

# Richard H Scheuermann

## List of Publications by Year in descending order

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145  
papers

15,849  
citations

44444

50  
h-index

24511

114  
g-index

176  
all docs

176  
docs citations

176  
times ranked

28827  
citing authors

#	ARTICLE	IF	CITATIONS
1	Defining the risk of SARS-CoV-2 variants on immune protection. <i>Nature</i> , 2022, 605, 640-652.	13.7	117
2	Genomic evolution of the Coronaviridae family. <i>Virology</i> , 2022, 570, 123-133.	1.1	13
3	The genome and preliminary single-nuclei transcriptome of <i>Lemna minuta</i> reveals mechanisms of invasiveness. <i>Plant Physiology</i> , 2022, 188, 879-897.	2.3	13
4	Cell type matching in single-cell RNA-sequencing data using FR-Match. <i>Scientific Reports</i> , 2022, 12, .	1.6	12
5	Acute flaccid myelitis: cause, diagnosis, and management. <i>Lancet</i> , The, 2021, 397, 334-346.	6.3	88
6	Standardization of assay representation in the Ontology for Biomedical Investigations. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	5
7	SARS-CoV-2 infection of the oral cavity and saliva. <i>Nature Medicine</i> , 2021, 27, 892-903.	15.2	527
8	A system-view of <i>Bordetella pertussis</i> booster vaccine responses in adults primed with whole-cell versus acellular vaccine in infancy. <i>JCI Insight</i> , 2021, 6, .	2.3	10
9	A machine learning method for the discovery of minimum marker gene combinations for cell type identification from single-cell RNA sequencing. <i>Genome Research</i> , 2021, 31, 1767-1780.	2.4	50
10	Impact of SARS-CoV-2 variants on the total CD4+ and CD8+ T cell reactivity in infected or vaccinated individuals. <i>Cell Reports Medicine</i> , 2021, 2, 100355.	3.3	490
11	Database and Analytical Resources for Viral Research Community. , 2021, , 141-152.		4
12	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021, 598, 111-119.	13.7	361
13	Machine Learning-Based Single Cell and Integrative Analysis Reveals That Baseline mDC Predisposition Correlates With Hepatitis B Vaccine Antibody Response. <i>Frontiers in Immunology</i> , 2021, 12, 690470.	2.2	8
14	Machine Learning of Discriminative Gate Locations for Clinical Diagnosis. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 97, 296-307.	1.1	8
15	Systems Biology Methods Applied to Blood and Tissue for a Comprehensive Analysis of Immune Response to Hepatitis B Vaccine in Adults. <i>Frontiers in Immunology</i> , 2020, 11, 580373.	2.2	28
16	Guidelines for reporting single-cell RNA-seq experiments. <i>Nature Biotechnology</i> , 2020, 38, 1384-1386.	9.4	27
17	Epidemiology and Sequence-Based Evolutionary Analysis of Circulating Non-Polio Enteroviruses. <i>Microorganisms</i> , 2020, 8, 1856.	1.6	23
18	A community-based transcriptomics classification and nomenclature of neocortical cell types. <i>Nature Neuroscience</i> , 2020, 23, 1456-1468.	7.1	183

