

Ryan R Brinkman

List of Publications by Year in descending order

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139
papers

11,211
citations

47006

47
h-index

32842

100
g-index

148
all docs

148
docs citations

148
times ranked

16743
citing authors

#	ARTICLE	IF	CITATIONS
1	flowCut : An R package for automated removal of outlier events and flagging of files based on time versus fluorescence analysis. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2023, 103, 71-81.	1.5	14
2	Automated identification of maximal differential cell populations in flow cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2022, 101, 177-184.	1.5	2
3	Occurrence of T cell and NK cell subsets with less well-recognized phenotypes in peripheral blood submitted for routine flow cytometry analysis. <i>Cytometry Part B - Clinical Cytometry</i> , 2021, 100, 235-239.	1.5	4
4	ISAC Probe Tag Dictionary: Standardized Nomenclature for Detection and Visualization Labels Used in Cytometry and Microscopy Imaging. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2021, 99, 103-106.	1.5	3
5	Data File Standard for Flow Cytometry, Version FCS 3.2. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2021, 99, 100-102.	1.5	6
6	Improving the Rigor and Reproducibility of Flow Cytometry-Based Clinical Research and Trials Through Automated Data Analysis. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 97, 107-112.	1.5	17
7	Single Cell Phenotypic Profiling of 27 DLBCL Cases Reveals Marked Intertumoral and Intratumoral Heterogeneity. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 97, 620-629.	1.5	12
8	High-throughput phenotyping reveals expansive genetic and structural underpinnings of immune variation. <i>Nature Immunology</i> , 2020, 21, 86-100.	14.5	32
9	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.	4.8	28
10	Age Related Differences in the Biology of Chronic Graft-Versus-Host Disease After Hematopoietic Stem Cell Transplantation. <i>Frontiers in Immunology</i> , 2020, 11, 571884.	4.8	16
11	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.	4.8	20
12	Clinical Protocol for a Longitudinal Cohort Study Employing Systems Biology to Identify Markers of Vaccine Immunogenicity in Newborn Infants in The Gambia and Papua New Guinea. <i>Frontiers in Pediatrics</i> , 2020, 8, 197.	1.9	12
13	BCG vaccination-induced emergency granulopoiesis provides rapid protection from neonatal sepsis. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	76
14	The miR-185/PAK6 axis predicts therapy response and regulates survival of drug-resistant leukemic stem cells in CML. <i>Blood</i> , 2020, 136, 596-609.	1.4	30
15	Improving the Quality and Reproducibility of Flow Cytometry in the Lung. An Official American Thoracic Society Workshop Report. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019, 61, 150-161.	2.9	49
16	Guidelines for the use of flow cytometry and cell sorting in immunological studies (second edition). <i>European Journal of Immunology</i> , 2019, 49, 1457-1973.	2.9	766
17	Flow cytometry data analysis: Recent tools and algorithms. <i>International Journal of Laboratory Hematology</i> , 2019, 41, 56-62.	1.3	53
18	Data-Driven Flow Cytometry Analysis. <i>Methods in Molecular Biology</i> , 2019, 1989, 245-265.	0.9	9

