

David Gfeller

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

8,620
citations

81900

39
h-index

106344

65
g-index

82
all docs

82
docs citations

82
times ranked

11924
citing authors

#	ARTICLE	IF	CITATIONS
1	Sensitive identification of neoantigens and cognate TCRs in human solid tumors. <i>Nature Biotechnology</i> , 2022, 40, 656-660.	17.5	41
2	Deciphering the landscape of phosphorylated HLA-II ligands. <i>Science</i> , 2022, 25, 104215.	4.1	3
3	Nongenetic Evolution Drives Lung Adenocarcinoma Spatial Heterogeneity and Progression. <i>Cancer Discovery</i> , 2021, 11, 1490-1507.	9.4	67
4	Prediction of neo-epitope immunogenicity reveals TCR recognition determinants and provides insight into immunoediting. <i>Cell Reports Medicine</i> , 2021, 2, 100194.	6.5	77
5	Tumor-specific cytolytic CD4 T cells mediate immunity against human cancer. <i>Science Advances</i> , 2021, 7, .	10.3	157
6	Inflammatory B cells correlate with failure to checkpoint blockade in melanoma patients. <i>Oncolmmunology</i> , 2021, 10, 1873585.	4.6	15
7	Key Parameters of Tumor Epitope Immunogenicity Revealed Through a Consortium Approach Improve Neoantigen Prediction. <i>Cell</i> , 2020, 183, 818-834.e13.	28.9	287
8	Structural dissimilarity from self drives neoepitope escape from immune tolerance. <i>Nature Chemical Biology</i> , 2020, 16, 1269-1276.	8.0	53
9	Single-cell transcriptomics identifies multiple pathways underlying antitumor function of TCR- and CD81±12-engineered human CD4 ⁺ T cells. <i>Science Advances</i> , 2020, 6, eaaz7809.	10.3	24
10	Mass Spectrometry Based Immunopeptidomics Leads to Robust Predictions of Phosphorylated HLA Class I Ligands. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 390-404.	3.8	47
11	Cathepsin S Regulates Antigen Processing and T Cell Activity in Non-Hodgkin Lymphoma. <i>Cancer Cell</i> , 2020, 37, 674-689.e12.	16.8	55
12	Deciphering the transcriptomic landscape of tumor-infiltrating CD8 lymphocytes in B16 melanoma tumors with single-cell RNA-Seq. <i>Oncolmmunology</i> , 2020, 9, 1737369.	4.6	42
13	EPIC: A Tool to Estimate the Proportions of Different Cell Types from Bulk Gene Expression Data. <i>Methods in Molecular Biology</i> , 2020, 2120, 233-248.	0.9	248
14	Robust prediction of HLA class II epitopes by deep motif deconvolution of immunopeptidomes. <i>Nature Biotechnology</i> , 2019, 37, 1283-1286.	17.5	208
15	Analysis of Secondary Structure Biases in Naturally Presented HLA-I Ligands. <i>Frontiers in Immunology</i> , 2019, 10, 2731.	4.8	8
16	A Phase Ib Study of the Combination of Personalized Autologous Dendritic Cell Vaccine, Aspirin, and Standard of Care Adjuvant Chemotherapy Followed by Nivolumab for Resected Pancreatic Adenocarcinomaâ€”A Proof of Antigen Discovery Feasibility in Three Patients. <i>Frontiers in Immunology</i> , 2019, 10, 1832.	4.8	73
17	CD56 as a marker of an ILC1-like population with NK cell properties that is functionally impaired in AML. <i>Blood Advances</i> , 2019, 3, 3674-3687.	5.2	40
18	Immunopeptidomics of colorectal cancer organoids reveals a sparse HLA class I neoantigen landscape and no increase in neoantigens with interferon or MEK-inhibitor treatment. , 2019, 7, 309.		112