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19	FR-Match: robust matching of cell type clusters from single cell RNA sequencing data using the Friedman-Rafsky non-parametric test. <i>Briefings in Bioinformatics</i> , 2020, 22, .	3.2	12
20	Multi-Omic Data Integration Allows Baseline Immune Signatures to Predict Hepatitis B Vaccine Response in a Small Cohort. <i>Frontiers in Immunology</i> , 2020, 11, 578801.	2.2	20
21	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	3.3	68
22	Unbiased analysis of peripheral blood mononuclear cells reveals CD4 T cell response to RSV matrix protein. <i>Vaccine: X</i> , 2020, 5, 100065.	0.9	0
23	A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. <i>Cell Host and Microbe</i> , 2020, 27, 671-680.e2.	5.1	893
24	Transcriptomic evidence that von Economo neurons are regionally specialized extratelencephalic-projecting excitatory neurons. <i>Nature Communications</i> , 2020, 11, 1172.	5.8	70
25	Candidate Targets for Immune Responses to 2019-Novel Coronavirus (nCoV): Sequence Homology- and Bioinformatic-Based Predictions. <i>SSRN Electronic Journal</i> , 2020, , 3541361.	0.4	13
26	1409. Genomic Variation Among Respiratory Syncytial Viruses. <i>Open Forum Infectious Diseases</i> , 2020, 7, S712-S712.	0.4	0
27	Classification of human Herpesviridae proteins using Domain-architecture Aware Inference of Orthologs (DAIO). <i>Virology</i> , 2019, 529, 29-42.	1.1	12
28	A survey of known immune epitopes in the enteroviruses strains associated with acute flaccid myelitis. <i>Human Immunology</i> , 2019, 80, 923-929.	1.2	11
29	Conserved cell types with divergent features in human versus mouse cortex. <i>Nature</i> , 2019, 573, 61-68.	13.7	1,198
30	Hepatitis C Virus Database and Bioinformatics Analysis Tools in the Virus Pathogen Resource (ViPR). <i>Methods in Molecular Biology</i> , 2019, 1911, 47-69.	0.4	4
31	Differential transcriptome and development of human peripheral plasma cell subsets. <i>JCI Insight</i> , 2019, 4, .	2.3	41
32	DAFi: A directed recursive data filtering and clustering approach for improving and interpreting data clustering identification of cell populations from polychromatic flow cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2018, 93, 597-610.	1.1	18
33	Cell type discovery using single-cell transcriptomics: implications for ontological representation. <i>Human Molecular Genetics</i> , 2018, 27, R40-R47.	1.4	63
34	Allergen-specific immunotherapy modulates the balance of circulating Tfh and Tfr cells. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 775-777.e6.	1.5	45
35	Single-nucleus and single-cell transcriptomes compared in matched cortical cell types. <i>PLoS ONE</i> , 2018, 13, e0209648.	1.1	400
36	Contemporary Circulating Enterovirus D68 Strains Have Acquired the Capacity for Viral Entry and Replication in Human Neuronal Cells. <i>MBio</i> , 2018, 9, .	1.8	79

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37	Chromosome Yâ€‘encoded antigens associate with acute graft-versus-host disease in sex-mismatched stem cell transplant. <i>Blood Advances</i> , 2018, 2, 2419-2429.	2.5	11
38	VDJServer: A Cloud-Based Analysis Portal and Data Commons for Immune Repertoire Sequences and Rearrangements. <i>Frontiers in Immunology</i> , 2018, 9, 976.	2.2	68
39	Bioinformatics Meets Virology: The European Virus Bioinformatics Centerâ€™s Second Annual Meeting. <i>Viruses</i> , 2018, 10, 256.	1.5	6
40	Transcriptomic and morphophysiological evidence for a specialized human cortical GABAergic cell type. <i>Nature Neuroscience</i> , 2018, 21, 1185-1195.	7.1	212
41	An Integrated Workflow To Assess Technical and Biological Variability of Cell Population Frequencies in Human Peripheral Blood by Flow Cytometry. <i>Journal of Immunology</i> , 2017, 198, 1748-1758.	0.4	69
42	A bioinformatics roadmap for the human vaccines project. <i>Expert Review of Vaccines</i> , 2017, 16, 535-544.	2.0	6
43	PRODUCTION OF A PRELIMINARY QUALITY CONTROL PIPELINE FOR SINGLE NUCLEI RNA-SEQ AND ITS APPLICATION IN THE ANALYSIS OF CELL TYPE DIVERSITY OF POST-MORTEM HUMAN BRAIN NEOCORTEX. , 2017, 22, 564-575.		8
44	Automated Analysis of Clinical Flow Cytometry Data. <i>Clinics in Laboratory Medicine</i> , 2017, 37, 931-944.	0.7	7
45	Fast and accurate HLA typing from short-read next-generation sequence data with xHLA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8059-8064.	3.3	118
46	Influenza Research Database: An integrated bioinformatics resource for influenza virus research. <i>Nucleic Acids Research</i> , 2017, 45, D466-D474.	6.5	293
47	Automated Analysis of Flow Cytometry Data to Reduce Inter-Lab Variation in the Detection of Major Histocompatibility Complex Multimer-Binding T Cells. <i>Frontiers in Immunology</i> , 2017, 8, 858.	2.2	9
48	Comprehensive Annotation of Mature Peptides and Genotypes for Zika Virus. <i>PLoS ONE</i> , 2017, 12, e0170462.	1.1	21
49	VDJPipe: a pipelined tool for pre-processing immune repertoire sequencing data. <i>BMC Bioinformatics</i> , 2017, 18, 448.	1.2	18
50	Cell type discovery and representation in the era of high-content single cell phenotyping. <i>BMC Bioinformatics</i> , 2017, 18, 559.	1.2	51
51	Identification of diagnostic peptide regions that distinguish Zika virus from related mosquito-borne Flaviviruses. <i>PLoS ONE</i> , 2017, 12, e0178199.	1.1	26
52	Genetic changes found in a distinct clade of Enterovirus D68 associated with paralysis during the 2014 outbreak. <i>Virus Evolution</i> , 2016, 2, vew015.	2.2	44
53	The Ontology for Biomedical Investigations. <i>PLoS ONE</i> , 2016, 11, e0154556.	1.1	217
54	A Phylogeny-Based Global Nomenclature System and Automated Annotation Tool for H1 Hemagglutinin Genes from Swine Influenza A Viruses. <i>MSphere</i> , 2016, 1, .	1.3	151

