

Kristina M Hettne

List of Publications by Citations

Source: <https://exaly.com/author-pdf/4398379/kristina-m-hettne-publications-by-citations.pdf>

Version: 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

44
papers

789
citations

18
h-index

27
g-index

49
ext. papers

1,000
ext. citations

5.8
avg, IF

3.44
L-index

| # | Paper | IF | Citations |
|----|--|------|-----------|
| 44 | A dictionary to identify small molecules and drugs in free text. <i>Bioinformatics</i> , 2009 , 25, 2983-91 | 7.2 | 95 |
| 43 | Using a suite of ontologies for preserving workflow-centric research objects. <i>Web Semantics</i> , 2015 , 32, 16-42 | 2.9 | 72 |
| 42 | FAIR Principles: Interpretations and Implementation Considerations. <i>Data Intelligence</i> , 2020 , 2, 10-29 | 3 | 66 |
| 41 | Chemical and biological profiling of an annotated compound library directed to the nuclear receptor family. <i>Current Topics in Medicinal Chemistry</i> , 2005 , 5, 763-72 | 3 | 39 |
| 40 | Why workflows break □ Understanding and combating decay in Taverna workflows 2012 , | | 34 |
| 39 | Automatic mining of the literature to generate new hypotheses for the possible link between periodontitis and atherosclerosis: lipopolysaccharide as a case study. <i>Journal of Clinical Periodontology</i> , 2007 , 34, 1016-24 | 7.7 | 34 |
| 38 | Tracking disease progression non-invasively in Duchenne and Becker muscular dystrophies. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2018 , 9, 715-726 | 10.3 | 32 |
| 37 | Transcriptional profiling and biomarker identification reveal tissue specific effects of expanded ataxin-3 in a spinocerebellar ataxia type 3 mouse model. <i>Molecular Neurodegeneration</i> , 2018 , 13, 31 | 19 | 29 |
| 36 | Integration of targeted metabolomics and transcriptomics identifies deregulation of phosphatidylcholine metabolism in Huntington's disease peripheral blood samples. <i>Metabolomics</i> , 2016 , 12, 137 | 4.7 | 29 |
| 35 | Automatic vs. manual curation of a multi-source chemical dictionary: the impact on text mining. <i>Journal of Cheminformatics</i> , 2010 , 2, 3 | 8.6 | 24 |
| 34 | Common disease signatures from gene expression analysis in Huntington's disease human blood and brain. <i>Orphanet Journal of Rare Diseases</i> , 2016 , 11, 97 | 4.2 | 24 |
| 33 | Selective Glucocorticoid Receptor Modulation Prevents and Reverses Nonalcoholic Fatty Liver Disease in Male Mice. <i>Endocrinology</i> , 2018 , 159, 3925-3936 | 4.8 | 22 |
| 32 | Structuring research methods and data with the research object model: genomics workflows as a case study. <i>Journal of Biomedical Semantics</i> , 2014 , 5, 41 | 2.2 | 21 |
| 31 | Applied information retrieval and multidisciplinary research: new mechanistic hypotheses in complex regional pain syndrome. <i>Journal of Biomedical Discovery and Collaboration</i> , 2007 , 2, 2 | | 21 |
| 30 | Literature-aided interpretation of gene expression data with the weighted global test. <i>Briefings in Bioinformatics</i> , 2011 , 12, 518-29 | 13.4 | 19 |
| 29 | Rewriting and suppressing UMLS terms for improved biomedical term identification. <i>Journal of Biomedical Semantics</i> , 2010 , 1, 5 | 2.2 | 19 |
| 28 | Early career researchers want Open Science. <i>Genome Biology</i> , 2017 , 18, 221 | 18.3 | 18 |