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19	Allosteric Modulation of Binding Specificity by Alternative Packing of Protein Cores. <i>Journal of Molecular Biology</i> , 2019, 431, 336-350.	4.2	20
20	Intratumoral Tcf1+PD-1+CD8+ T Cells with Stem-like Properties Promote Tumor Control in Response to Vaccination and Checkpoint Blockade Immunotherapy. <i>Immunity</i> , 2019, 50, 195-211.e10.	14.3	924
21	Single Cell RNA Sequencing Identifies Transcriptional Programs That Enhance Anti-Tumor Function of Transgenic CD4+ T Cells Redirected with TCR and CD8 $\hat{+}$ 1 $\hat{2}$. <i>Blood</i> , 2019, 134, 250-250.	1.4	0
22	Computational KIR copy number discovery reveals interaction between inhibitory receptor burden and survival. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019, 24, 148-159.	0.7	1
23	Personalized cancer vaccine effectively mobilizes antitumor T cell immunity in ovarian cancer. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	326
24	High-throughput and Sensitive Immunopeptidomics Platform Reveals Profound Interferon $\hat{3}$ -Mediated Remodeling of the Human Leukocyte Antigen (HLA) Ligandome. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 533-548.	3.8	224
25	The C-terminal extension landscape of naturally presented HLA-I ligands. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5083-5088.	7.1	48
26	Sensitive and frequent identification of high avidity neo-epitope \hat{A} specific CD8 + T cells in immunotherapy-naive ovarian cancer. <i>Nature Communications</i> , 2018, 9, 1092.	12.8	122
27	The Length Distribution and Multiple Specificity of Naturally Presented HLA-I Ligands. <i>Journal of Immunology</i> , 2018, 201, 3705-3716.	0.8	145
28	Estimating the Contribution of Proteasomal Spliced Peptides to the HLA-I Ligandome*. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2347-2357.	3.8	105
29	Deciphering the Evolution of Vertebrate Immune Cell Types with Single-Cell RNA-Seq. , 2018, , 95-111.		1
30	Polymorphic sites preferentially avoid co-evolving residues in MHC class I proteins. <i>PLoS Computational Biology</i> , 2018, 14, e1006188.	3.2	6
31	Predicting Antigen Presentation \hat{e} ”What Could We Learn From a Million Peptides?. <i>Frontiers in Immunology</i> , 2018, 9, 1716.	4.8	159
32	Broad and Conserved Immune Regulation by Genetically Heterogeneous Melanoma Cells. <i>Cancer Research</i> , 2017, 77, 1623-1636.	0.9	13
33	Single-cell transcriptome analysis of fish immune cells provides insight into the evolution of vertebrate immune cell types. <i>Genome Research</i> , 2017, 27, 451-461.	5.5	126
34	Identification of innate lymphoid cells in single-cell RNA-Seq data. <i>Immunogenetics</i> , 2017, 69, 439-450.	2.4	13
35	The pathogen-related yeast protein Pry1, a member of the CAP protein superfamily, is a fatty acid-binding protein. <i>Journal of Biological Chemistry</i> , 2017, 292, 8304-8314.	3.4	40
36	Tumour-derived PGD2 and NKp30-B7H6 engagement drives an immunosuppressive ILC2-MDSC axis. <i>Nature Communications</i> , 2017, 8, 593.	12.8	175