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19	Dynamic molecular changes during the first week of human life follow a robust developmental trajectory. <i>Nature Communications</i> , 2019, 10, 1092.	12.8	151
20	Implementation and Validation of an Automated Flow Cytometry Analysis Pipeline for Human Immune Profiling. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2019, 95, 183-191.	1.5	18
21	flowLearn: fast and precise identification and quality checking of cell populations in flow cytometry. <i>Bioinformatics</i> , 2018, 34, 2245-2253.	4.1	37
22	High throughput automated analysis of big flow cytometry data. <i>Methods</i> , 2018, 134-135, 164-176.	3.8	25
23	ddPCRclust: an R package and Shiny app for automated analysis of multiplexed ddPCR data. <i>Bioinformatics</i> , 2018, 34, 2687-2689.	4.1	14
24	Use FlowRepository to share your clinical data upon study publication. <i>Cytometry Part B - Clinical Cytometry</i> , 2018, 94, 196-198.	1.5	10
25	Methodology for evaluating and comparing flow cytometers: A multisite study of 23 instruments. , 2018, 93, 1087-1091.		14
26	A standardized immune phenotyping and automated data analysis platform for multicenter biomarker studies. <i>JCI Insight</i> , 2018, 3, .	5.0	29
27	Single-Cell Profiling Reveals Distinct Tumor Subtypes and Their Associated T-Cell Environments in Follicular Lymphoma. <i>Blood</i> , 2018, 132, 1577-1577.	1.4	0
28	Global Transcriptome Profiling Identifies a Key Mir-185-PAK6 Axis That Promotes Survival of Leukemic Stem Cells and Drug-Insensitive Blasts in BCR-ABL+ Human Leukemia. <i>Blood</i> , 2018, 132, 931-931.	1.4	0
29	Evaluating flow cytometer performance with weighted quadratic least squares analysis of L _{ED} and multi-level bead data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2017, 91, 232-249.	1.5	18
30	Guidelines for the use of flow cytometry and cell sorting in immunological studies [*] . <i>European Journal of Immunology</i> , 2017, 47, 1584-1797.	2.9	505
31	An Early Naïve T Cell Population Lacking PD1 Expression at Day 100 As A Prognostic Biomarker of Chronic GVHD. <i>Transplantation</i> , 2017, 101, S40.	1.0	0
32	Standardized Immunophenotyping in the Canadian National Transplant Research Program. <i>Transplantation</i> , 2017, 101, S62.	1.0	0
33	Cell Phenotypes Predictive of Frailty and Mortality in Elderly Nursing Home Residents. <i>Journal of the American Geriatrics Society</i> , 2017, 65, 153-159.	2.6	46
34	The Ontology for Biomedical Investigations. <i>PLoS ONE</i> , 2016, 11, e0154556.	2.5	217
35	flowC _{lean} : Automated identification and removal of fluorescence anomalies in flow cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2016, 89, 461-471.	1.5	52
36	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.	1.5	65

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37	Publishing code is essential for reproducible flow cytometry bioinformatics. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 10-11.	1.5	10
38	Automated analysis of flow cytometry data comes of age. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 13-15.	1.5	23
39	Standardizing Flow Cytometry Immunophenotyping Analysis from the Human ImmunoPhenotyping Consortium. Scientific Reports, 2016, 6, 20686.	3.3	240
40	State-of-the-Art in the Computational Analysis of Cytometry Data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2015, 87, 591-593.	1.5	13
41	Comparative RNA-seq analyses identify new microRNA biomarkers and candidate target genes in patients' drug-resistant CD34+ CML stem/progenitor cells. Experimental Hematology, 2015, 43, S63.	0.4	0
42	A randomized controlled trial on the effects of goal-directed therapy on the inflammatory response open abdominal aortic aneurysm repair. Critical Care, 2015, 19, 247.	5.8	28
43	<sc>ISAC</sc>'s <sc>G</sc>ating <sc>ML</sc> 2.0 data exchange standard for gating description. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2015, 87, 683-687.	1.5	13
44	flowDensity: reproducing manual gating of flow cytometry data by automated density-based cell population identification. Bioinformatics, 2015, 31, 606-607.	4.1	105
45	Thinking Outside the Gate: Single-Cell Assessments in Multiple Dimensions. Immunity, 2015, 42, 591-592.	14.3	67
46	Deep profiling of multitube flow cytometry data. Bioinformatics, 2015, 31, 1623-1631.	4.1	13
47	ISAC's classification results file format. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2015, 87, 86-88.	1.5	4
48	flowCL: ontology-based cell population labelling in flow cytometry. Bioinformatics, 2015, 31, 1337-1339.	4.1	25
49	The Logic of Surveillance Guidelines: An Analysis of Vaccine Adverse Event Reports from an Ontological Perspective. PLoS ONE, 2014, 9, e92632.	2.5	10
50	Enhanced flowType/RchyOptimyx: a Bioconductor pipeline for discovery in high-dimensional cytometry data. Bioinformatics, 2014, 30, 1329-1330.	4.1	33
51	Bim Regulates Alloimmune-Mediated Vascular Injury Through Effects on T-Cell Activation and Death. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 1290-1297.	2.4	8
52	Computational analysis optimizes the flow cytometric evaluation for lymphoma. , 2014, 86, 18-24.		6
53	The core autophagy protein ATG4B is a potential biomarker and therapeutic target in CML stem/progenitor cells. Blood, 2014, 123, 3622-3634.	1.4	177
54	Identification of New microRNA Biomarkers and Candidate Target Genes in Primitive CML Cells Using Global Comparative RNA analyses. Blood, 2014, 124, 3133-3133.	1.4	2

