembolism in <scp>COVID</scp>‐19. American Journal of Hematology, 2021, 96, E468-E471.	2.0	17
33	Identifying Cell Type-Specific Chemokine Correlates with Hierarchical Signal Extraction from Single-Cell Transcriptomes. , 2021, , .		0
34	Reprogramming NK cells and macrophages via combined antibody and cytokine therapy primes tumors for elimination by checkpoint blockade. Cell Reports, 2021, 37, 110021.	2.9	21
35	Differential pre-malignant programs and microenvironment chart distinct paths to malignancy in human colorectal polyps. Cell, 2021, 184, 6262-6280.e26.	13.5	125
36	Radiation therapy enhances immunotherapy response in microsatellite stable colorectal and pancreatic adenocarcinoma in a phase II trial. Nature Cancer, 2021, 2, 1124-1135.	5.7	112

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37	Transcriptomic Analysis and High-dimensional Phenotypic Mapping of Mononuclear Phagocytes in Mesenteric Lymph Nodes Reveal Differences Between Ulcerative Colitis and Crohnâ€™s Disease. Journal of Crohn's and Colitis, 2020, 14, 393-405.	0.6	12
38	Accelerating Medicines Partnership: Organizational Structure and Preliminary Data From the Phase 1 Studies of Lupus Nephritis. Arthritis Care and Research, 2020, 72, 233-242.	1.5	17
39	Genome-wide CRISPR screen identifies host dependency factors for influenza A virus infection. Nature Communications, 2020, 11, 164.	5.8	136
40	A large peptidome dataset improves HLA class I epitope prediction across most of the human population. Nature Biotechnology, 2020, 38, 199-209.	9.4	324
41	Viral epitope profiling of COVID-19 patients reveals cross-reactivity and correlates of severity. Science, 2020, 370, .	6.0	511
42	Key Parameters of Tumor Epitope Immunogenicity Revealed Through a Consortium Approach Improve Neoantigen Prediction. Cell, 2020, 183, 818-834.e13.	13.5	287
43	Personal Neoantigen Cancer Vaccines: A Road Not Fully Paved. Cancer Immunology Research, 2020, 8, 1465-1469.	1.6	20
44	Cumulus provides cloud-based data analysis for large-scale single-cell and single-nucleus RNA-seq. Nature Methods, 2020, 17, 793-798.	9.0	134
45	Loss of the Nuclear Protein RTF2 Enhances Influenza Virus Replication. Journal of Virology, 2020, 94, .	1.5	5
46	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. Cell, 2020, 182, 1474-1489.e23.	13.5	126
47	Temporal and spatial heterogeneity of host response to SARS-CoV-2 pulmonary infection. Nature Communications, 2020, 11, 6319.	5.8	203
48	MAUDE: inferring expression changes in sorting-based CRISPR screens. Genome Biology, 2020, 21, 134.	3.8	18
49	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. Nature Communications, 2020, 11, 1237.	5.8	38
50	An immune-cell signature of bacterial sepsis. Nature Medicine, 2020, 26, 333-340.	15.2	261
51	B cells and tertiary lymphoid structures promote immunotherapy response. Nature, 2020, 577, 549-555.	13.7	1,421
52	Automated Flow Synthesis of Tumor Neoantigen Peptides for Personalized Immunotherapy. Scientific Reports, 2020, 10, 723.	1.6	21
53	Systematic comparison of single-cell and single-nucleus RNA-sequencing methods. Nature Biotechnology, 2020, 38, 737-746.	9.4	527
54	Single cell transcriptomics identifies focal segmental glomerulosclerosis remission endothelial biomarker. JCI Insight, 2020, 5, .	2.3	108