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55	A benchmark for evaluation of algorithms for identification of cellular correlates of clinical outcomes. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2016, 89, 16-21.	1.1	65
56	Mapping cell populations in flow cytometry data for cross-sample comparison using the Friedman-Rafsky test statistic as a distance measure. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2016, 89, 71-88.	1.1	20
57	Automated analysis of flow cytometry data comes of age. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2016, 89, 13-15.	1.1	23
58	Standardizing Flow Cytometry Immunophenotyping Analysis from the Human Immunophenotyping Consortium. <i>Scientific Reports</i> , 2016, 6, 20686.	1.6	240
59	VDJML: a file format with tools for capturing the results of inferring immune receptor rearrangements. <i>BMC Bioinformatics</i> , 2016, 17, 333.	1.2	16
60	Using single nuclei for RNA-seq to capture the transcriptome of postmortem neurons. <i>Nature Protocols</i> , 2016, 11, 499-524.	5.5	358
61	Zika virus: designate standardized names. <i>Nature</i> , 2016, 531, 173-173.	13.7	3
62	State-of-the-Art in the Computational Analysis of Cytometry Data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2015, 87, 591-593.	1.1	13
63	A RESTful API for Access to Phylogenetic Tools via the CIPRES Science Gateway. <i>Evolutionary Bioinformatics</i> , 2015, 11, EBO.S21501.	0.6	390
64	FlowGate. , 2015, , .		5
65	Thinking Outside the Gate: Single-Cell Assessments in Multiple Dimensions. <i>Immunity</i> , 2015, 42, 591-592.	6.6	67
66	Diversifying Selection Analysis Predicts Antigenic Evolution of 2009 Pandemic H1N1 Influenza A Virus in Humans. <i>Journal of Virology</i> , 2015, 89, 5427-5440.	1.5	21
67	flowCL: ontology-based cell population labelling in flow cytometry. <i>Bioinformatics</i> , 2015, 31, 1337-1339.	1.8	25
68	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. <i>PLoS ONE</i> , 2014, 9, e99979.	1.1	34
69	A comprehensive collection of systems biology data characterizing the host response to viral infection. <i>Scientific Data</i> , 2014, 1, 140033.	2.4	62
70	Toward a method for tracking virus evolutionary trajectory applied to the pandemic H1N1 2009 influenza virus. <i>Infection, Genetics and Evolution</i> , 2014, 28, 351-357.	1.0	3
71	Response of human skin to esthetic scarification. <i>Burns</i> , 2014, 40, 1338-1344.	1.1	5
72	GenePattern flow cytometry suite. <i>Source Code for Biology and Medicine</i> , 2013, 8, 14.	1.7	16