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55	Immune Biomarkers Predictive of Respiratory Viral Infection in Elderly Nursing Home Residents. PLoS ONE, 2014, 9, e108481.	2.5	43
56	GenePattern flow cytometry suite. Source Code for Biology and Medicine, 2013, 8, 14.	1.7	16
57	Cerebral oxygen desaturation during one-lung ventilation: correlation with hemodynamic variables. Canadian Journal of Anaesthesia, 2013, 60, 660-666.	1.6	21
58	Scoring relevancy of features based on combinatorial analysis of Lasso with application to lymphoma diagnosis. BMC Genomics, 2013, 14, S14.	2.8	22
59	BAIT: Organizing genomes and mapping rearrangements in single cells. Genome Medicine, 2013, 5, 82.	8.2	32
60	Critical assessment of automated flow cytometry data analysis techniques. Nature Methods, 2013, 10, 228-238.	19.0	509
61	The Luminal Progenitor Compartment of the Normal Human Mammary Gland Constitutes a Unique Site of Telomere Dysfunction. Stem Cell Reports, 2013, 1, 28-37.	4.8	50
62	Computational Analysis of High-Dimensional Flow Cytometric Data for Diagnosis and Discovery. Current Topics in Microbiology and Immunology, 2013, 377, 159-175.	1.1	3
63	Flow Cytometry Bioinformatics. PLoS Computational Biology, 2013, 9, e1003365.	3.2	79
64	Computational analysis optimizes the flow cytometric evaluation for lymphoma. , 2013, , n/a-n/a.		4
65	Integration of Lyoplate Based Flow Cytometry and Computational Analysis for Standardized Immunological Biomarker Discovery. PLoS ONE, 2013, 8, e65485.	2.5	16
66	MIFlowCyt. , 2013, , 1358-1360.		0
67	Automated Analysis of Multidimensional Flow Cytometry Data Improves Diagnostic Accuracy Between Mantle Cell Lymphoma and Small Lymphocytic Lymphoma. American Journal of Clinical Pathology, 2012, 137, 75-85.	0.7	36
68	Distinct but phenotypically heterogeneous human cell populations produce rapid recovery of platelets and neutrophils after transplantation. Blood, 2012, 119, 3431-3439.	1.4	23
69	B Cells With High Side Scatter Parameter by Flow Cytometry Correlate With Inferior Survival in Diffuse Large B-Cell Lymphoma. American Journal of Clinical Pathology, 2012, 137, 805-814.	0.7	12
70	Early immunologic correlates of HIV protection can be identified from computational analysis of complex multivariate T-cell flow cytometry assays. Bioinformatics, 2012, 28, 1009-1016.	4.1	70
71	RchyOptimyx: Cellular hierarchy optimization for flow cytometry. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2012, 81A, 1022-1030.	1.5	53
72	Hematopoietic Stem Cell Subtypes Expand Differentially during Development and Display Distinct Lymphopoietic Programs. Cell Stem Cell, 2012, 10, 273-283.	11.1	277

