

Eugene Kolker

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

97
papers

12,031
citations

31
h-index

108
g-index

108
ext. papers

13,282
ext. citations

6.4
avg, IF

5.94
L-index

#	Paper	IF	Citations
97	Data Science Community Matures with Diversity: Conference Observations, Highlights, and Interviews Strata Data Conference, New York, September 11-13, 2018. <i>Big Data</i> , 2018 , 6, 305-313	3.1	
96	Integrated Proteomic and Transcriptomic-Based Approaches to Identifying Signature Biomarkers and Pathways for Elucidation of Daoy and UW228 Subtypes. <i>Proteomes</i> , 2017 , 5,	4.6	15
95	How Healthcare Can Refocus on Its Super-Customers (Patients, n =1) and Customers (Doctors and Nurses) by Leveraging Lessons from Amazon, Uber, and Watson. <i>OMICS A Journal of Integrative Biology</i> , 2016 , 20, 329-33	3.8	19
94	Precision Nutrition 4.0: A Big Data and Ethics Foresight Analysis--Convergence of Agrigenomics, Nutrigenomics, Nutriproteomics, and Nutrimetabolomics. <i>OMICS A Journal of Integrative Biology</i> , 2016 , 20, 69-75	3.8	35
93	Dynamic Proteomic Analysis of Pancreatic Mesenchyme Reveals Novel Factors That Enhance Human Embryonic Stem Cell to Pancreatic Cell Differentiation. <i>Stem Cells International</i> , 2016 , 2016, 6183562	5.562	18
92	Health Care Transformation: A Strategy Rooted in Data and Analytics. <i>Academic Medicine</i> , 2016 , 91, 165-3.9	3.9	10
91	Genic insights from integrated human proteomics in GeneCards. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	85
90	A Case Study: Analyzing City Vitality with Four Pillars of Activity-Live, Work, Shop, and Play. <i>Big Data</i> , 2016 , 4, 60-6	3.1	3
89	Beyond protein expression, MOPED goes multi-omics. <i>Nucleic Acids Research</i> , 2015 , 43, D1145-51	20.1	15
88	Can "normal" protein expression ranges be estimated with high-throughput proteomics?. <i>Journal of Proteome Research</i> , 2015 , 14, 2398-407	5.6	7
87	The promise of multi-omics and clinical data integration to identify and target personalized healthcare approaches in autism spectrum disorders. <i>OMICS A Journal of Integrative Biology</i> , 2015 , 19, 197-208	3.8	71
86	An Appeal to the Global Health Community for a Tripartite Innovation: An "Essential Diagnostics List," "Health in All Policies," and "See-Through 21(st) Century Science and Ethics". <i>OMICS A Journal of Integrative Biology</i> , 2015 , 19, 435-42	3.8	6
85	Finding Text-Supported Gene-to-Disease Co-appearances with MOPED-Digger. <i>OMICS A Journal of Integrative Biology</i> , 2015 , 19, 754-6	3.8	4
84	Biomarker differences between cadaveric grafts used in human orthotopic liver transplantation as identified by coulometric electrochemical array detection (CEAD) metabolomics. <i>OMICS A Journal of Integrative Biology</i> , 2014 , 18, 767-77	3.8	10
83	Healthcare Analytics: Creating a Prioritized Improvement System with Performance Benchmarking. <i>Big Data</i> , 2014 , 2, 50-4	3.1	8
82	Big data and ethics review for health systems research in LMICs: understanding risk, uncertainty and ignorance -- and catching the black swans?. <i>American Journal of Bioethics</i> , 2014 , 14, 48-50	1.1	28
81	Toward more transparent and reproducible omics studies through a common metadata checklist and data publications. <i>OMICS A Journal of Integrative Biology</i> , 2014 , 18, 10-4	3.8	44