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73	Metadata-driven comparative analysis tool for sequences (meta-CATS): An automated process for identifying significant sequence variations that correlate with virus attributes. <i>Virology</i> , 2013, 447, 45-51.	1.1	35
74	Critical assessment of automated flow cytometry data analysis techniques. <i>Nature Methods</i> , 2013, 10, 228-238.	9.0	509
75	Virus Pathogen Database and Analysis Resource (ViPR): A Comprehensive Bioinformatics Database and Analysis Resource for the Coronavirus Research Community. <i>Viruses</i> , 2012, 4, 3209-3226.	1.5	156
76	ViPR: an open bioinformatics database and analysis resource for virology research. <i>Nucleic Acids Research</i> , 2012, 40, D593-D598.	6.5	610
77	Influenza Virus Sequence Feature Variant Type Analysis: Evidence of a Role for NS1 in Influenza Virus Host Range Restriction. <i>Journal of Virology</i> , 2012, 86, 5857-5866.	1.5	35
78	FCSTrans: An open source software system for FCS file conversion and data transformation. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2012, 81A, 353-356.	1.1	15
79	Influenza Research Database: an integrated bioinformatics resource for influenza research and surveillance. <i>Influenza and Other Respiratory Viruses</i> , 2012, 6, 404-416.	1.5	270
80	Minimum Information about a Genotyping Experiment (MIGEN). <i>Standards in Genomic Sciences</i> , 2011, 5, 224-229.	1.5	3
81	Hematopoietic cell types: Prototype for a revised cell ontology. <i>Journal of Biomedical Informatics</i> , 2011, 44, 75-79.	2.5	35
82	Toward an ontology-based framework for clinical research databases. <i>Journal of Biomedical Informatics</i> , 2011, 44, 48-58.	2.5	28
83	Ontologies for clinical and translational research: Introduction. <i>Journal of Biomedical Informatics</i> , 2011, 44, 3-7.	2.5	14
84	A gene selection method for GeneChip array data with small sample sizes. <i>BMC Genomics</i> , 2011, 12, S7.	1.2	6
85	Overcoming the ontology enrichment bottleneck with Quick Term Templates. <i>Applied Ontology</i> , 2011, 6, 13-22.	1.0	7
86	Identifying Differentially Expressed Genes based on probe level data for GeneChip arrays. <i>International Journal of Computational Biology and Drug Design</i> , 2010, 3, 237.	0.3	5
87	Personalized care, comparative effectiveness research and the electronic health record. <i>Current Opinion in Allergy and Clinical Immunology</i> , 2010, 10, 168-170.	1.1	2
88	Deterministic graph-theoretic algorithm for detecting modules in biological interaction networks. <i>International Journal of Bioinformatics Research and Applications</i> , 2010, 6, 101.	0.1	3
89	Elucidation of seventeen human peripheral blood B cell subsets and quantification of the tetanus response using a density-based method for the automated identification of cell populations in multidimensional flow cytometry data. <i>Cytometry Part B - Clinical Cytometry</i> , 2010, 78B, S69-82.	0.7	178
90	Novel sequence feature variant type analysis of the HLA genetic association in systemic sclerosis. <i>Human Molecular Genetics</i> , 2010, 19, 707-719.	1.4	37

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91	GO-Bayes: Gene Ontology-based overrepresentation analysis using a Bayesian approach. <i>Bioinformatics</i> , 2010, 26, 905-911.	1.8	29
92	Towards Viral Genome Annotation Standards, Report from the 2010 NCBI Annotation Workshop. <i>Viruses</i> , 2010, 2, 2258-2268.	1.5	27
93	Technical and Policy Approaches to Balancing Patient Privacy and Data Sharing in Clinical and Translational Research. <i>Journal of Investigative Medicine</i> , 2010, 58, 11-18.	0.7	97
94	An Ontology-Based Framework for Clinical Research Databases. <i>Nature Precedings</i> , 2009, , .	0.1	0
95	Hematopoietic Cell Types: Prototype for a Revised Cell Ontology. <i>Nature Precedings</i> , 2009, , .	0.1	0
96	Pre-existing immunity against swine-origin H1N1 influenza viruses in the general human population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20365-20370.	3.3	298
97	FuGEFlow: data model and markup language for flow cytometry. <i>BMC Bioinformatics</i> , 2009, 10, 184.	1.2	6
98	An improved ontological representation of dendritic cells as a paradigm for all cell types. <i>BMC Bioinformatics</i> , 2009, 10, 70.	1.2	29
99	Core and periphery structures in protein interaction networks. <i>BMC Bioinformatics</i> , 2009, 10, S8.	1.2	36
100	A distribution-free convolution model for background correction of oligonucleotide microarray data. <i>BMC Genomics</i> , 2009, 10, S19.	1.2	13
101	Synergies and Distinctions Between Computational Disciplines in Biomedical Research: Perspective From the Clinical and Translational Science Award Programs. <i>Academic Medicine</i> , 2009, 84, 964-970.	0.8	39
102	SEQUENCE FEATURE VARIANT TYPE (SFVT) ANALYSIS OF THE HLA GENETIC ASSOCIATION IN JUVENILE IDIOPATHIC ARTHRITIS. , 2009, , 359-370.		12
103	Complete Genome Sequence of <i>Francisella tularensis</i> Subspecies <i>holarctica</i> FTNF002-00. <i>PLoS ONE</i> , 2009, 4, e7041.	1.1	47
104	Toward an ontological treatment of disease and diagnosis. <i>Summit on Translational Bioinformatics</i> , 2009, 2009, 116-20.	0.7	85
105	MIFlowCyt: The minimum information about a flow cytometry experiment. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2008, 73A, 926-930.	1.1	381
106	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896.	9.4	506
107	BioHealthBase: informatics support in the elucidation of influenza virus host-pathogen interactions and virulence. <i>Nucleic Acids Research</i> , 2008, 36, D497-D503.	6.5	71
108	Exploring Core/Periphery Structures in Protein Interaction Networks Provides Structure-Property Relation Insights. , 2008, , .		0

