Ulf Leser

List of Publications by Year
in descending order

93 papers	**3,386** citations	147801 **31** h-index	168389 **53** g-index
97 all docs	**97** docs citations	**97** times ranked	**4192** citing authors

#	Article	IF	Citations
1	DNA methylation reveals distinct cells of origin for pancreatic neuroendocrine carcinomas and pancreatic neuroendocrine tumors. Genome Medicine, 2022, 14, 24.	8.2	12
2	Large-scale entity representation learning for biomedical relationship extraction. Bioinformatics, 2021, 37, 236-242.	4.1	6
3	Earthquake magnitude and location estimation from real time seismic waveforms with a transformer network. Geophysical Journal International, 2021, 226, 1086-1104.	2.4	37
4	Annotation and initial evaluation of a large annotated German oncological corpus. JAMIA Open, 2021, 4, ooab025.	2.0	14
5	Elevated Flt3L Predicts Long-Term Survival in Patients with High-Grade Gastroenteropancreatic Neuroendocrine Neoplasms. Cancers, 2021, 13, 4463.	3.7	2
6	HunFlair: an easy-to-use tool for state-of-the-art biomedical named entity recognition. Bioinformatics, 2021, 37, 2792-2794.	4.1	53
7	The transformer earthquake alerting model: a new versatile approach to earthquake early warning. Geophysical Journal International, 2021, 225, 646-656.	2.4	49
8	The Collaborative Research Center FONDA. Datenbank-Spektrum, 2021, 21, 255-260.	1.3	3
9	Public data sources for regulatory genomic features. Medizinische Genetik, 2021, 33, 167-177.	0.2	1
10	HUNER: improving biomedical NER with pretraining. Bioinformatics, 2020, 36, 295-302.	4.1	38
11	Low uncertainty multifeature magnitude estimation with 3-D corrections and boosting tree regression: application to North Chile. Geophysical Journal International, 2020, 220, 142-159.	2.4	14
12	H3K9me3-mediated epigenetic regulation of senescence in mice predicts outcome of lymphoma patients. Nature Communications, 2020, 11, 3651.	12.8	15
13	PEDL: extracting protein–protein associations using deep language models and distant supervision. Bioinformatics, 2020, 36, i490-i498.	4.1	8
14	DeepTable: a permutation invariant neural network for table orientation classification. Data Mining and Knowledge Discovery, 2020, 34, 1963-1983.	3.7	1
15	TEASER: early and accurate time series classification. Data Mining and Knowledge Discovery, 2020, 34, 1336-1362.	3.7	32
16	Finding k-shortest paths with limited overlap. VLDB Journal, 2020, 29, 1023-1047.	4.1	29
17	VIST - a Variant-Information Search Tool for precision oncology. BMC Bioinformatics, 2019, 20, 429.	2.6	8
18	Estimation of Transcription Factor Activity in Knockdown Studies. Scientific Reports, 2019, 9, 9593.	3.3	4

#	Article	IF	Citations
19	BB-Tree: A Main-Memory Index Structure for Multidimensional Range Queries. , 2019, , .		10
20	Predictive performance modeling for distributed batch processing using black box monitoring and machine learning. Information Systems, 2019, 82, 33-52.	3.6	43
21	Robust in-silico identification of Cancer Cell Lines based on RNA and targeted DNA sequencing data. Scientific Reports, 2019, 9, 367.	3.3	1
22	Feedback-Based Resource Allocation for Batch Scheduling of Scientific Workflows. , 2019, , .		7
23	Optimization of Complex Dataflows with User-Defined Functions. ACM Computing Surveys, 2018, 50, 1-39.	23.0	23
24	POS: Online learning for memory-aware scheduling of scientific workflows. , 2018, , .		0
25	Variant information systems for precision oncology. BMC Medical Informatics and Decision Making, 2018, 18, 107.	3.0	10
26	Exploiting Automatic Vectorization to Employ SPMD on SIMD Registers. , 2018, , .		3
27	Set similarity joins on mapreduce. Proceedings of the VLDB Endowment, 2018, 11, 1110-1122.	3.8	33
28	Semantic Data Integration for Life Science Entities. , 2018, , 3387-3391.		0
29	Senescence Markers from a DLBCL-Reminiscent Mouse Lymphoma Model Predict Patient Outcome. Blood, 2018, 132, 2850-2850.	1.4	0
30	Comparative assessment of differential network analysis methods. Briefings in Bioinformatics, 2017, 18, bbw061.	6.5	65
31	DNA copy number changes define spatial patterns of heterogeneity in colorectal cancer. Nature Communications, 2017, 8, 14093.	12.8	85
32	How to improve information extraction from German medical records. IT - Information Technology, 2017, 59, 171-179.	0.9	8
33	Deep learning with word embeddings improves biomedical named entity recognition. Bioinformatics, 2017, 33, i37-i48.	4.1	400
34	Modeling Data Flow Execution in a Parallel Environment. Lecture Notes in Computer Science, 2017, , 183-196.	1.3	4
35	Estimating genome-wide regulatory activity from multi-omics data sets using mathematical optimization. BMC Systems Biology, 2017, 11, 41.	3.0	15
36	Fast and Accurate Time Series Classification with WEASEL. , 2017, , .		137