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37	“Hotspots”™ of Antigen Presentation Revealed by Human Leukocyte Antigen Ligandomics for Neoantigen Prioritization. <i>Frontiers in Immunology</i> , 2017, 8, 1367.	4.8	133
38	Simultaneous enumeration of cancer and immune cell types from bulk tumor gene expression data. <i>ELife</i> , 2017, 6, .	6.0	795
39	ILC2-modulated T cell-to-MDSC balance is associated with bladder cancer recurrence. <i>Journal of Clinical Investigation</i> , 2017, 127, 2916-2929.	8.2	176
40	Deciphering HLA-I motifs across HLA peptidomes improves neo-antigen predictions and identifies allosteric regulating HLA specificity. <i>PLoS Computational Biology</i> , 2017, 13, e1005725.	3.2	250
41	Current tools for predicting cancer-specific T cell immunity. <i>Oncotarget</i> , 2016, 5, e1177691.	4.6	45
42	Unsupervised HLA Peptidome Deconvolution Improves Ligand Prediction Accuracy and Predicts Cooperative Effects in Peptide-HLA Interactions. <i>Journal of Immunology</i> , 2016, 197, 2492-2499.	0.8	150
43	The SIB Swiss Institute of Bioinformatics™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	14.5	64
44	Protein homology reveals new targets for bioactive small molecules. <i>Bioinformatics</i> , 2015, 31, 2721-2727.	4.1	9
45	Baseline serum predictors of clinical response to CTLA4 inhibitor therapy in melanoma patients.. <i>Journal of Clinical Oncology</i> , 2015, 33, 3025-3025.	1.6	0
46	Prediction and Experimental Characterization of nsSNPs Altering Human PDZ-Binding Motifs. <i>PLoS ONE</i> , 2014, 9, e94507.	2.5	10
47	SwissTargetPrediction: a web server for target prediction of bioactive small molecules. <i>Nucleic Acids Research</i> , 2014, 42, W32-W38.	14.5	977
48	A Structural Portrait of the PDZ Domain Family. <i>Journal of Molecular Biology</i> , 2014, 426, 3509-3519.	4.2	71
49	The caveolin-binding motif of the pathogen-related yeast protein Pry1, a member of the CAP protein superfamily, is required for in vivo export of cholesteryl acetate. <i>Journal of Lipid Research</i> , 2014, 55, 883-894.	4.2	35
50	Shaping the interaction landscape of bioactive molecules. <i>Bioinformatics</i> , 2013, 29, 3073-3079.	4.1	327
51	Improving Binding Affinity and Stability of Peptide Ligands by Substituting Glycines with Amino Acids. <i>ChemBioChem</i> , 2013, 14, 1316-1322.	2.6	56
52	Susceptibility and adaptation to human TRIM5 α alleles at positive selected sites in HIV-1 capsid. <i>Virology</i> , 2013, 441, 162-170.	2.4	12
53	SH3 interactome conserves general function over specific form. <i>Molecular Systems Biology</i> , 2013, 9, 652.	7.2	61
54	Beyond the Binding Site: The Role of the β 2- β 3 Loop and Extra-Domain Structures in PDZ Domains. <i>PLoS Computational Biology</i> , 2012, 8, e1002429.	3.2	40

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55	SwissSidechain: a molecular and structural database of non-natural sidechains. <i>Nucleic Acids Research</i> , 2012, 41, D327-D332.	14.5	100
56	Sequence Determinants of a Microtubule Tip Localization Signal (MtLS). <i>Journal of Biological Chemistry</i> , 2012, 287, 28227-28242.	3.4	44
57	MUSI: an integrated system for identifying multiple specificity from very large peptide or nucleic acid data sets. <i>Nucleic Acids Research</i> , 2012, 40, e47-e47.	14.5	45
58	Uncovering new aspects of protein interactions through analysis of specificity landscapes in peptide recognition domains. <i>FEBS Letters</i> , 2012, 586, 2764-2772.	2.8	13
59	Expanding molecular modeling and design tools to non-natural sidechains. <i>Journal of Computational Chemistry</i> , 2012, 33, 1525-1535.	3.3	27
60	The multiple-specificity landscape of modular peptide recognition domains. <i>Molecular Systems Biology</i> , 2011, 7, 484.	7.2	78
61	Functional complexes between YAP2 and ZO-2 are PDZ domain-dependent, and regulate YAP2 nuclear localization and signalling. <i>Biochemical Journal</i> , 2010, 432, 461-478.	3.7	180
62	Coevolution of PDZ domain-ligand interactions analyzed by high-throughput phage display and deep sequencing. <i>Molecular BioSystems</i> , 2010, 6, 1782.	2.9	107
63	Bayesian Modeling of the Yeast SH3 Domain Interactome Predicts Spatiotemporal Dynamics of Endocytosis Proteins. <i>PLoS Biology</i> , 2009, 7, e1000218.	5.6	172
64	How to visually interpret biological data using networks. <i>Nature Biotechnology</i> , 2009, 27, 921-924.	17.5	93
65	Spectral Coarse Graining and Synchronization in Oscillator Networks. <i>Physical Review Letters</i> , 2008, 100, 174104.	7.8	68
66	Uncovering the topology of configuration space networks. <i>Physical Review E</i> , 2007, 76, 026113.	2.1	29
67	Complex network analysis of free-energy landscapes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1817-1822.	7.1	159
68	Spectral Coarse Graining of Complex Networks. <i>Physical Review Letters</i> , 2007, 99, 038701.	7.8	95
69	Finding instabilities in the community structure of complex networks. <i>Physical Review E</i> , 2005, 72, 056135.	2.1	109