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55	Integrated urine proteomics and renal single-cell genomics identify an IFN-Î³ response gradient in lupus nephritis. JCI Insight, 2020, 5, .	2.3	57
56	PD-1 blockade in subprimed CD8 cells induces dysfunctional PD-1+CD38hi cells and anti-PD-1 resistance. Nature Immunology, 2019, 20, 1231-1243.	7.0	217
57	1830. Single-cell Transcriptional Profiling Reveals an Immune Cell State Signature of Bacterial Sepsis. Open Forum Infectious Diseases, 2019, 6, S42-S42.	0.4	1
58	Two distinct colonic CD14+ subsets characterized by single-cell RNA profiling in Crohn's disease. Mucosal Immunology, 2019, 12, 703-719.	2.7	44
59	Multiplexed enrichment and genomic profiling of peripheral blood cells reveal subset-specific immune signatures. Science Advances, 2019, 5, eaau9223.	4.7	25
60	Extranuclear DNA accumulates in aged cells and contributes to senescence and inflammation. Aging Cell, 2019, 18, e12901.	3.0	84
61	The immune cell landscape in kidneys of patients with lupus nephritis. Nature Immunology, 2019, 20, 902-914.	7.0	501
62	Defining inflammatory cell states in rheumatoid arthritis joint synovial tissues by integrating single-cell transcriptomics and mass cytometry. Nature Immunology, 2019, 20, 928-942.	7.0	760
63	Streamlined Protocol for Deep Proteomic Profiling of FAC-sorted Cells and Its Application to Freshly Isolated Murine Immune Cells*. Molecular and Cellular Proteomics, 2019, 18, 995a-1009.	2.5	69
64	Landscape of B cell immunity and related immune evasion in human cancers. Nature Genetics, 2019, 51, 560-567.	9.4	115
65	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. Cell, 2019, 176, 1325-1339.e22.	13.5	345
66	204â€¦The immune cell landscape in kidneys of lupus nephritis patients. , 2019, , .		2
67	AB0167â€¦SINGLE CELL RNA EXPRESSION IN LUPUS NEPHRITIS COMPARING AFRICAN-AMERICAN AND CAUCASIAN PATIENTS IDENTIFIES DIFFERENTIAL EXPRESSION OF TYPE I INTERFERON PATHWAY. , 2019, , .		0
68	205â€¦Single cell RNA expression in lupus nephritis comparing african-american and caucasian patients identifies differential expression of type I interferon pathway. , 2019, , .		0
69	Immune receptor repertoires in pediatric and adult acute myeloid leukemia. Genome Medicine, 2019, 11, 73.	3.6	38
70	A secreted PD-L1 splice variant that covalently dimerizes and mediates immunosuppression. Cancer Immunology, Immunotherapy, 2019, 68, 421-432.	2.0	93
71	Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial. Nature, 2019, 565, 234-239.	13.7	956
72	Targeting individual cells by barcode in pooled sequence libraries. Nucleic Acids Research, 2019, 47, e4-e4.	6.5	13

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73	Damaged DNA marching out of aging nucleus. Aging, 2019, 11, 8039-8040.	1.4	2
74	Systems Immunology: Learning the Rules of the Immune System. Annual Review of Immunology, 2018, 36, 813-842.	9.5	70
75	ATIM-32. PERSONALIZED NEOANTIGEN-TARGETING VACCINE GENERATES ROBUST SYSTEMIC AND INTRATUMORAL T CELL RESPONSES IN GLIOBLASTOMA (GBM) PATIENTS. Neuro-Oncology, 2018, 20, vi8-vi8.	0.6	0
76	Defining T Cell States Associated with Response to Checkpoint Immunotherapy in Melanoma. Cell, 2018, 175, 998-1013.e20.	13.5	1,260
77	The Chaperone UNC93B1 Regulates Toll-like Receptor Stability Independently of Endosomal TLR Transport. Immunity, 2018, 48, 911-922.e7.	6.6	92
78	An eQTL Landscape of Kidney Tissue in Human Nephrotic Syndrome. American Journal of Human Genetics, 2018, 103, 232-244.	2.6	147
79	Methods for high-dimensional analysis of cells dissociated from cryopreserved synovial tissue. Arthritis Research and Therapy, 2018, 20, 139.	1.6	93
80	Positional specificity of different transcription factor classes within enhancers. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7222-E7230.	3.3	72
81	A cloning and expression system to probe T-cell receptor specificity and assess functional avidity to neoantigens. Blood, 2018, 132, 1911-1921.	0.6	44
82	Mass Spectrometry Profiling of HLA-Associated Peptidomes in Mono-allelic Cells Enables More Accurate Epitope Prediction. Immunity, 2017, 46, 315-326.	6.6	596
83	Single-cell RNA-seq reveals new types of human blood dendritic cells, monocytes, and progenitors. Science, 2017, 356, .	6.0	1,846
84	Functional screen of MSI2 interactors identifies an essential role for SYNCRIP in myeloid leukemia stem cells. Nature Genetics, 2017, 49, 866-875.	9.4	75
85	Heavy Metal Enlightens Tumor Immunity. Cell, 2017, 169, 567-569.	13.5	6
86	A genome-wide CRISPR screen identifies a restricted set of HIV host dependency factors. Nature Genetics, 2017, 49, 193-203.	9.4	290
87	Resistance to checkpoint blockade therapy through inactivation of antigen presentation. Nature Communications, 2017, 8, 1136.	5.8	686
88	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	13.7	764
89	Aryl Hydrocarbon Receptor Controls Monocyte Differentiation into Dendritic Cells versus Macrophages. Immunity, 2017, 47, 582-596.e6.	6.6	282
90	Challenges and recommendations for epigenomics in precision health. Nature Biotechnology, 2017, 35, 1128-1132.	9.4	19

