Benjamin D Greenbaum

List of Publications by Year in descending order

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54 papers

7,441 citations

30 h-index 55 g-index

59 all docs 59 docs citations

59 times ranked

16517 citing authors

#	Article	IF	Citations
1	Clinical and Genomic Characterization of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS) Tj ETQq1 1 C Diseases, 2022, 75, e774-e782.).784314 ı 5.8	rgBT /Overlock 5
2	Prolonged SARS-CoV-2 Infection in Patients with Lymphoid Malignancies. Cancer Discovery, 2022, 12, 62-73.	9.4	65
3	The genotypes and phenotypes of missense mutations in the proline domain of the p53 protein. Cell Death and Differentiation, 2022, 29, 938-945.	11.2	18
4	Fundamental immune–oncogenicity trade-offs define driver mutationÂfitness. Nature, 2022, 606, 172-179.	27.8	23
5	Neoantigen quality predicts immunoediting in survivors of pancreatic cancer. Nature, 2022, 606, 389-395.	27.8	80
6	Calreticulin mutant myeloproliferative neoplasms induce MHC-I skewing, which can be overcome by an optimized peptide cancer vaccine. Science Translational Medicine, 2022, 14, .	12.4	10
7	Biomarkers of response to neoadjuvant atezolizumab with gemcitabine and cisplatin in muscle-invasive bladder cancer Journal of Clinical Oncology, 2022, 40, 4584-4584.	1.6	1
8	Frontiers in cancer immunotherapyâ€"a symposium report. Annals of the New York Academy of Sciences, 2021, 1489, 30-47.	3.8	39
9	The Heterogeneous Landscape and Early Evolution of Pathogen-Associated CpG Dinucleotides in SARS-CoV-2. Molecular Biology and Evolution, 2021, 38, 2428-2445.	8.9	15
10	HNRNPM controls circRNA biogenesis and splicing fidelity to sustain cancer cell fitness. ELife, 2021, 10,	6.0	27
11	Pharmacologic modulation of RNA splicing enhances anti-tumor immunity. Cell, 2021, 184, 4032-4047.e31.	28.9	131
12	Probing T-cell response by sequence-based probabilistic modeling. PLoS Computational Biology, 2021, 17, e1009297.	3.2	9
13	Lynch Syndrome and MSI-H Cancers: From Mechanisms to "Off-The-Shelf―Cancer Vaccines. Frontiers in Immunology, 2021, 12, 757804.	4.8	31
14	Mutation-derived Neoantigen-specific T-cell Responses in Multiple Myeloma. Clinical Cancer Research, 2020, 26, 450-464.	7.0	62
15	Role of AID in the temporal pattern of acquisition of driver mutations in multiple myeloma. Leukemia, 2020, 34, 1476-1480.	7.2	39
16	Shared Immunogenic Poly-Epitope Frameshift Mutations in Microsatellite Unstable Tumors. Cell, 2020, 183, 1634-1649.e17.	28.9	103
17	Immunology of COVID-19: Current State of the Science. Immunity, 2020, 52, 910-941.	14.3	1,387
18	Hybrid Gene Origination Creates Human-Virus Chimeric Proteins during Infection. Cell, 2020, 181, 1502-1517.e23.	28.9	33