80	MOPED enables discoveries through consistently processed proteomics data. <i>Journal of Proteome Research</i> , 2014 , 13, 107-13	5.6	20
79	OMICS studies: How about metadata checklist and data publications?. <i>Journal of Proteome Research</i> , 2014 , 13, 1783-4	5.6	4
78	MOPED 2.5--an integrated multi-omics resource: multi-omics profiling expression database now includes transcriptomics data. <i>OMICS A Journal of Integrative Biology</i> , 2014 , 18, 335-43	3.8	37
77	Metadata checklist for the integrated personal OMICS study: proteomics and metabolomics experiments. <i>OMICS A Journal of Integrative Biology</i> , 2014 , 18, 81-5	3.8	13
76	Visualizing the Protein Sequence Universe. <i>Concurrency Computation Practice and Experience</i> , 2014 , 26, 1313-1325	1.4	4
75	Ready to put metadata on the post-2015 development agenda? Linking data publications to responsible innovation and science diplomacy. <i>OMICS A Journal of Integrative Biology</i> , 2014 , 18, 1-9	3.8	26
74	Optimizing high performance computing workflow for protein functional annotation. <i>Concurrency Computation Practice and Experience</i> , 2014 , 26, 2112-2121	1.4	1
73	Bernard Lerer: recipient of the 2014 inaugural Werner Kalow Responsible Innovation Prize in Global Omics and Personalized Medicine (Pacific Rim Association for Clinical Pharmacogenetics). <i>OMICS A Journal of Integrative Biology</i> , 2014 , 18, 211-21	3.8	6
72	Reproducibility: In praise of open research measures. <i>Nature</i> , 2013 , 498, 170	50.4	10
71	Unraveling the Complexities of Life Sciences Data. <i>Big Data</i> , 2013 , 1, 42-50	3.1	34
70	Predictive Analytics In Healthcare: Medications as a Predictor of Medical Complexity. <i>Big Data</i> , 2013 , 1, 237-44	3.1	11
69	Toward More Transparent and Reproducible Omics Studies Through a Common Metadata Checklist and Data Publications. <i>Big Data</i> , 2013 , 1, 196-201	3.1	5
68	Introducing a Metadata Checklist for Omics Data. <i>Big Data</i> , 2013 , 1, 195	3.1	2
67	Delsa Workshop IV: Launching the Quantified Human Initiative. <i>Big Data</i> , 2013 , 1, 187-90	3.1	4
66	Metadata Checklist for the Integrated Personal Omics Study: Proteomics and Metabolomics Experiments. <i>Big Data</i> , 2013 , 1, 202-6	3.1	6
65	Integrative analysis of longitudinal metabolomics data from a personal multi-omics profile. <i>Metabolites</i> , 2013 , 3, 741-60	5.6	46
64	Differential expression analysis for pathways. <i>PLoS Computational Biology</i> , 2013 , 9, e1002967	5	54
63	Designing a post-genomics knowledge ecosystem to translate pharmacogenomics into public health action. <i>Genome Medicine</i> , 2012 , 4, 91	14.4	18

62	MOPED: Model Organism Protein Expression Database. <i>Nucleic Acids Research</i> , 2012 , 40, D1093-9	20.1	93
61	Visualizing the protein sequence universe 2012 ,		2
60	Opportunities and challenges for the life sciences community. <i>OMICS A Journal of Integrative Biology</i> , 2012 , 16, 138-47	3.8	18
59	DELSA Global for Big Data and the Bioeconomy: Catalyzing Collective Innovation. <i>Industrial Biotechnology</i> , 2012 , 8, 176-178	1.3	8
58	Classifying proteins into functional groups based on all-versus-all BLAST of 10 million proteins. <i>OMICS A Journal of Integrative Biology</i> , 2011 , 15, 513-21	3.8	9
57	Towards an Ecology of Collective Innovation: Human Variome Project (HVP), Rare Disease Consortium for Autosomal Loci (RaDiCAL) and Data-Enabled Life Sciences Alliance (DELSA). <i>Current Pharmacogenomics and Personalized Medicine</i> , 2011 , 9, 243-251	0.4	17
56	In-silico human genomics with GeneCards. <i>Human Genomics</i> , 2011 , 5, 709-17	6.8	143
55	SPIRE: Systematic protein investigative research environment. <i>Journal of Proteomics</i> , 2011 , 75, 122-6	3.9	23
54	IPM: An integrated protein model for false discovery rate estimation and identification in high-throughput proteomics. <i>Journal of Proteomics</i> , 2011 , 75, 116-21	3.9	12
53	Policy and data-intensive scientific discovery in the beginning of the 21st century. <i>OMICS A Journal of Integrative Biology</i> , 2011 , 15, 221-5	3.8	13
52	Communication and data-intensive science in the beginning of the 21st century. <i>OMICS A Journal of Integrative Biology</i> , 2011 , 15, 213-5	3.8	14
51	Design and initial characterization of the SC-200 proteomics standard mixture. <i>OMICS A Journal of Integrative Biology</i> , 2011 , 15, 73-82	3.8	6
50	Bioinformatics and data-intensive scientific discovery in the beginning of the 21st century. <i>OMICS A Journal of Integrative Biology</i> , 2011 , 15, 199-201	3.8	15
49	Technology and data-intensive science in the beginning of the 21st century. <i>OMICS A Journal of Integrative Biology</i> , 2011 , 15, 203-7	3.8	5
48	Biology and data-intensive scientific discovery in the beginning of the 21st century. <i>OMICS A Journal of Integrative Biology</i> , 2011 , 15, 209-12	3.8	13
47	Education and data-intensive science in the beginning of the 21st century. <i>OMICS A Journal of Integrative Biology</i> , 2011 , 15, 217-9	3.8	8
46	The United States of America and scientific research. <i>PLoS ONE</i> , 2010 , 5, e12203	3.7	22
45	The necessity of adjusting tests of protein category enrichment in discovery proteomics. <i>Bioinformatics</i> , 2010 , 26, 3007-11	7.2	8

