David S Deluca

List of Publications by Year
in descending order

39 papers	16,234 citations	394421 19 h-index	345221 36 g-index
40 all docs	40 docs citations	40 times ranked	38082 citing authors

#	Article	IF	Citations
1	MicroRNA-449a Inhibits Triple Negative Breast Cancer by Disturbing DNA Repair and Chromatid Separation. International Journal of Molecular Sciences, 2022, 23, 5131.	4.1	1
2	Single cell versus single nucleus: transcriptome differences in the murine kidney after ischemia-reperfusion injury. American Journal of Physiology - Renal Physiology, 2022, 323, F171-F181.	2.7	5
3	Polymerization of misfolded Z alpha-1 antitrypsin protein lowers CX3CR1 expression in human PBMCs. ELife, 2021, 10, .	6.0	4
4	The Delivery of Î±1-Antitrypsin Therapy Through Transepidermal Route: Worthwhile to Explore. Frontiers in Pharmacology, 2020, 11, 983.	3.5	9
5	ILâ€17 regulates DC migration to the peribronchial LNs and allergen presentation in experimental allergic asthma. European Journal of Immunology, 2020, 50, 1019-1033.	2.9	14
6	Smokers with COPD Show a Shift in Energy and Nitrogen Metabolism at Rest and During Exercise . International Journal of COPD, 2020, Volume 15, 1-13.	2.3	4
7	Serum Levels of Alpha1-antitrypsin and Their Relationship With COPD in the General Spanish Population. Archivos De Bronconeumologia, 2020, 56, 76-83.	0.8	22
8	A comparison of curated gene sets versus transcriptomics-derived gene signatures for detecting pathway activation in immune cells. BMC Bioinformatics, 2020, 21, 28.	2.6	4
9	SERPINA1 gene polymorphisms in a populationâ€based ALSPAC cohort. Pediatric Pulmonology, 2019, 54, 1474-1478.	2.0	6
10	Clinical Significance of SERPINA1 Gene and Its Encoded Alpha1-antitrypsin Protein in NSCLC. Cancers, 2019, 11, 1306.	3.7	52
11	The FMS-like tyrosine kinase-3 ligand/lung dendritic cell axis contributes to regulation of pulmonary fibrosis. Thorax, 2019, 74, 947-957.	5.6	24
12	Complications and risk factors in pediatric bronchoscopy in a tertiary pediatric respiratory center. Pediatric Pulmonology, 2018, 53, 619-627.	2.0	24
13	Transcriptomic Characterization of SF3B1 Mutation Reveals Its Pleiotropic Effects in Chronic Lymphocytic Leukemia. Cancer Cell, 2016, 30, 750-763.	16.8	173
14	Filtration and Normalization of Sequencing Read Data in Whole-Metagenome Shotgun Samples. PLoS ONE, 2016, 11, e0165015.	2.5	22
15	The human transcriptome across tissues and individuals. Science, 2015, 348, 660-665.	12.6	1,127
16	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	12.6	4,659
17	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	12.6	252
18	A Novel Approach to High-Quality Postmortem Tissue Procurement: The GTEx Project. Biopreservation and Biobanking, 2015, 13, 311-319.	1.0	674

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19	A Pan-Cancer Analysis of Transcriptome Changes Associated with Somatic Mutations in U2AF1 Reveals Commonly Altered Splicing Events. PLoS ONE, 2014, 9, e87361.	2.5	168
20	Complementary genomic approaches highlight the PI3K/mTOR pathway as a common vulnerability in osteosarcoma. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5564-73.	7.1	355
21	Human Leukocyte Antigen Typing Using a Knowledge Base Coupled with a High-Throughput Oligonucleotide Probe Array Analysis. Frontiers in Immunology, 2014, 5, 597.	4.8	3
22	SOX2 and p63 colocalize at genetic loci in squamous cell carcinomas. Journal of Clinical Investigation, 2014, 124, 1636-1645.	8.2	151
23	Comparative analysis of RNA sequencing methods for degraded or low-input samples. Nature Methods, 2013, 10, 623-629.	19.0	419
24	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	21.4	6,815
25	SF3B1 Mutation Alters The Selection Of 3' RNA Splice Sites In Chronic Lymphocytic Leukemia. Blood, 2013, 122, 117-117.	1.4	2
26	Tumor Neoantigens Are Abundant Across Cancers. Blood, 2013, 122, 3265-3265.	1.4	0
27	Mutated BCR-ABL Generates Immunogenic T-cell Epitopes in CML Patients. Clinical Cancer Research, 2012, 18, 5761-5772.	7.0	57
28	Systematic Identification of Personal Mutated Tumor-Specific Neoantigens in CLL. Blood, 2012, 120, 954-954.	1.4	0
29	SF3B1and Other Novel Cancer Genes in Chronic Lymphocytic Leukemia. New England Journal of Medicine, 2011, 365, 2497-2506.	27.0	1,021
30	MULTIPRED2: A computational system for large-scale identification of peptides predicted to bind to HLA supertypes and alleles. Journal of Immunological Methods, 2011, 374, 53-61.	1.4	55
31	Novel sequence feature variant type analysis of the HLA genetic association in systemic sclerosis. Human Molecular Genetics, 2010, 19, 707-719.	2.9	37
32	Peptides Derived From Mutated BCR-ABL Elicit T Cell Immunity In CML Patients. Blood, 2010, 116, 887-887.	1.4	1
33	High-throughput minor histocompatibility antigen prediction. Bioinformatics, 2009, 25, 2411-2417.	4.1	11
34	MaHCO: an ontology of the major histocompatibility complex for immunoinformatic applications and text mining. Bioinformatics, 2009, 25, 2064-2070.	4.1	9
35	Factor VIII Is a Potential Autosomal B Cell Minor Histocompatibility Antigen in Chronic Gvhd.. Blood, 2009, 114, 1167-1167.	1.4	0
36	Amino acid 95 causes strong alteration of peptide position PÎ© in HLA-B*41 variants. Immunogenetics, 2007, 59, 253-259.	2.4	25

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37	Implementing the Modular MHC Model for Predicting Peptide Binding. Methods in Molecular Biology, 2007, 409, 261-271.	0.9	4
38	A modular concept of HLA for comprehensive peptide binding prediction. Immunogenetics, 2006, 59, 25-35.	2.4	22
39	The Replacement Mutation in HLA-DRB1*1211 Affects a Likely Keystone Position. Human Immunology, 2005, 66, 1254-1257.	2.4	3