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73	FlowRepository: A resource of annotated flow cytometry datasets associated with peer-reviewed publications. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2012, 81A, 727-731.	1.5	159
74	The phenotypic distribution and functional profile of tuberculin-specific CD4 T cells characterizes different stages of TB infection. <i>Cytometry Part B - Clinical Cytometry</i> , 2012, 82B, 360-368.	1.5	17
75	Preparing a Minimum Information about a Flow Cytometry Experiment (MIFlowCyt) Compliant Manuscript Using the International Society for Advancement of Cytometry (ISAC) FCS File Repository (FlowRepository.org). <i>Current Protocols in Cytometry</i> , 2012, 61, Unit 10.18.	3.7	27
76	FCS 3.1 Implementation Guidance. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2012, 81A, 523-526.	1.5	8
77	Short Term Signalling Responses of the Most Primitive Subsets of Human Hematopoietic Cells Stimulated in Vitro Correlate with Their Subsequent Self-Renewal Behaviour.. <i>Blood</i> , 2012, 120, 2341-2341.	1.4	0
78	Flow cytometry data standards. <i>BMC Research Notes</i> , 2011, 4, 50.	1.4	12
79	Rapid cell population identification in flow cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2011, 79A, 6-13.	1.5	183
80	Overcoming the ontology enrichment bottleneck with Quick Term Templates. <i>Applied Ontology</i> , 2011, 6, 13-22.	2.0	7
81	MIREOT: The minimum information to reference an external ontology term. <i>Applied Ontology</i> , 2011, 6, 23-33.	2.0	78
82	Per-channel basis normalization methods for flow cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2010, 77A, 121-131.	1.5	79
83	Data File Standard for Flow Cytometry, version FCS 3.1. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2010, 77A, 97-100.	1.5	49
84	Properties of CD34+ CML stem/progenitor cells that correlate with different clinical responses to imatinib mesylate. <i>Blood</i> , 2010, 116, 2112-2121.	1.4	56
85	Data reduction for spectral clustering to analyze high throughput flow cytometry data. <i>BMC Bioinformatics</i> , 2010, 11, 403.	2.6	139
86	OntoFox: web-based support for ontology reuse. <i>BMC Research Notes</i> , 2010, 3, 175.	1.4	145
87	Modeling biomedical experimental processes with OBI. <i>Journal of Biomedical Semantics</i> , 2010, 1, S7.	1.6	207
88	Identification of B cells through negative gating—An example of the MIFlowCyt standard applied. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2010, 77A, 546-551.	1.5	17
89	Correlation analysis of intracellular and secreted cytokines via the generalized integrated mean fluorescence intensity. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2010, 77A, 873-880.	1.5	50
90	Merging Mixture Components for Cell Population Identification in Flow Cytometry. <i>Advances in Bioinformatics</i> , 2009, 2009, 1-12.	5.7	92

