## Atsuko Yamaguchi

List of Publications by Year in descending order

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759233 752698 33 446 12 20 citations h-index g-index papers 33 33 33 604 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Advances in the development of PubCaseFinder, including the new application programming interface and matching algorithm. Human Mutation, 2022, , .	2.5	3
2	O-JMeSH: creating a bilingual English-Japanese controlled vocabulary of MeSH UIDs through machine translation and mutual information. Genomics and Informatics, 2021, 19, e26.	0.8	2
3	Constructing Japanese MeSH term dictionaries related to the COVID-19 literature. Genomics and Informatics, 2021, 19, e25.	0.8	1
4	BioHackathon 2015: Semantics of data for life sciences and reproducible research. F1000Research, 2020, 9, 136.	1.6	5
5	A proof-of-concept study of extracting patient histories for rare/intractable diseases from social media. Genomics and Informatics, 2020, 18, e17.	0.8	4
6	Investigating Schema Definitions Using RDFS and OWL 2 for RDF Databases in Life Sciences. Communications in Computer and Information Science, 2020, , 137-144.	0.5	0
7	Split4Blank: Maintaining consistency while improving efficiency of loading RDF data with blank nodes. PLoS ONE, 2019, 14, e0217852.	2.5	O
8	YummyData: providing high-quality open life science data. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	17
9	Implementing LOD Surfer as a Search System for the Annotation of Multiple Protein Sequence Alignment. Lecture Notes in Computer Science, 2018, , 418-426.	1.3	1
10	Semantic Graph Analysis for Federated LOD Surfing in Life Sciences. Lecture Notes in Computer Science, 2017, , 268-276.	1.3	1
11	Efficiently Finding Paths Between Classes to Build a SPARQL Query for Life-Science Databases. Lecture Notes in Computer Science, 2016, , 321-330.	1.3	4
12	Semantic Data Acquisition by Traversing Class–Class Relationships Over Linked Open Data. Lecture Notes in Computer Science, 2016, , 136-151.	1.3	7
13	The health care and life sciences community profile for dataset descriptions. PeerJ, 2016, 4, e2331.	2.0	18
14	Semantic Web technologies for the big data in life sciences. BioScience Trends, 2014, 8, 192-201.	3.4	11
15	TogoTable: cross-database annotation system using the Resource Description Framework (RDF) data model. Nucleic Acids Research, 2014, 42, W442-W448.	14.5	7
16	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. Journal of Biomedical Semantics, 2014, 5, 5.	1.6	47
17	BioBenchmark Toyama 2012: an evaluation of the performance of triple stores on biological data. Journal of Biomedical Semantics, 2014, 5, 32.	1.6	25
18	Building Linked Open Data towards integration of biomedical scientific literature with DBpedia. Journal of Biomedical Semantics, 2013, 4, 8.	1.6	12

#	Article	IF	CITATIONS
19	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. Journal of Biomedical Semantics, 2013, 4, 6.	1.6	26
20	Building linked open data using approximate string matching methods and domain specific resources. , $2012, \dots$		1
21	Discriminative application of string similarity methods to chemical and non-chemical names for biomedical abbreviation clustering. BMC Genomics, 2012, 13, S8.	2.8	4
22	Discriminative Application of String Similarity Methods to Chemical and Non-chemical Names for Biomedical Abbreviation Clustering. , $2011, \dots$		0
23	Discriminative Optimization of String Similarity and Its Application to Biomedical Abbreviation Clustering., 2011,,.		0
24	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. Journal of Biomedical Semantics, 2011, 2, 4.	1.6	19
25	Allie: a database and a search service of abbreviations and long forms. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar013-bar013.	3.0	33
26	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. Journal of Biomedical Semantics, 2010, 1, 8.	1.6	31
27	Natural Language Query Processing for Life Science Knowledge. Lecture Notes in Computer Science, 2010, , 158-165.	1.3	1
28	Application of a new probabilistic model for recognizing complex patterns in glycans. Bioinformatics, 2004, 20, i6-i14.	4.1	13
29	Finding the maximum common subgraph of a partial k-tree and a graph with a polynomially bounded number of spanning trees. Information Processing Letters, 2004, 92, 57-63.	0.6	23
30	KCaM (KEGG Carbohydrate Matcher): a software tool for analyzing the structures of carbohydrate sugar chains. Nucleic Acids Research, 2004, 32, W267-W272.	14.5	95
31	Efficient tree-matching methods for accurate carbohydrate database queries. Genome Informatics, 2003, 14, 134-43.	0.4	20
32	An Approximation Algorithm for the Two-Layered Graph Drawing Problem. Lecture Notes in Computer Science, 1999, , 81-91.	1.3	15
33	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. F1000Research, 0, 8, 1677.	1.6	0