

Eugene Kolker

List of Publications by Year in descending order

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105
papers

14,058
citations

126858

33
h-index

29127

104
g-index

108
all docs

108
docs citations

108
times ranked

18833
citing authors

#	ARTICLE	IF	CITATIONS
1	Empirical Statistical Model To Estimate the Accuracy of Peptide Identifications Made by MS/MS and Database Search. <i>Analytical Chemistry</i> , 2002, 74, 5383-5392.	3.2	4,503
2	A Statistical Model for Identifying Proteins by Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 4646-4658.	3.2	4,283
3	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008, 26, 541-547.	9.4	1,069
4	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896.	9.4	506
5	Differential stable isotope labeling of peptides for quantitation and de novo sequence derivation. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 1214-1221.	0.7	277
6	Experimental Protein Mixture for Validating Tandem Mass Spectral Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2002, 6, 207-212.	1.0	246
7	Meeting Report: The Terabase Metagenomics Workshop and the Vision of an Earth Microbiome Project. <i>Standards in Genomic Sciences</i> , 2010, 3, 243-248.	1.5	228
8	In-silico human genomics with GeneCards. <i>Human Genomics</i> , 2011, 5, 709.	1.4	186
9	Transcriptome analysis of <i>Escherichia coli</i> using high-density oligonucleotide probe arrays. <i>Nucleic Acids Research</i> , 2002, 30, 3732-3738.	6.5	167
10	Genic insights from integrated human proteomics in GeneCards. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw030.	1.4	145
11	'Omics Data Sharing. <i>Science</i> , 2009, 326, 234-236.	6.0	136
12	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, 2099-2104.	3.3	113
13	MOPED: Model Organism Protein Expression Database. <i>Nucleic Acids Research</i> , 2012, 40, D1093-D1099.	6.5	106
14	Interplay of heritage and habitat in the distribution of bacterial signal transduction systems. <i>Molecular BioSystems</i> , 2010, 6, 721.	2.9	87
15	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.	1.0	84
16	Differential Expression Analysis for Pathways. <i>PLoS Computational Biology</i> , 2013, 9, e1002967.	1.5	78
17	Randomized Sequence Databases for Tandem Mass Spectrometry Peptide and Protein Identification. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 364-379.	1.0	77
18	Identification and functional analysis of 'hypothetical' genes expressed in <i>Haemophilus influenzae</i> . <i>Nucleic Acids Research</i> , 2004, 32, 2353-2361.	6.5	75

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19	Initial Proteome Analysis of Model Microorganism <i>Haemophilus influenzae</i> Strain Rd KW20. <i>Journal of Bacteriology</i> , 2003, 185, 4593-4602.	1.0	66
20	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.	1.0	58
21	A predictive model for identifying proteins by a single peptide match. <i>Bioinformatics</i> , 2007, 23, 277-280.	1.8	57
22	Integrative Analysis of Longitudinal Metabolomics Data from a Personal Multi-Omics Profile. <i>Metabolites</i> , 2013, 3, 741-760.	1.3	56
23	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, 10-14.	1.0	54
24	Spectral Quality Assessment for High-Throughput Tandem Mass Spectrometry Proteomics. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 255-265.	1.0	51
25	Standard Mixtures for Proteome Studies. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 79-92.	1.0	48
26	Unraveling the Complexities of Life Sciences Data. <i>Big Data</i> , 2013, 1, 42-50.	2.1	46
27	Identifying operons and untranslated regions of transcripts using <i>Escherichia coli</i> RNA expression analysis. <i>Bioinformatics</i> , 2002, 18, S337-S344.	1.8	43
28	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.	1.0	42
29	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, 335-343.	1.0	42
30	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.	1.0	40
31	Protein identification and expression analysis using mass spectrometry. <i>Trends in Microbiology</i> , 2006, 14, 229-235.	3.5	38
32	A note on the false discovery rate and inconsistent comparisons between experiments. <i>Bioinformatics</i> , 2008, 24, 1225-1228.	1.8	35
33	Toward a Standards-Compliant Genomic and Metagenomic Publication Record. <i>OMICS A Journal of Integrative Biology</i> , 2008, 12, 157-160.	1.0	33
34	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.	0.5	33
35	Estimating false discovery rates for peptide and protein identification using randomized databases. <i>Proteomics</i> , 2010, 10, 2369-2376.	1.3	32
36	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.	1.0	31

