

Elena Zaslavsky

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

2,168
citations

394421

19
h-index

361022

35
g-index

50
all docs

50
docs citations

50
times ranked

4656
citing authors

#	ARTICLE	IF	CITATIONS
1	Anti-invasive efficacy and survival benefit of the YAP-TEAD inhibitor verteporfin in preclinical glioblastoma models. <i>Neuro-Oncology</i> , 2022, 24, 694-707.	1.2	29
2	Skeletal muscle transcriptome response to a bout of endurance exercise in physically active and sedentary older adults. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2022, 322, E260-E277.	3.5	13
3	Single nucleus transcriptome and chromatin accessibility of postmortem human pituitaries reveal diverse stem cell regulatory mechanisms. <i>Cell Reports</i> , 2022, 38, 110467.	6.4	27
4	Asymptomatic SARS-CoV-2 Infection Is Associated With Higher Levels of Serum IL-17C, Matrix Metalloproteinase 10 and Fibroblast Growth Factors Than Mild Symptomatic COVID-19. <i>Frontiers in Immunology</i> , 2022, 13, 821730.	4.8	21
5	Comparing Host Module Activation Patterns and Temporal Dynamics in Infection by Influenza H1N1 Viruses. <i>Frontiers in Immunology</i> , 2021, 12, 691758.	4.8	0
6	Advances in the computational landscape for repurposed drugs against COVID-19. <i>Drug Discovery Today</i> , 2021, 26, 2800-2815.	6.4	19
7	Attenuated activation of pulmonary immune cells in mRNA-1273 vaccinated hamsters after SARS-CoV-2 infection. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	23
8	EPCO-05. GENOME-WIDE ANALYSIS OF TEAD1 OCCUPANCY IN BIOLOGICALLY DISTINCT GLIOBLASTOMA SAMPLES. <i>Neuro-Oncology</i> , 2021, 23, vi2-vi2.	1.2	0
9	Distinct peripheral blood molecular signature emerges with successful tacrolimus withdrawal in kidney transplant recipients. <i>American Journal of Transplantation</i> , 2020, 20, 3477-3485.	4.7	4
10	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. <i>Cell</i> , 2020, 181, 1464-1474.	28.9	147
11	Single-cell transcriptional profiles in human skeletal muscle. <i>Scientific Reports</i> , 2020, 10, 229.	3.3	188
12	Deciphering the combinatorial landscape of immunity. <i>ELife</i> , 2020, 9, .	6.0	6
13	Abstract 1111: Verteporfin inhibits GBM growth and migration and confers survival benefit in xenograft models. , 2020, , .		0
14	EXTH-51. ANTI-INVASIVE EFFICACY AND SURVIVAL BENEFIT OF THE YAP-TEAD INHIBITOR VERTEPORFIN IN PRECLINICAL GLIOBLASTOMA MODELS. <i>Neuro-Oncology</i> , 2020, 22, ii98-ii98.	1.2	0
15	Innate Immune Response to Influenza Virus at Single-Cell Resolution in Human Epithelial Cells Revealed Paracrine Induction of Interferon Lambda 1. <i>Journal of Virology</i> , 2019, 93, .	3.4	65
16	Pathway-level information extractor (PLIER) for gene expression data. <i>Nature Methods</i> , 2019, 16, 607-610.	19.0	74
17	ANGI-04. TEAD1 REGULATES CELL MIGRATION IN HUMAN GLIOBLASTOMA IN PART THROUGH EMT-ASSOCIATED CADHERINS. <i>Neuro-Oncology</i> , 2018, 20, vi29-vi29.	1.2	0
18	Interpretation of an individual functional genomics experiment guided by massive public data. <i>Nature Methods</i> , 2018, 15, 1049-1052.	19.0	5