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91	Analysis of High-Throughput Flow Cytometry Data Using plateCore. <i>Advances in Bioinformatics</i> , 2009, 2009, 1-10.	5.7	9
92	A Survey of Flow Cytometry Data Analysis Methods. <i>Advances in Bioinformatics</i> , 2009, 2009, 1-19.	5.7	84
93	Recent Bioinformatics Advances in the Analysis of High Throughput Flow Cytometry Data. <i>Advances in Bioinformatics</i> , 2009, 2009, 1-2.	5.7	1
94	A Pipeline for automated analysis of flow cytometry data: Preliminary results on lymphoma sub-type diagnosis. , 2009, 2009, 4945-8.		8
95	A container for the advanced cytometry standard (ACS). <i>Proceedings of SPIE</i> , 2009, , .	0.8	4
96	flowCore: a Bioconductor package for high throughput flow cytometry. <i>BMC Bioinformatics</i> , 2009, 10, 106.	2.6	484
97	flowClust: a Bioconductor package for automated gating of flow cytometry data. <i>BMC Bioinformatics</i> , 2009, 10, 145.	2.6	171
98	FuGEFlow: data model and markup language for flow cytometry. <i>BMC Bioinformatics</i> , 2009, 10, 184.	2.6	6
99	Reply to 'Reassessing the human mammary stem cell concept by modeling limiting dilution transplantation assays'. <i>Nature Medicine</i> , 2009, 15, 604-605.	30.7	0
100	Cytogenetic and molecular responses to standard-dose imatinib in chronic myeloid leukemia are correlated with Sokal risk scores and duration of therapy but not trough imatinib plasma levels. <i>Leukemia Research</i> , 2009, 33, 271-275.	0.8	74
101	Correlation between trough imatinib plasma concentration and clinical response in chronic myeloid leukemia. <i>Leukemia Research</i> , 2009, 33, 1149-1150.	0.8	0
102	Reduction in multi-lineage and erythroid progenitors distinguishes myelodysplastic syndromes from non-malignant cytopenias. <i>Leukemia Research</i> , 2009, 33, 1636-1642.	0.8	2
103	Diffuse large B-cell lymphoma: reduced CD20 expression is associated with an inferior survival. <i>Blood</i> , 2009, 113, 3773-3780.	1.4	133
104	Automated gating of flow cytometry data via robust model-based clustering. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2008, 73A, 321-332.	1.5	224
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.	1.5	381
106	Gatingâ€MML: XML-based gating descriptions in flow cytometry. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2008, 73A, 1151-1157.	1.5	36
107	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896.	17.5	506
108	Allogeneic SCT for relapsed composite and transformed lymphoma using related and unrelated donors: long-term results. <i>Bone Marrow Transplantation</i> , 2008, 42, 601-608.	2.4	21

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109	Cytometry standards continuum. Proceedings of SPIE, 2008, , .	0.8	3
110	Salvage Therapy with Allogeneic Stem Cell Transplantation Results in Better Outcome for Patients with Relapsed/Refractory Follicular Lymphoma Compared to Those with Transformed Non-Hodgkin Lymphoma: A Population-Based Comparative Study.. Blood, 2008, 112, 975-975.	1.4	29
111	Impact of Comorbidity Index on Outcome with Allogeneic Hematopoietic Stem Cell Transplantation for Chronic Lymphocytic Leukemia. Blood, 2008, 112, 3305-3305.	1.4	0
112	Long-Term Propagation of Distinct Hematopoietic Differentiation Programs In Vivo. Cell Stem Cell, 2007, 1, 218-229.	11.1	520
113	High-Content Flow Cytometry and Temporal Data Analysis for Defining a Cellular Signature of Graft-Versus-Host Disease. Biology of Blood and Marrow Transplantation, 2007, 13, 691-700.	2.0	67
114	Data quality assessment of ungated flow cytometry data in high throughput experiments. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2007, 71A, 393-403.	1.5	38
115	The Relationship Between CAG Repeat Length and Age of Onset Differs for Huntington's Disease Patients with Juvenile Onset or Adult Onset. Annals of Human Genetics, 2007, 71, 295-301.	0.8	110
116	Allogeneic Stem Cell Transplant in First Complete Remission Overcomes the Poor Prognosis Associated with the FLT-3 Internal Tandem Duplication in Acute Myeloid Leukemia.. Blood, 2007, 110, 3491-3491.	1.4	0
117	Data Standards for Flow Cytometry. OMICS A Journal of Integrative Biology, 2006, 10, 209-214.	2.0	23
118	Human monogenic disorders " a source of novel drug targets. Nature Reviews Genetics, 2006, 7, 249-260.	16.3	81
119	Wrestling with SUMO and bio-ontologies. Nature Biotechnology, 2006, 24, 21-21.	17.5	8
120	Wrestling with SUMO and bio-ontologies. Nature Biotechnology, 2006, 24, 21-22.	17.5	5
121	Development of FuGO: An Ontology for Functional Genomics Investigations. OMICS A Journal of Integrative Biology, 2006, 10, 199-204.	2.0	56
122	Long Term Results of Myeloablative Allogeneic Stem Cell Transplantation Using Related and Unrelated Donors in Patients with Relapsed Composite Low and Intermediate Grade (Including Transformed) Lymphoma.. Blood, 2006, 108, 3139-3139.	1.4	0
123	Prior Rituximab Reduces Relapse and Improves Survival Following High Dose Chemotherapy and Stem Cell Transplantation for Relapsed Composite Low and Intermediate Grade (Including Transformed) Lymphoma.. Blood, 2006, 108, 3662-3662.	1.4	7
124	Induction Therapy with High-Dose Dex Alone in Newly Diagnosed Myeloma Patients Produces a 57% Partial Response and Is Predictive of Progression Free Survival.. Blood, 2006, 108, 3098-3098.	1.4	0
125	A new model for prediction of the age of onset and penetrance for Huntington's disease based on CAG length. Clinical Genetics, 2004, 65, 267-277.	2.0	738
126	Evidence for a modifier of onset age in Huntington disease linked to the HD gene in 4p16. Neurogenetics, 2004, 5, 109-114.	1.4	67