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37	LIP Index for Peptide Classification Using MS/MS and SEQUEST Search via Logistic Regression. OMICS A Journal of Integrative Biology, 2004, 8, 357-369.	1.0	30
38	<i>Staphylococcus aureus</i> Elicits Marked Alterations in the Airway Proteome during Early Pneumonia. Infection and Immunity, 2008, 76, 5862-5872.	1.0	30
39	The United States of America and Scientific Research. PLoS ONE, 2010, 5, e12203.	1.1	30
40	SPIRE: Systematic protein investigative research environment. Journal of Proteomics, 2011, 75, 122-126.	1.2	30
41	New metrics for comparative genomics. Current Opinion in Biotechnology, 2006, 17, 440-447.	3.3	29
42	Statistical analysis of global gene expression data: some practical considerations. Current Opinion in Biotechnology, 2004, 15, 52-57.	3.3	28
43	How Healthcare Can Refocus on Its Super-Customers (Patients, $n=1$) and Customers (Doctors) Tj ETQq1 1 0.784314 rgBT (Biology, 2016, 20, 329-333.	1.0	28
44	Opportunities and Challenges for the Life Sciences Community. OMICS A Journal of Integrative Biology, 2012, 16, 138-147.	1.0	27
45	A Statistical Model of Protein Sequence Similarity and Function Similarity Reveals Overly-Specific Function Predictions. PLoS ONE, 2009, 4, e7546.	1.1	26
46	Editorial [Towards an Ecology of Collective Innovation: Human Variome Project (HVP), Rare Disease Consortium for Autosomal Loci (RaDiCAL) and Data-Enabled Life Sciences Alliance (DELSA)]. Current Pharmacogenomics and Personalized Medicine, 2011, 9, 243-251.	0.2	24
47	Experiment-Specific Estimation of Peptide Identification Probabilities Using a Randomized Database. OMICS A Journal of Integrative Biology, 2007, 11, 351-366.	1.0	23
48	Designing a post-genomics knowledge ecosystem to translate pharmacogenomics into public health action. Genome Medicine, 2012, 4, 91.	3.6	22
49	Experimental Standards for High-Throughput Proteomics. OMICS A Journal of Integrative Biology, 2006, 10, 152-157.	1.0	21
50	Policy and Data-Intensive Scientific Discovery in the Beginning of the 21st Century. OMICS A Journal of Integrative Biology, 2011, 15, 221-225.	1.0	21
51	MOPED Enables Discoveries through Consistently Processed Proteomics Data. Journal of Proteome Research, 2014, 13, 107-113.	1.8	20
52	Integrated Proteomic and Transcriptomic-Based Approaches to Identifying Signature Biomarkers and Pathways for Elucidation of Daoy and UW228 Subtypes. Proteomes, 2017, 5, 5.	1.7	20
53	Host Airway Proteins Interact with <i>Staphylococcus aureus</i> during Early Pneumonia. Infection and Immunity, 2008, 76, 888-898.	1.0	19
54	Communication and Data-Intensive Science in the Beginning of the 21st Century. OMICS A Journal of Integrative Biology, 2011, 15, 213-215.	1.0	18

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55	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, 1-9.	1.2	18
56	Meta-analysis for Protein Identification: A Case Study on Yeast Data. <i>OMICS A Journal of Integrative Biology</i> , 2010, 14, 309-314.	1.0	17
57	Beyond protein expression, MOPED goes multi-omics. <i>Nucleic Acids Research</i> , 2015, 43, D1145-D1151.	6.5	17
58	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.	1.0	16
59	Vaccines of the 21st Century and Vaccinomics: Data-Enabled Science Meets Global Health to Spark Collective Action for Vaccine Innovation. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 523-527.	1.0	16
60	Biology and Data-Intensive Scientific Discovery in the Beginning of the 21st Century. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 209-212.	1.0	16
61	Predictive Analytics In Healthcare: Medications as a Predictor of Medical Complexity. <i>Big Data</i> , 2013, 1, 237-244.	2.1	16
62	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, 333-335.	1.0	15
63	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.	1.0	15
64	Metadata Checklist for the Integrated Personal OMICS Study: Proteomics and Metabolomics Experiments. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 81-85.	1.0	14
65	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, 435-442.	1.0	14
66	Charge State Estimation for Tandem Mass Spectrometry Proteomics. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 233-250.	1.0	13
67	Health Care Transformation. <i>Academic Medicine</i> , 2016, 91, 165-167.	0.8	13
68	IPM: An integrated protein model for false discovery rate estimation and identification in high-throughput proteomics. <i>Journal of Proteomics</i> , 2011, 75, 116-121.	1.2	12
69	DELTA Global for "Big Data" and the Bioeconomy: Catalyzing Collective Innovation. <i>Industrial Biotechnology</i> , 2012, 8, 176-178.	0.5	12
70	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, 767-777.	1.0	12
71	Development of BIATECH-54 standard mixtures for assessment of protein identification and relative expression. <i>Proteomics</i> , 2007, 7, 3693-3698.	1.3	11
72	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, 513-521.	1.0	11