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19	Analysis of chromatin accessibility uncovers TEAD1 as a regulator of migration in human glioblastoma. <i>Nature Communications</i> , 2018, 9, 4020.	12.8	64
20	High resolution annotation of zebrafish transcriptome using long-read sequencing. <i>Genome Research</i> , 2018, 28, 1415-1425.	5.5	69
21	Regulatory Architecture of the L ¹ T ² Gonadotrope Cell Underlying the Response to Gonadotropin-Releasing Hormone. <i>Frontiers in Endocrinology</i> , 2018, 9, 34.	3.5	15
22	Prospective Isolation and Comparison of Human Germinal Matrix and Glioblastoma EGFR + Populations with Stem Cell Properties. <i>Stem Cell Reports</i> , 2017, 8, 1421-1429.	4.8	16
23	Pandemic H1N1 influenza A viruses suppress immunogenic RIPK3-driven dendritic cell death. <i>Nature Communications</i> , 2017, 8, 1931.	12.8	44
24	GENE-11. CHROMATIN ACCESSIBILITY DEFINES TRANSCRIPTIONAL DRIVERS OF MIGRATION IN HUMAN GLIOBLASTOMA. <i>Neuro-Oncology</i> , 2017, 19, vi94-vi95.	1.2	0
25	The Transcriptional Activator KrÄ½ppel-like Factor-6 Is Required for CNS Myelination. <i>PLoS Biology</i> , 2016, 14, e1002467.	5.6	31
26	STMC-28. INTACT EGFR DEFINES HUMAN GERMINAL MATRIX AND GLIOBLASTOMA POPULATIONS WITH SHARED AND EPIGENETICALLY IMPRINTED STEM CELL PROPERTIES. <i>Neuro-Oncology</i> , 2016, 18, vi188-vi188.	1.2	0
27	CellCODE: a robust latent variable approach to differential expression analysis for heterogeneous cell populations. <i>Bioinformatics</i> , 2015, 31, 1584-1591.	4.1	96
28	Human Dendritic Cell Response Signatures Distinguish 1918, Pandemic, and Seasonal H1N1 Influenza Viruses. <i>Journal of Virology</i> , 2015, 89, 10190-10205.	3.4	27
29	Understanding multicellular function and disease with human tissue-specific networks. <i>Nature Genetics</i> , 2015, 47, 569-576.	21.4	738
30	Astrocytic TYMP and VEGFA drive blood-brain barrier opening in inflammatory central nervous system lesions. <i>Brain</i> , 2015, 138, 1548-1567.	7.6	123
31	Interactive Big Data Resource to Elucidate Human Immune Pathways and Diseases. <i>Immunity</i> , 2015, 43, 605-614.	14.3	49
32	Reconstruction of regulatory networks through temporal enrichment profiling and its application to H1N1 influenza viral infection. <i>BMC Bioinformatics</i> , 2013, 14, S1.	2.6	11
33	Î²-Catenin Regulates GnRH-Induced FSHÎ² Gene Expression. <i>Molecular Endocrinology</i> , 2013, 27, 224-237.	3.7	17
34	Computational approaches to understanding dendritic cell responses to influenza virus infection. <i>Immunologic Research</i> , 2012, 54, 160-168.	2.9	3
35	A cost-aggregating integer linear program for motif finding. <i>Journal of Discrete Algorithms</i> , 2011, 9, 326-334.	0.7	2
36	Inferring PDZ Domain Multi-Mutant Binding Preferences from Single-Mutant Data. <i>PLoS ONE</i> , 2010, 5, e12787.	2.5	7

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37	Antiviral Response Dictated by Choreographed Cascade of Transcription Factors. Journal of Immunology, 2010, 184, 2908-2917.	0.8	46
38	The Construction and Use of Log-Odds Substitution Scores for Multiple Sequence Alignment. PLoS Computational Biology, 2010, 6, e1000852.	3.2	58
39	<i>M</i> are better than one: an ensemble-based motif finder and its application to regulatory element prediction. Bioinformatics, 2009, 25, 868-874.	4.1	19
40	Graph-based Approaches for Motif Discovery. , 2009, , 83-99.		0
41	A combinatorial optimization approach for diverse motif finding applications. Algorithms for Molecular Biology, 2006, 1, 13.	1.2	25
42	A Compact Mathematical Programming Formulation for DNA Motif Finding. Lecture Notes in Computer Science, 2006, , 233-245.	1.3	7
43	Comparative analysis of methods for representing and searching for transcription factor binding sites. Bioinformatics, 2004, 20, 3516-3525.	4.1	62