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109	Ontology development for biological systems: immunology. <i>Bioinformatics</i> , 2007, 23, 913-915.	1.8	49
110	Modular organization of protein interaction networks. <i>Bioinformatics</i> , 2007, 23, 207-214.	1.8	151
111	National Institute of Allergy and Infectious Diseases Bioinformatics Resource Centers: New Assets for Pathogen Informatics. <i>Infection and Immunity</i> , 2007, 75, 3212-3219.	1.0	50
112	A distribution free summarization method for Affymetrix GeneChip(R) arrays. <i>Bioinformatics</i> , 2007, 23, 321-327.	1.8	89
113	The OBO Foundry: coordinated evolution of ontologies to support biomedical data integration. <i>Nature Biotechnology</i> , 2007, 25, 1251-1255.	9.4	1,955
114	Complete Genomic Characterization of a Pathogenic A.II Strain of <i>Francisella tularensis</i> Subspecies <i>tularensis</i> . <i>PLoS ONE</i> , 2007, 2, e947.	1.1	46
115	Nucleic acid testing for viral burden and viral genotyping. <i>Clinica Chimica Acta</i> , 2006, 363, 197-205.	0.5	16
116	Application of random matrix theory to biological networks. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 2006, 357, 420-423.	0.9	172
117	Components of the antigen processing and presentation pathway revealed by gene expression microarray analysis following B cell antigen receptor (BCR) stimulation. <i>BMC Bioinformatics</i> , 2006, 7, 237.	1.2	33
118	Detecting Functional Modules from Protein Interaction Networks. , 2006, , .		1
119	Analysis of the Major Patterns of B Cell Gene Expression Changes in Response to Short-Term Stimulation with 33 Single Ligands. <i>Journal of Immunology</i> , 2004, 173, 7141-7149.	0.4	55
120	Development of Real-Time PCR Assays for the Quantitative Detection of Epstein-Barr Virus and Cytomegalovirus, Comparison of TaqMan Probes, and Molecular Beacons. <i>Journal of Molecular Diagnostics</i> , 2003, 5, 15-20.	1.2	50
121	A Novel Colonic Repressor Element Regulates Intestinal Gene Expression by Interacting with Cux/CDP. <i>Molecular and Cellular Biology</i> , 2002, 22, 5467-5478.	1.1	29
122	Presence of simian virus 40 DNA sequences in human lymphomas. <i>Lancet, The</i> , 2002, 359, 851-852.	6.3	142
123	Activation of the Syk tyrosine kinase is insufficient for downstream signal transduction in B lymphocytes. <i>BMC Immunology</i> , 2002, 3, 16.	0.9	9
124	Lymphoid apoptosis and myeloid hyperplasia in CCAAT displacement protein mutant mice. <i>Blood</i> , 2001, 98, 3658-3667.	0.6	96
125	Prevalence and Cellular Reservoir of Latent Human Herpesvirus 6 in Tonsillar Lymphoid Tissue. <i>American Journal of Clinical Pathology</i> , 2001, 116, 648-654.	0.4	42
126	Transcriptional Activation by a Matrix Associating Region-binding Protein. <i>Journal of Biological Chemistry</i> , 2001, 276, 21325-21330.	1.6	30