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127	Identification of a Novel Gene (HSN2) Causing Hereditary Sensory and Autonomic Neuropathy Type II through the Study of Canadian Genetic Isolates. <i>American Journal of Human Genetics</i> , 2004, 74, 1064-1073.	6.2	133
128	Interaction of normal and expanded CAG repeat sizes influences age at onset of Huntington disease. , 2003, 119A, 279-282.		146
129	Psychological consequences and predictors of adverse events in the first 5 years after predictive testing for Huntington's disease. <i>Clinical Genetics</i> , 2003, 64, 300-309.	2.0	107
130	A Genome Scan for Modifiers of Age at Onset in Huntington Disease: The HD MAPS Study. <i>American Journal of Human Genetics</i> , 2003, 73, 682-687.	6.2	148
131	Familial influence on age of onset among siblings with Huntington disease. <i>American Journal of Medical Genetics Part A</i> , 2001, 105, 399-403.	2.4	92
132	Clinical markers of early disease in persons near onset of Huntington's disease. <i>Neurology</i> , 2001, 57, 658-662.	1.1	197
133	A Worldwide Assessment of the Frequency of Suicide, Suicide Attempts, or Psychiatric Hospitalization after Predictive Testing for Huntington Disease. <i>American Journal of Human Genetics</i> , 1999, 64, 1293-1304.	6.2	271
134	A Yeast Artificial Chromosome-Based Physical Map of the Juvenile Amyotrophic Lateral Sclerosis (ALS2) Critical Region on Human Chromosome 2q33-q34. <i>Genomics</i> , 1999, 55, 106-112.	2.9	18
135	Representation of cloned genomic sequences in two sequencing vectors: correlation of DNA sequence and subclone distribution. <i>Nucleic Acids Research</i> , 1997, 25, 2960-2966.	14.5	19
136	Toward Understanding the Molecular Pathology of Huntington's Disease. <i>Brain Pathology</i> , 1997, 7, 979-1002.	4.1	69
137	The construction and analysis of M13 libraries prepared from YAC DNA. <i>Nucleic Acids Research</i> , 1995, 23, 670-674.	14.5	25
138	Complete nucleotide sequence of <i>Saccharomyces cerevisiae</i> chromosome VIII. <i>Science</i> , 1994, 265, 2077-2082.	12.6	303
139	Overcoming the Ontology Enrichment Bottleneck with Quick Term Templates. <i>Nature Precedings</i> , 0, , .	0.1	6