#	Article	IF	Citations
37	Basal subtype is predictive for response to cetuximab treatment in patient-derived xenografts of squamous cell head and neck cancer. International Journal of Cancer, 2017, 141, 1215-1221.	5.1	24
38	Robust <i>in-silico</i> identification of cancer cell lines based on next generation sequencing. Oncotarget, 2017, 8, 34310-34320.	1.8	12
39	SoFIA: a data integration framework for annotating high-throughput datasets. Bioinformatics, 2016, 32, 2590-2597.	4.1	10
40	Potential and Pitfalls of Domain-Specific Information Extraction at Web Scale. , 2016, , .		5
41	Reflection of successful anticancer drug development processes in the literature. Drug Discovery Today, 2016, 21, 1740-1744.	6.4	11
42	Recognizing chemicals in patents: a comparative analysis. Journal of Cheminformatics, 2016, 8, 59.	6.1	12
43	SETH detects and normalizes genetic variants in text. Bioinformatics, 2016, 32, 2883-2885.	4.1	30
44	Effective and efficient similarity search in scientific workflow repositories. Future Generation Computer Systems, 2016, 56, 584-594.	7.5	14
45	Alternative routing. , 2015, , .		25
46	MRCSI. Proceedings of the VLDB Endowment, 2015, 8, 461-472.	3.8	11
47	Assembly of a Comprehensive Regulatory Network for the Mammalian Circadian Clock: A Bioinformatics Approach. PLoS ONE, 2015, 10, e0126283.	2.5	43
48	On-Demand Indexing for Referential Compression of DNA Sequences. PLoS ONE, 2015, 10, e0132460.	2.5	8
49	Question answering for Biology. Methods, 2015, 74, 36-46.	3.8	31
50	Deregulation of the endogenous C/EBPβ LIP isoform predisposes to tumorigenesis. Journal of Molecular Medicine, 2015, 93, 39-49.	3.9	28
51	SOFA: An extensible logical optimizer for UDF-heavy data flows. Information Systems, 2015, 52, 96-125.	3.6	25
52	Algorithms for differential splicing detection using exon arrays: a comparative assessment. BMC Genomics, 2015, 16, 136.	2.8	3
53	SAASFEE. Proceedings of the VLDB Endowment, 2015, 8, 1892-1895.	3.8	17
54	Computer-assisted curation of a human regulatory core network from the biological literature. Bioinformatics, 2015, 31, 1258-1266.	4.1	10