44	Meta-analysis for protein identification: a case study on yeast data. <i>OMICS A Journal of Integrative Biology</i> , 2010 , 14, 309-14	3.8	15
43	Modeling sequence and function similarity between proteins for protein functional annotation 2010 , 2010, 499-502		4
42	Interplay of heritage and habitat in the distribution of bacterial signal transduction systems. <i>Molecular BioSystems</i> , 2010 , 6, 721-8		76
41	A vision for 21st century U.S. Policy to support sustainable advancement of scientific discovery and technological innovation. <i>OMICS A Journal of Integrative Biology</i> , 2010 , 14, 333-5	3.8	11
40	Meeting report: the terabase metagenomics workshop and the vision of an Earth microbiome project. <i>Standards in Genomic Sciences</i> , 2010 , 3, 243-8		187
39	Quantifying protein function specificity in the gene ontology. <i>Standards in Genomic Sciences</i> , 2010 , 2, 238-44		6
38	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 9. <i>Standards in Genomic Sciences</i> , 2010 , 3, 216-24		2
37	Meeting Report: "Metagenomics, Metadata and Meta-analysis" (M3) Workshop at the Pacific Symposium on Biocomputing 2010. <i>Standards in Genomic Sciences</i> , 2010 , 2, 357-60		2
36	Estimating false discovery rates for peptide and protein identification using randomized databases. <i>Proteomics</i> , 2010 , 10, 2369-76	4.8	26
35	Risk assessment and communication tools for genotype associations with multifactorial phenotypes: the concept of "edge effect" and cultivating an ethical bridge between omics innovations and society. <i>OMICS A Journal of Integrative Biology</i> , 2009 , 13, 43-61	3.8	45
34	Genome-environment interactions and prospective technology assessment: evolution from pharmacogenomics to nutrigenomics and ecogenomics. <i>OMICS A Journal of Integrative Biology</i> , 2009 , 13, 1-6	3.8	14
33	Megascience. 'Omics data sharing. <i>Science</i> , 2009 , 326, 234-6	33.3	117
32	A statistical model of protein sequence similarity and function similarity reveals overly-specific function predictions. <i>PLoS ONE</i> , 2009 , 4, e7546	3.7	23
31	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008 , 26, 889-96	44.5	417
30	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008 , 26, 541-7	44.5	964
29	Host airway proteins interact with <i>Staphylococcus aureus</i> during early pneumonia. <i>Infection and Immunity</i> , 2008 , 76, 888-98	3.7	15
28	A note on the false discovery rate and inconsistent comparisons between experiments. <i>Bioinformatics</i> , 2008 , 24, 1225-8	7.2	29
27	<i>Staphylococcus aureus</i> elicits marked alterations in the airway proteome during early pneumonia. <i>Infection and Immunity</i> , 2008 , 76, 5862-72	3.7	27