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19	Genomic analysis of metastatic melanoma in an adult with giant congenital melanocytic nevus. Pigment Cell and Melanoma Research, 2020, 33, 633-636.	3.3	1
20	The Heterogeneous Landscape and Early Evolution of Pathogen-Associated CpG Dinucleotides in SARS-CoV-2. SSRN Electronic Journal, 2020, , 3611280.	0.4	3
21	Phase II study of lamivudine in p53 mutant metastatic colorectal cancer (mCRC) Journal of Clinical Oncology, 2020, 38, 149-149.	1.6	2
22	Reply to †Reconciling disparate estimates of viral genetic diversity during human influenza infections'. Nature Genetics, 2019, 51, 1301-1303.	21.4	3
23	A tumor-specific endogenous repetitive element is induced by herpesviruses. Nature Communications, 2019, 10, 90.	12.8	25
24	Muscle invasive bladder cancer (MIBC) demonstrates neoadjuvant cisplatin-based chemotherapy (NAC) related changes in molecular subtype and immune infiltration Journal of Clinical Oncology, 2019, 37, 443-443.	1.6	0
25	FBXW 7 regulates a mitochondrial transcription program by modulating MITF. Pigment Cell and Melanoma Research, 2018, 31, 636-640.	3.3	13
26	Global Cancer Transcriptome Quantifies Repeat Element Polarization between Immunotherapy Responsive and T Cell Suppressive Classes. Cell Reports, 2018, 23, 512-521.	6.4	90
27	Patient HLA class I genotype influences cancer response to checkpoint blockade immunotherapy. Science, 2018, 359, 582-587.	12.6	834
28	Influenza virus infection causes global RNAPII termination defects. Nature Structural and Molecular Biology, 2018, 25, 885-893.	8.2	48
29	Therapeutic Immune Modulation against Solid Cancers with Intratumoral Poly-ICLC: A Pilot Trial. Clinical Cancer Research, 2018, 24, 4937-4948.	7. O	95
30	Chromatin dependencies in cancer and inflammation. Nature Reviews Molecular Cell Biology, 2018, 19, 245-261.	37.0	64
31	Stage-Specific Human Induced Pluripotent Stem Cells Map the Progression of Myeloid Transformation to Transplantable Leukemia. Cell Stem Cell, 2017, 20, 315-328.e7.	11.1	114
32	Innate Immune Landscape in Early Lung Adenocarcinoma by Paired Single-Cell Analyses. Cell, 2017, 169, 750-765.e17.	28.9	937
33	Transmission Bottleneck Size Estimation from Pathogen Deep-Sequencing Data, with an Application to Human Influenza A Virus. Journal of Virology, 2017, 91, .	3.4	100
34	Innate immune driven evolution via immunostimulatory RNA: Viruses that mimic hosts, tumors that mimic viruses. Current Opinion in Systems Biology, 2017, 1, 137-142.	2.6	3
35	Dengue virus NS2B protein targets cGAS for degradation and prevents mitochondrial DNA sensing during infection. Nature Microbiology, 2017, 2, 17037.	13.3	292
36	Identification of unique neoantigen qualities in long-term survivors of pancreatic cancer. Nature, 2017, 551, 512-516.	27.8	854

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37	A neoantigen fitness model predicts tumour response to checkpoint blockade immunotherapy. Nature, 2017, 551, 517-520.	27.8	532
38	Sequence-Specific Sensing of Nucleic Acids. Trends in Immunology, 2017, 38, 53-65.	6.8	45
39	Diverse repetitive element RNA expression defines epigenetic and immunologic features of colon cancer. JCl Insight, 2017, 2, e91078.	5.0	23
40	Host-Protozoan Interactions Protect from Mucosal Infections through Activation of the Inflammasome. Cell, 2016, 167, 444-456.e14.	28.9	251
41	P53 and the defenses against genome instability caused by transposons and repetitive elements. BioEssays, 2016, 38, 508-513.	2.5	60
42	Fundamental amino acid mass distributions and entropy costs in proteomes. Journal of Theoretical Biology, 2016, 410, 119-124.	1.7	7
43	Targeting Viral Proteostasis Limits Influenza Virus, HIV, and Dengue Virus Infection. Immunity, 2016, 44, 46-58.	14.3	110
44	Quantifying influenza virus diversity and transmission in humans. Nature Genetics, 2016, 48, 195-200.	21.4	182
45	Ion efflux and influenza infection trigger NLRP3 inflammasome signaling in human dendritic cells. Journal of Leukocyte Biology, 2016, 99, 723-734.	3.3	43
46	Revelation of Influencing Factors in Overall Codon Usage Bias of Equine Influenza Viruses. PLoS ONE, 2016, 11, e0154376.	2.5	95
47	Distinguishing the immunostimulatory properties of noncoding RNAs expressed in cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15154-15159.	7.1	69
48	Intrahost Dynamics of Antiviral Resistance in Influenza A Virus Reflect Complex Patterns of Segment Linkage, Reassortment, and Natural Selection. MBio, 2015, 6, .	4.1	58
49	Using First Passage Statistics to Extract Environmentally Dependent Amino Acid Correlations. PLoS ONE, 2014, 9, e101665.	2.5	3
50	Quantitative theory of entropic forces acting on constrained nucleotide sequences applied to viruses. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5054-5059.	7.1	37
51	Bird to Human Transmission Biases and Vaccine Escape Mutants in H5N1 Infections. PLoS ONE, 2014, 9, e100754.	2.5	2
52	Viral reassortment as an information exchange between viral segments. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3341-3346.	7.1	61
53	Oligonucleotide Motifs That Disappear during the Evolution of Influenza Virus in Humans Increase Alpha Interferon Secretion by Plasmacytoid Dendritic Cells. Journal of Virology, 2011, 85, 3893-3904.	3.4	56
54	Patterns of Evolution and Host Gene Mimicry in Influenza and Other RNA Viruses. PLoS Pathogens, 2008, 4, e1000079.	4.7	236