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127	Tyrosine kinase activation in the decision between growth, differentiation, and death responses initiated from the B cell antigen receptor. <i>Advances in Immunology</i> , 2000, 75, 283-316.	1.1	67
128	Predictive Value of Quantitative PCR-Based Viral Burden Analysis for Eight Human Herpesviruses in Pediatric Solid Organ Transplant Patients. <i>Journal of Molecular Diagnostics</i> , 2000, 2, 191-201.	1.2	36
129	MARs of Antigen Receptor and Co-Receptor Genes. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 1999, 9, 295-310.	0.4	34
130	Annexin V Staining Due to Loss of Membrane Asymmetry Can Be Reversible and Precede Commitment to Apoptotic Death. <i>Experimental Cell Research</i> , 1999, 251, 16-21.	1.2	172
131	Quantitation of 8 Human Herpesviruses in Peripheral Blood of Human Immunodeficiency Virus-Infected Patients and Healthy Blood Donors by Polymerase Chain Reaction. <i>American Journal of Clinical Pathology</i> , 1999, 111, 655-659.	0.4	15
132	Cux/CDP Homeoprotein Is a Component of NF- $\kappa$ B and Represses the Immunoglobulin Heavy Chain Intronic Enhancer by Antagonizing the Bright Transcription Activator. <i>Molecular and Cellular Biology</i> , 1999, 19, 284-295.	1.1	76
133	Human Herpesvirus-6 and Sudden Death in Infancy: Report of a Case and Review of the Literature. <i>Journal of Forensic Sciences</i> , 1999, 44, 432-437.	0.9	12
134	Bcl-2 Expression in Langerhans' Cell Histiocytosis. <i>Pediatric and Developmental Pathology</i> , 1998, 1, 210-215.	0.5	21
135	Epstein-Barr Virus Polymerase Chain Reaction and Serology in Pediatric Post-Transplant Lymphoproliferative Disorder: Three-Year Experience. <i>Pediatric and Developmental Pathology</i> , 1998, 1, 480-486.	0.5	17
136	Polymerase chain reaction amplification of archival material for Epstein-Barr virus, cytomegalovirus, human herpesvirus 6, and parvovirus B19 in children with bone marrow hemophagocytosis. <i>Human Pathology</i> , 1998, 29, 1074-1077.	1.1	40
137	Benefits and dangers of genetic tests. <i>Nature</i> , 1998, 392, 14-14.	13.7	1
138	Quantitative polymerase chain reaction for human herpesvirus diagnosis and measurement of Epstein-Barr virus burden in posttransplant lymphoproliferative disorder. <i>Clinical Chemistry</i> , 1997, 43, 1843-1849.	1.5	111
139	Tumor Dormancy and Cell Signaling. V. Regrowth of the BCL1 Tumor After Dormancy Is Established. <i>Blood</i> , 1997, 89, 4425-4436.	0.6	51
140	Cancer dormancy: Opportunities for new therapeutic approaches. <i>Nature Medicine</i> , 1997, 3, 505-509.	15.2	191
141	Mutually Exclusive Interaction of a Novel Matrix Attachment Region Binding Protein and the NF- $\kappa$ B Enhancer Repressor. <i>Journal of Biological Chemistry</i> , 1995, 270, 24010-24018.	1.6	27
142	Induction of B cell tumor dormancy by anti-idiotypic antibodies. <i>Current Opinion in Immunology</i> , 1993, 5, 740-744.	2.4	20
143	[33] Polymerase chain reaction-based mRNA quantification using an internal standard: Analysis of oncogene expression. <i>Methods in Enzymology</i> , 1993, 218, 446-473.	0.4	55
144	Analysis of cis- and trans-Acting Factors Regulating Gene Transcription. , 1990, , 75-93.		3

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145	UmuD mutagenesis protein of Escherichia coli: overproduction, purification, and cleavage by RecA.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 1811-1815.	3.3	325