26	Toward a standards-compliant genomic and metagenomic publication record. <i>OMICS A Journal of Integrative Biology</i> , 2008 , 12, 157-60	3.8	31
25	Validating annotations for uncharacterized proteins in <i>Shewanella oneidensis</i> . <i>OMICS A Journal of Integrative Biology</i> , 2008 , 12, 211-5	3.8	5
24	Development of BIATECH-54 standard mixtures for assessment of protein identification and relative expression. <i>Proteomics</i> , 2007 , 7, 3693-8	4.8	10
23	Experiment-specific estimation of peptide identification probabilities using a randomized database. <i>OMICS A Journal of Integrative Biology</i> , 2007 , 11, 351-65	3.8	23
22	A predictive model for identifying proteins by a single peptide match. <i>Bioinformatics</i> , 2007 , 23, 277-80	7.2	50
21	Experimental standards for high-throughput proteomics. <i>OMICS A Journal of Integrative Biology</i> , 2006 , 10, 152-7	3.8	20
20	Protein identification and expression analysis using mass spectrometry. <i>Trends in Microbiology</i> , 2006 , 14, 229-35	12.4	31
19	New metrics for comparative genomics. <i>Current Opinion in Biotechnology</i> , 2006 , 17, 440-7	11.4	26
18	Randomized sequence databases for tandem mass spectrometry peptide and protein identification. <i>OMICS A Journal of Integrative Biology</i> , 2005 , 9, 364-79	3.8	75
17	Charge state estimation for tandem mass spectrometry proteomics. <i>OMICS A Journal of Integrative Biology</i> , 2005 , 9, 233-50	3.8	11
16	Global profiling of <i>Shewanella oneidensis</i> MR-1: expression of hypothetical genes and improved functional annotations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 2099-104	11.5	106
15	Standard mixtures for proteome studies. <i>OMICS A Journal of Integrative Biology</i> , 2004 , 8, 79-92	3.8	43
14	Spectral quality assessment for high-throughput tandem mass spectrometry proteomics. <i>OMICS A Journal of Integrative Biology</i> , 2004 , 8, 255-65	3.8	42
13	LIP index for peptide classification using MS/MS and SEQUEST search via logistic regression. <i>OMICS A Journal of Integrative Biology</i> , 2004 , 8, 357-69	3.8	29
12	In Silico Metabolic Model and Protein Expression of <i>Haemophilus influenzae</i> Strain Rd KW20 in Rich Medium. <i>OMICS A Journal of Integrative Biology</i> , 2004 , 8, 25-41	3.8	35
11	Identification and functional analysis of 'hypothetical' genes expressed in <i>Haemophilus influenzae</i> . <i>Nucleic Acids Research</i> , 2004 , 32, 2353-61	20.1	64
10	Statistical analysis of global gene expression data: some practical considerations. <i>Current Opinion in Biotechnology</i> , 2004 , 15, 52-7	11.4	24
9	Initial proteome analysis of model microorganism <i>Haemophilus influenzae</i> strain Rd KW20. <i>Journal of Bacteriology</i> , 2003 , 185, 4593-602	3.5	60

8	A statistical model for identifying proteins by tandem mass spectrometry. <i>Analytical Chemistry</i> , 2003 , 75, 4646-58	7.8	3620
7	H. influenzae Consortium: integrative study of H. influenzae-human interactions. <i>OMICS A Journal of Integrative Biology</i> , 2002 , 6, 341-8	3.8	4
6	Spectral analysis of distributions: finding periodic components in eukaryotic enzyme length data. <i>OMICS A Journal of Integrative Biology</i> , 2002 , 6, 123-30	3.8	3
5	Transcriptome analysis of Escherichia coli using high-density oligonucleotide probe arrays. <i>Nucleic Acids Research</i> , 2002 , 30, 3732-8	20.1	144
4	Identifying operons and untranslated regions of transcripts using Escherichia coli RNA expression analysis. <i>Bioinformatics</i> , 2002 , 18 Suppl 1, S337-44	7.2	35
3	Experimental protein mixture for validating tandem mass spectral analysis. <i>OMICS A Journal of Integrative Biology</i> , 2002 , 6, 207-12	3.8	221
2	Empirical statistical model to estimate the accuracy of peptide identifications made by MS/MS and database search. <i>Analytical Chemistry</i> , 2002 , 74, 5383-92	7.8	3930
1	Differential stable isotope labeling of peptides for quantitation and de novo sequence derivation. <i>Rapid Communications in Mass Spectrometry</i> , 2001 , 15, 1214-21	2.2	258