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73	Education and Data-Intensive Science in the Beginning of the 21st Century. OMICS A Journal of Integrative Biology, 2011, 15, 217-219.	1.0	11
74	In praise of open research measures. Nature, 2013, 498, 170-170.	13.7	11
75	Special Issue on Data-Intensive Science. OMICS A Journal of Integrative Biology, 2011, 15, 197-198.	1.0	10
76	Healthcare Analytics: Creating a Prioritized Improvement System with Performance Benchmarking. Big Data, 2014, 2, 50-54.	2.1	10
77	Can "Normal" Protein Expression Ranges Be Estimated with High-Throughput Proteomics?. Journal of Proteome Research, 2015, 14, 2398-2407.	1.8	9
78	The necessity of adjusting tests of protein category enrichment in discovery proteomics. Bioinformatics, 2010, 26, 3007-3011.	1.8	8
79	Metadata Checklist for the Integrated Personal Omics Study: Proteomics and Metabolomics Experiments. Big Data, 2013, 1, 202-206.	2.1	8
80	A Case Study: Analyzing City Vitality with Four Pillars of Activity "Live, Work, Shop, and Play. Big Data, 2016, 4, 60-66.	2.1	8
81	Quantifying Protein Function Specificity in the Gene Ontology. Standards in Genomic Sciences, 2010, 2, 238-244.	1.5	7
82	Bernard Lerer: Recipient of the 2014 Inaugural Werner Kalow Responsible Innovation Prize in Global Omics and Personalized Medicine (Pacific Rim Association for Clinical Pharmacogenetics). OMICS A Journal of Integrative Biology, 2014, 18, 211-221.	1.0	7
83	Modeling sequence and function similarity between proteins for protein functional annotation. , 2010, 2010, 499-502.		6
84	Design and Initial Characterization of the SC-200 Proteomics Standard Mixture. OMICS A Journal of Integrative Biology, 2011, 15, 73-82.	1.0	6
85	OMICS Studies: How about Metadata Checklist and Data Publications?. Journal of Proteome Research, 2014, 13, 1783-1784.	1.8	6
86	Spectral Analysis of Distributions: Finding Periodic Components in Eukaryotic Enzyme Length Data. OMICS A Journal of Integrative Biology, 2002, 6, 123-130.	1.0	5
87	Validating Annotations for Uncharacterized Proteins in <i>Shewanella oneidensis</i> . OMICS A Journal of Integrative Biology, 2008, 12, 211-215.	1.0	5
88	Technology and Data-Intensive Science in the Beginning of the 21st Century. OMICS A Journal of Integrative Biology, 2011, 15, 203-207.	1.0	5
89	Collective theranostics and postgenomics entrepreneurship: rethinking innovations as knowledge ecosystems built by complex collaboration. Expert Review of Molecular Diagnostics, 2012, 12, 787-790.	1.5	5
90	Toward More Transparent and Reproducible Omics Studies Through a Common Metadata Checklist and Data Publications. Big Data, 2013, 1, 196-201.	2.1	5

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91	Visualizing the Protein Sequence Universe. Concurrency Computation Practice and Experience, 2014, 26, 1313-1325.	1.4	5
92	Finding Text-Supported Gene-to-Disease Co-appearances with MOPED-Digger. OMICS A Journal of Integrative Biology, 2015, 19, 754-756.	1.0	5
93	H. influenzae Consortium: Integrative Study of H. influenzae-Human Interactions. OMICS A Journal of Integrative Biology, 2002, 6, 341-348.	1.0	4
94	Delsa Workshop IV: Launching the Quantified Human Initiative. Big Data, 2013, 1, 187-190.	2.1	4
95	Precision Medicine 2.0: The Rise of Glocal Innovation, Superconnectors, and Design Thinking. OMICS A Journal of Integrative Biology, 2016, 20, 493-495.	1.0	4
96	OMICS: 2009, 2010, and Beyond. OMICS A Journal of Integrative Biology, 2009, 13, 451-451.	1.0	3
97	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 9. Standards in Genomic Sciences, 2010, 3, 216-224.	1.5	3
98	Visualizing the protein sequence universe. , 2012, , .		3
99	Meeting Report: "Metagenomics, Metadata and Meta-analysis" (M3) Workshop at the Pacific Symposium on Biocomputing 2010. Standards in Genomic Sciences, 2010, 2, 357-360.	1.5	2
100	Introducing a Metadata Checklist for Omics Data. Big Data, 2013, 1, 195-195.	2.1	2
101	Optimizing high performance computing workflow for protein functional annotation. Concurrency Computation Practice and Experience, 2014, 26, 2112-2121.	1.4	2
102	Integrative Microbiology, 2003. OMICS A Journal of Integrative Biology, 2002, 6, 285-285.	1.0	1
103	Editorial. OMICS A Journal of Integrative Biology, 2010, 14, 229-229.	1.0	1
104	Statistical Methods in Systems Biology. , 2013, , 1985-1986.		1
105	Data Science Community Matures with Diversity: Conference Observations, Highlights, and Interviews" Strata Data Conference, New York, September 11-13, 2018. Big Data, 2018, 6, 305-313.	2.1	0