| | | | |
|----|---|------|----|
| 27 | The Implicitome: A Resource for Rationalizing Gene-Disease Associations. <i>PLoS ONE</i> , 2016 , 11, e0149621 | 3.7 | 18 |
| 26 | Recognition of chemical entities: combining dictionary-based and grammar-based approaches. <i>Journal of Cheminformatics</i> , 2015 , 7, S10 | 8.6 | 17 |
| 25 | Drug prioritization using the semantic properties of a knowledge graph. <i>Scientific Reports</i> , 2019 , 9, 62814 | 4.9 | 16 |
| 24 | Cross-sectional serum metabolomic study of multiple forms of muscular dystrophy. <i>Journal of Cellular and Molecular Medicine</i> , 2018 , 22, 2442-2448 | 5.6 | 14 |
| 23 | Chemical entity recognition in patents by combining dictionary-based and statistical approaches. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016, | 5 | 13 |
| 22 | Next-generation text-mining mediated generation of chemical response-specific gene sets for interpretation of gene expression data. <i>BMC Medical Genomics</i> , 2013 , 6, 2 | 3.7 | 13 |
| 21 | Automated workflow-based exploitation of pathway databases provides new insights into genetic associations of metabolite profiles. <i>BMC Genomics</i> , 2013 , 14, 865 | 4.5 | 13 |
| 20 | Nanopublications for exposing experimental data in the life-sciences: a Huntington's Disease case study. <i>Journal of Biomedical Semantics</i> , 2015 , 6, 5 | 2.2 | 10 |
| 19 | Brain Transcriptomic Analysis of Hereditary Cerebral Hemorrhage With Amyloidosis-Dutch Type. <i>Frontiers in Aging Neuroscience</i> , 2018 , 10, 102 | 5.3 | 9 |
| 18 | Training multidisciplinary biomedical informatics students: three years of experience. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2008 , 15, 246-54 | 8.6 | 8 |
| 17 | Connecting small molecules to nuclear receptor pathways. <i>Current Topics in Medicinal Chemistry</i> , 2007 , 7, 1530-6 | 3 | 8 |
| 16 | How to automatically turn patient experience free-text responses into actionable insights: a natural language programming (NLP) approach. <i>BMC Medical Informatics and Decision Making</i> , 2020 , 20, 97 | 3.6 | 7 |
| 15 | Prioritization of novel ADPKD drug candidates from disease-stage specific gene expression profiles. <i>EBioMedicine</i> , 2020 , 51, 102585 | 8.8 | 7 |
| 14 | Longitudinal metabolomic analysis of plasma enables modeling disease progression in Duchenne muscular dystrophy mouse models. <i>Human Molecular Genetics</i> , 2020 , 29, 745-755 | 5.6 | 6 |
| 13 | Simultaneous Enrichment Analysis of all Possible Gene-sets: Unifying Self-Contained and Competitive Methods. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1302-1312 | 13.4 | 5 |
| 12 | Explain your data by Concept Profile Analysis Web Services. <i>F1000Research</i> , 3 , 173 | 3.6 | 4 |
| 11 | Workflow forever 2012 , | | 3 |
| 10 | Reusable FAIR Implementation Profiles as Accelerators of FAIR Convergence. <i>Lecture Notes in Computer Science</i> , 2020 , 138-147 | 0.9 | 3 |

| | | | |
|---|---|-----|---|
| 9 | Multidisciplinary Collaboration to Facilitate Hypotheses Generation in Huntington's Disease 2015 , | | 2 |
| 8 | Reusable FAIR Implementation Profiles as Accelerators of FAIR Convergence | | 2 |
| 7 | Knowledge.Bio: A Web Application for Exploring, Building and Sharing Webs of Biomedical Relationships Mined from PubMed | | 2 |
| 6 | Peripheral blood transcriptome profiling enables monitoring disease progression in dystrophic mice and patients. <i>EMBO Molecular Medicine</i> , 2021 , 13, e13328 | 12 | 2 |
| 5 | From FAIR Leading Practices to FAIR Implementation and Back: An Inclusive Approach to FAIR at Leiden University Libraries. <i>Data Science Journal</i> , 2020 , 19, | 2 | 1 |
| 4 | Bioinformatics Methods for Interpreting Toxicogenomics Data: The Role of Text-Mining 2014 , 291-304 | | 0 |
| 3 | Huntington Disease Gene Expression Signatures in Blood Compared to Brain of YAC128 Mice as Candidates for Monitoring of Pathology.. <i>Molecular Neurobiology</i> , 2022 , 1 | 6.2 | |
| 2 | A putative role for genome-wide epigenetic regulatory mechanisms in Huntington's disease: A computational assessment. <i>F1000Research</i> , 6 , 1888 | 3.6 | |
| 1 | B16 Common disease signatures from gene expression analysis in huntington's disease human blood and brain. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2016 , 87, A14.2-A15 | 5.5 | |