## Kristina M Hettne

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4398379/publications.pdf

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44 papers 1,165 citations

18 h-index 433756 31 g-index

49 all docs 49 docs citations

49 times ranked 2206 citing authors

#	Article	IF	CITATIONS
1	FAIR Principles: Interpretations and Implementation Considerations. Data Intelligence, 2020, 2, 10-29.	0.8	149
2	A dictionary to identify small molecules and drugs in free text. Bioinformatics, 2009, 25, 2983-2991.	1.8	116
3	Using a suite of ontologies for preserving workflow-centric research objects. Web Semantics, 2015, 32, 16-42.	2.2	94
4	Why workflows break & mp; #x2014; Understanding and combating decay in Taverna workflows. , 2012, , .		48
5	Tracking disease progression nonâ€invasively in Duchenne and Becker muscular dystrophies. Journal of Cachexia, Sarcopenia and Muscle, 2018, 9, 715-726.	2.9	47
6	Transcriptional profiling and biomarker identification reveal tissue specific effects of expanded ataxin-3 in a spinocerebellar ataxia type 3 mouse model. Molecular Neurodegeneration, 2018, 13, 31.	4.4	47
7	Chemical and Biological Profiling of an Annotated Compound Library Directed to the Nuclear Receptor Family. Current Topics in Medicinal Chemistry, 2005, 5, 763-772.	1.0	45
8	Integration of targeted metabolomics and transcriptomics identifies deregulation of phosphatidylcholine metabolism in Huntington's disease peripheral blood samples. Metabolomics, 2016, 12, 137.	1.4	43
9	Automatic mining of the literature to generate new hypotheses for the possible link between periodontitis and atherosclerosis: lipopolysaccharide as a case study. Journal of Clinical Periodontology, 2007, 34, 1016-1024.	2.3	40
10	Automatic vs. manual curation of a multi-source chemical dictionary: the impact on text mining. Journal of Cheminformatics, 2010, 2, 3.	2.8	33
11	Drug prioritization using the semantic properties of a knowledge graph. Scientific Reports, 2019, 9, 6281.	1.6	33
12	Common disease signatures from gene expression analysis in Huntington's disease human blood and brain. Orphanet Journal of Rare Diseases, 2016, 11, 97.	1.2	32
13	Selective glucocorticoid receptor modulation prevents and reverses non-alcoholic fatty liver disease in male mice. Endocrinology, 2018, 159, 3925-3936.	1.4	27
14	Structuring research methods and data with the research object model: genomics workflows as a case study. Journal of Biomedical Semantics, 2014, 5, 41.	0.9	26
15	Early career researchers want Open Science. Genome Biology, 2017, 18, 221.	3.8	26
16	Recognition of chemical entities: combining dictionary-based and grammar-based approaches. Journal of Cheminformatics, 2015, 7, S10.	2.8	25
17	Crossâ€sectional serum metabolomic study of multiple forms of muscular dystrophy. Journal of Cellular and Molecular Medicine, 2018, 22, 2442-2448.	1.6	25
18	Rewriting and suppressing UMLS terms for improved biomedical term identification. Journal of Biomedical Semantics, 2010, $1, 5$ .	0.9	24

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19	Applied information retrieval and multidisciplinary research: new mechanistic hypotheses in Complex Regional Pain Syndrome. Journal of Biomedical Discovery and Collaboration, 2007, 2, 2.	2.0	23
20	The Implicitome: A Resource for Rationalizing Gene-Disease Associations. PLoS ONE, 2016, 11, e0149621.	1.1	22
21	Literature-aided interpretation of gene expression data with the weighted global test. Briefings in Bioinformatics, 2011, 12, 518-529.	3.2	19
22	Longitudinal metabolomic analysis of plasma enables modeling disease progression in Duchenne muscular dystrophy mouse models. Human Molecular Genetics, 2020, 29, 745-755.	1.4	19
23	Chemical entity recognition in patents by combining dictionary-based and statistical approaches. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw061.	1.4	17
24	Prioritization of novel ADPKD drug candidates from disease-stage specific gene expression profiles. EBioMedicine, 2020, 51, 102585.	2.7	16
25	Peripheral blood transcriptome profiling enables monitoring disease progression in dystrophic mice and patients. EMBO Molecular Medicine, 2021, 13, e13328.	3.3	16
26	Next-generation text-mining mediated generation of chemical response-specific gene sets for interpretation of gene expression data. BMC Medical Genomics, 2013, 6, 2.	0.7	15
27	How to automatically turn patient experience free-text responses into actionable insights: a natural language programming (NLP) approach. BMC Medical Informatics and Decision Making, 2020, 20, 97.	1.5	15
28	Reusable FAIR Implementation Profiles as Accelerators of FAIR Convergence. Lecture Notes in Computer Science, 2020, , 138-147.	1.0	15
29	Automated workflow-based exploitation of pathway databases provides new insights into genetic associations of metabolite profiles. BMC Genomics, 2013, 14, 865.	1.2	14
30	Brain Transcriptomic Analysis of Hereditary Cerebral Hemorrhage With Amyloidosis-Dutch Type. Frontiers in Aging Neuroscience, 2018, 10, 102.	1.7	13
31	Simultaneous Enrichment Analysis of all Possible Gene-sets: Unifying Self-Contained and Competitive Methods. Briefings in Bioinformatics, 2020, 21, 1302-1312.	3.2	13
32	Nanopublications for exposing experimental data in the life-sciences: a Huntington's Disease case study. Journal of Biomedical Semantics, 2015, 6, 5.	0.9	12
33	Training Multidisciplinary Biomedical Informatics Students: Three Years of Experience. Journal of the American Medical Informatics Association: JAMIA, 2008, 15, 246-254.	2.2	11
34	Connecting Small Molecules to Nuclear Receptor Pathways. Current Topics in Medicinal Chemistry, 2007, 7, 1530-1536.	1.0	8
35	Workflow forever., 2011, , .		6
36	Explain your data by Concept Profile Analysis Web Services. F1000Research, 0, 3, 173.	0.8	5

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37	Multidisciplinary Collaboration to Facilitate Hypotheses Generation in Huntington's Disease. , 2015, , .		3
38	From FAIR Leading Practices to FAIR Implementation and Back: An Inclusive Approach to FAIR at Leiden University Libraries. Data Science Journal, 2020, 19, .	0.6	2
39	Bioinformatics Methods for Interpreting Toxicogenomics Data. , 2014, , 291-304.		1
40	ReprohackNL 2019: how libraries can promote research reproducibility through community engagement. IASSIST Quarterly, 2020, 44, 1-10.	0.1	1
41	Huntington Disease Gene Expression Signatures in Blood Compared to Brain of YAC128 Mice as Candidates for Monitoring of Pathology. Molecular Neurobiology, 2022, 59, 2532-2551.	1.9	1
42	B16â€Common disease signatures from gene expression analysis in huntington's disease human blood and brain. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, A14.2-A15.	0.9	0
43	Using a Suite of Ontologies for Preserving Workflow-Centric Research Objects. SSRN Electronic Journal, 0, , .	0.4	0
44	A putative role for genome-wide epigenetic regulatory mechanisms in Huntington's disease: A computational assessment. F1000Research, 0, 6, 1888.	0.8	0