Sebastian Bauer

List of Publications by Year
in descending order

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26 papers	5,413 citations	448610 19 h-index	651938 25 g-index
27 all docs	27 docs citations	27 times ranked	10268 citing authors

#	Article	IF	Citations
1	Gene-Category Analysis. Methods in Molecular Biology, 2017, 1446, 175-188.	0.4	11
2	Improved exome prioritization of disease genes through cross-species phenotype comparison. Genome Research, 2014, 24, 340-348.	2.4	300
3	Use of animal models for exome prioritization of rare disease genes. Orphanet Journal of Rare Diseases, 2014, 9, O19.	1.2	0
4	Deletions of chromosomal regulatory boundaries are associated with congenital disease. Genome Biology, 2014, 15, 423.	3.8	144
5	The Human Phenotype Ontology project: linking molecular biology and disease through phenotype data. Nucleic Acids Research, 2014, 42, D966-D974.	6.5	698
6	Phenotypic overlap in the contribution of individual genes to CNV pathogenicity revealed by cross-species computational analysis of single-gene mutations in humans, mice and zebrafish. DMM Disease Models and Mechanisms, 2013, 6, 358-72.	1.2	43
7	Construction and accessibility of a cross-species phenotype ontology along with gene annotations for biomedical research. F1000Research, 2013, 2, 30.	0.8	72
8	Construction and accessibility of a cross-species phenotype ontology along with gene annotations for biomedical research. F1000Research, 2013, 2, 30.	0.8	64
9	Bayesian ontology querying for accurate and noise-tolerant semantic searches. Bioinformatics, 2012, 28, 2502-2508.	1.8	55
10	The allele distribution in next-generation sequencing data sets is accurately described as the result of a stochastic branching process. Nucleic Acids Research, 2012, 40, 2426-2431.	6.5	40
11	Improving ontologies by automatic reasoning and evaluation of logical definitions. BMC Bioinformatics, 2011, 12, 418.	1.2	29
12	Exact score distribution computation for ontological similarity searches. BMC Bioinformatics, 2011, 12, 441.	1.2	15
13	Integrative analysis of genomic, functional and protein interaction data predicts long-range enhancer-target gene interactions. Nucleic Acids Research, 2011, 39, 2492-2502.	6.5	22
14	Model-based gene set analysis for Bioconductor. Bioinformatics, 2011, 27, 1882-1883.	1.8	56
15	Identity-by-descent filtering of exome sequence data for diseaseâ€“gene identification in autosomal recessive disorders. Bioinformatics, 2011, 27, 829-836.	1.8	30
16	Identity-by-descent filtering of exome sequence data identifies PIGV mutations in hyperphosphatasia mental retardation syndrome. Nature Genetics, 2010, 42, 827-829.	9.4	286
17	GOing Bayesian: model-based gene set analysis of genome-scale data. Nucleic Acids Research, 2010, 38, 3523-3532.	6.5	190
18	Microindel detection in short-read sequence data. Bioinformatics, 2010, 26, 722-729.	1.8	90

#	Article	IF	Citations
19	Clinical Diagnostics in Human Genetics with Semantic Similarity Searches in Ontologies. American Journal of Human Genetics, 2009, 85, 457-464.	2.6	444
20	Short ultraconserved promoter regions delineate a class of preferentially expressed alternatively spliced transcripts. Genomics, 2009, 94, 308-316.	1.3	11
21	Exact Score Distribution Computation for Similarity Searches in Ontologies. Lecture Notes in Computer Science, 2009, , 298-309.	1.0	3
22	Walking the Interactome for Prioritization of Candidate Disease Genes. American Journal of Human Genetics, 2008, 82, 949-958.	2.6	1,111
23	The Human Phenotype Ontology: A Tool for Annotating and Analyzing Human Hereditary Disease. American Journal of Human Genetics, 2008, 83, 610-615.	2.6	797
24	A short ultraconserved sequence drives transcription from an alternate FBN1 promoter. International Journal of Biochemistry and Cell Biology, 2008, 40, 638-650.	1.2	15
25	Ontologizer 2.0â€”a multifunctional tool for GO term enrichment analysis and data exploration. Bioinformatics, 2008, 24, 1650-1651.	1.8	466
26	Improved detection of overrepresentation of Gene-Ontology annotations with parentâ€“child analysis. Bioinformatics, 2007, 23, 3024-3031.	1.8	370