#	ARTICLE	IF	CITATIONS
55	DynamicCloudSim: Simulating heterogeneity in computational clouds. Future Generation Computer Systems, 2015, 46, 85-99.	7.5	54
56	Sequence Factorization with Multiple References. PLoS ONE, 2015, 10, e0139000.	2.5	6
57	Ras-Mediated Deregulation of the Circadian Clock in Cancer. PLoS Genetics, 2014, 10, e1004338.	3.5	140
58	State-of-the-art in string similarity search and join. SIGMOD Record, 2014, 43, 64-76.	1.2	33
59	CellFinder: a cell data repository. Nucleic Acids Research, 2014, 42, D950-D958.	14.5	26
60	A survey on annotation tools for the biomedical literature. Briefings in Bioinformatics, 2014, 15, 327-340.	6.5	47
61	The Stratosphere platform for big data analytics. VLDB Journal, 2014, 23, 939-964.	4.1	348
62	Similarity search for scientific workflows. Proceedings of the VLDB Endowment, 2014, 7, 1143-1154.	3.8	33
63	Trends in Genome Compression. Current Bioinformatics, 2014, 9, 315-326.	1.5	38
64	Histone acetylation and DNA demethylation of T cells result in an anaplastic large cell lymphoma-like phenotype. Haematologica, 2013, 98, 247-254.	3.5	15
65	Cross talk between Wnt/Î²-catenin and Irf8 in leukemia progression and drug resistance. Journal of Experimental Medicine, 2013, 210, 2239-2256.	8.5	47
66	RCSI. Proceedings of the VLDB Endowment, 2013, 6, 1534-1545.	3.8	36
67	Tools for managing and analyzing microarray data. Briefings in Bioinformatics, 2012, 13, 46-60.	6.5	28
68	GeneView: a comprehensive semantic search engine for PubMed. Nucleic Acids Research, 2012, 40, W585-W591.	14.5	62
69	Data Management Challenges in Next Generation Sequencing. Datenbank-Spektrum, 2012, 12, 161-171.	1.3	25
70	Regular Path Queries on Large Graphs. Lecture Notes in Computer Science, 2012, , 177-194.	1.3	44
71	Classical Hodgkin's lymphoma shows epigenetic features of abortive plasma cell differentiation. Haematologica, 2011, 96, 863-870.	3.5	20
72	Search, adapt, and reuse. SIGMOD Record, 2011, 40, 6-16.	1.2	39

#	Article	IF	Citations
73	Deep web integration with VisQI. Proceedings of the VLDB Endowment, 2010, 3, 1613-1616.	3.8	21
74	Simple tricks for improving pattern-based information extraction from the biomedical literature. Journal of Biomedical Semantics, 2010, 1, 9.	1.6	12
75	A Comprehensive Benchmark of Kernel Methods to Extract Protein–Protein Interactions from Literature. PLoS Computational Biology, 2010, 6, e1000837.	3.2	124
76	Inference of Surface Membrane Factors of HIV-1 Infection through Functional Interaction Networks. PLoS ONE, 2010, 5, e13139.	2.5	7
77	High-performance information extraction with AliBaba. , 2009, , .		18
78	A hierarchical approach to model web query interfaces for web source integration. Proceedings of the VLDB Endowment, 2009, 2, 325-336.	3.8	52
79	SOA-Based Integration of Text Mining Services. , 2009, , .		4
80	Semantic Data Integration for Life Science Entities. , 2009, , 2555-2559.		0
81	Graph Management in the Life Sciences. , 2009, , 1266-1271.		1
82	Gene mention normalization and interaction extraction with context models and sentence motifs. Genome Biology, 2008, 9, S14.	9.6	47
83	Implications for Molecular Mechanisms of Glycoprotein Hormone Receptors Using a New Sequence-Structure-Function Analysis Resource. Molecular Endocrinology, 2007, 21, 574-580.	3.7	50
84	Efficiently Detecting Inclusion Dependencies. , 2007, , .		30
85	A structural keystone for drug design. Journal of Integrative Bioinformatics, 2006, 3, 21-31.	1.5	2
86	ALIBABA: PubMed as a graph. Bioinformatics, 2006, 22, 2444-2445.	4.1	114
87	How well are protein structures annotated in secondary databases?. Proteins: Structure, Function and Bioinformatics, 2005, 60, 571-576.	2.6	5
88	A query language for biological networks. Bioinformatics, 2005, 21, ii33-ii39.	4.1	69
89	What makes a gene name? Named entity recognition in the biomedical literature. Briefings in Bioinformatics, 2005, 6, 357-369.	6.5	134
90	Completeness of integrated information sources. Information Systems, 2004, 29, 583-615.	3.6	100

#	Article	IF	Citations
91	Finding Kinetic Parameters Using Text Mining. OMICS A Journal of Integrative Biology, 2004, 8, 131-152.	2.0	47
92	Query Planning with Information Quality Bounds. , 2001, , 85-94.		10
93	IXDB, an X chromosome integrated database (update). Nucleic Acids Research, 1999, 27, 123-127.	14.5	6