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91	An immunogenic personal neoantigen vaccine for patients with melanoma. Nature, 2017, 547, 217-221.	13.7	2,112
92	An Integrative Framework Reveals Signaling-to-Transcription Events in Toll-like Receptor Signaling. Cell Reports, 2017, 19, 2853-2866.	2.9	26
93	How T cells spot tumour cells. Nature, 2017, 551, 444-446.	13.7	15
94	Editorial overview: Cancer immunology: genomics & biomarkers: Cancer immunity through the prism of genomics and proteomics. Current Opinion in Immunology, 2016, 41, ix-x.	2.4	0
95	Neoantigens encoded in the cancer genome. Current Opinion in Immunology, 2016, 41, 98-103.	2.4	65
96	Landscape of tumor-infiltrating T cell repertoire of human cancers. Nature Genetics, 2016, 48, 725-732.	9.4	288
97	Impact of autoimmune risk alleles on the immune system. Genome Medicine, 2015, 7, 57.	3.6	3
98	A Regression-Based Analysis of Ribosome-Profiling Data Reveals a Conserved Complexity to Mammalian Translation. Molecular Cell, 2015, 60, 816-827.	4.5	200
99	Meta- and Orthogonal Integration of Influenza â€œOMICsâ€•Data Defines a Role for UBR4 in Virus Budding. Cell Host and Microbe, 2015, 18, 723-735.	5.1	868
100	Dynamic profiling of the protein life cycle in response to pathogens. Science, 2015, 347, 1259038.	6.0	408
101	Molecular and Genetic Properties of Tumors Associated with Local Immune Cytolytic Activity. Cell, 2015, 160, 48-61.	13.5	2,948
102	A Genome-wide CRISPR Screen in Primary Immune Cells to Dissect Regulatory Networks. Cell, 2015, 162, 675-686.	13.5	383
103	ImmVar project: Insights and design considerations for future studies of â€œhealthyâ€•immune variation. Seminars in Immunology, 2015, 27, 51-57.	2.7	53
104	The receptor TREML4 amplifies TLR7-mediated signaling during antiviral responses and autoimmunity. Nature Immunology, 2015, 16, 495-504.	7.0	67
105	Genetic Control of Immune Variation across the Human Population. FASEB Journal, 2015, 29, 369.2.	0.2	0
106	Dnase2a Deficiency Uncovers Lysosomal Clearance of Damaged Nuclear DNA via Autophagy. Cell Reports, 2014, 9, 180-192.	2.9	182
107	Personal neoantigen cancer vaccines. OncoImmunology, 2014, 3, e29311.	2.1	55
108	Locally Disordered Methylation Forms the Basis of Intratumor Methylome Variation in Chronic Lymphocytic Leukemia. Cancer Cell, 2014, 26, 813-825.	7.7	323

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109	Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. Blood, 2014, 124, 453-462.	0.6	286
110	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. Science, 2014, 343, 1246980.	6.0	391
111	Somatic mutation as a mechanism of Wnt/Î²-catenin pathway activation in CLL. Blood, 2014, 124, 1089-1098.	0.6	65
112	Perturbation of m6A Writers Reveals Two Distinct Classes of mRNA Methylation at Internal and 5â€² Sites. Cell Reports, 2014, 8, 284-296.	2.9	972
113	Intersection of population variation and autoimmunity genetics in human T cell activation. Science, 2014, 345, 1254665.	6.0	218
114	CRISPR-Cas9 Knockin Mice for Genome Editing and Cancer Modeling. Cell, 2014, 159, 440-455.	13.5	1,566
115	HLA-Binding Properties of Tumor Neoepitopes in Humans. Cancer Immunology Research, 2014, 2, 522-529.	1.6	194
116	Single-cell RNA-seq reveals dynamic paracrine control of cellular variation. Nature, 2014, 510, 363-369.	13.7	872
117	Getting Personal with Neoantigen-Based Therapeutic Cancer Vaccines. Cancer Immunology Research, 2013, 1, 11-15.	1.6	167
118	Tumor Neoantigens Are Abundant Across Cancers. Blood, 2013, 122, 3265-3265.	0.6	0
119	Reversal of T Cell Exhaustion in Pre-Treatment Marrow T Cells Is Associated with Effective Graft-Versus-Leukemia Responses to Donor Lymphocyte Infusion. Blood, 2012, 120, 1903-1903.	0.6	0
120	A Physical and Regulatory Map of Host-Influenza Interactions Reveals Pathways in H1N1 Infection. Cell, 2009, 139, 1255-1267.	13.5	593