

# Susanna-Assunta Sansone

## List of Publications by Year in descending order

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Version: 2024-02-01

112  
papers

21,858  
citations

47409

49  
h-index

27587

110  
g-index

136  
all docs

136  
docs citations

136  
times ranked

37646  
citing authors

#	ARTICLE	IF	CITATIONS
1	FAIRsharing: Data and Metadata Standards and Data Policies for Biomedical Research. , 2021, , 544-546.		1
2	Barely sufficient practices in scientific computing. Patterns, 2021, 2, 100206.	3.1	5
3	ISA API: An open platform for interoperable life science experimental metadata. GigaScience, 2021, 10, .	3.3	19
4	Orchestrating and sharing large multimodal data for transparent and reproducible research. Nature Communications, 2021, 12, 5797.	5.8	10
5	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	15.2	170
6	FAIR Convergence Matrix: Optimizing the Reuse of Existing FAIR-Related Resources. Data Intelligence, 2020, 2, 158-170.	0.8	10
7	Community standards for open cell migration data. GigaScience, 2020, 9, .	3.3	12
8	FAIR Principles: Interpretations and Implementation Considerations. Data Intelligence, 2020, 2, 10-29.	0.8	149
9	COVID-19 pandemic reveals the peril of ignoring metadata standards. Scientific Data, 2020, 7, 188.	2.4	56
10	TeSS: a platform for discovering life-science training opportunities. Bioinformatics, 2020, 36, 3290-3291.	1.8	15
11	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. New Phytologist, 2020, 227, 260-273.	3.5	84
12	Semantic concept schema of the linear mixed model of experimental observations. Scientific Data, 2020, 7, 70.	2.4	8
13	Fostering global data sharing: highlighting the recommendations of the Research Data Alliance COVID-19 working group. Wellcome Open Research, 2020, 5, 267.	0.9	11
14	Helping the Consumers and Producers of Standards, Repositories and Policies to Enable FAIR Data. Data Intelligence, 2020, 2, 151-157.	0.8	10
15	Fostering global data sharing: highlighting the recommendations of the Research Data Alliance COVID-19 working group. Wellcome Open Research, 2020, 5, 267.	0.9	6
16	Evaluating FAIR maturity through a scalable, automated, community-governed framework. Scientific Data, 2019, 6, 174.	2.4	82
17	Toward unrestricted use of public genomic data. Science, 2019, 363, 350-352.	6.0	45
18	Consent insufficient for data release—Response. Science, 2019, 364, 446-446.	6.0	5

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19	Interoperable and scalable data analysis with microservices: applications in metabolomics. <i>Bioinformatics</i> , 2019, 35, 3752-3760.	1.8	22
20	FAIRsharing as a community approach to standards, repositories and policies. <i>Nature Biotechnology</i> , 2019, 37, 358-367.	9.4	228
21	FAIRshake: Toolkit to Evaluate the FAIRness of Research Digital Resources. <i>Cell Systems</i> , 2019, 9, 417-421.	2.9	33
22	Experiment design driven FAIRification of omics data matrices, an exemplar. <i>Scientific Data</i> , 2019, 6, 271.	2.4	14
23	PhenoMeNal: processing and analysis of metabolomics data in the cloud. <i>GigaScience</i> , 2019, 8, .	3.3	60
24	DataMed â€” an open source discovery index for finding biomedical datasets. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2018, 25, 300-308.	2.2	54
25	Data discovery with DATS: exemplar adoptions and lessons learned. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2018, 25, 13-16.	2.2	5
26	CEDAR. , 2018, , .		3
27	High-quality science requires high-quality open data infrastructure. <i>Scientific Data</i> , 2018, 5, 180027.	2.4	6
28	A design framework and exemplar metrics for FAIRness. <i>Scientific Data</i> , 2018, 5, 180118.	2.4	145
29	Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , 2017, 35, 406-409.	9.4	159
30	Finding useful data across multiple biomedical data repositories using DataMed. <i>Nature Genetics</i> , 2017, 49, 816-819.	9.4	77
31	DATS, the data tag suite to enable discoverability of datasets. <i>Scientific Data</i> , 2017, 4, 170059.	2.4	67
32	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. <i>Nature Biotechnology</i> , 2017, 35, 1127-1128.	9.4	32
33	Developing a strategy for computational lab skills training through Software and Data Carpentry: Experiences from the ELIXIR Pilot action. <i>F1000Research</i> , 2017, 6, 1040.	0.8	8
34	The future of metabolomics in ELIXIR. <i>F1000Research</i> , 2017, 6, 1649.	0.8	19
35	The future of metabolomics in ELIXIR. <i>F1000Research</i> , 2017, 6, 1649.	0.8	11
36	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data. <i>PLoS Biology</i> , 2017, 15, e2001414.	2.6	97

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37	The Ontology for Biomedical Investigations. PLoS ONE, 2016, 11, e0154556.	1.1	217
38	BioSharing: curated and crowd-sourced metadata standards, databases and data policies in the life sciences. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw075.	1.4	84
39	Measures for interoperability of phenotypic data: minimum information requirements and formatting. Plant Methods, 2016, 12, 44.	1.9	109
40	The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 2016, 3, 160018.	2.4	8,670
41	Publishing descriptions of non-public clinical datasets: proposed guidance for researchers, repositories, editors and funding organisations. Research Integrity and Peer Review, 2016, 1, 6.	2.2	16
42	Data standards can boost metabolomics research, and if there is a will, there is a way. Metabolomics, 2016, 12, 14.	1.4	97
43	COordination of Standards in MetabOlomics (COSMOS): facilitating integrated metabolomics data access. Metabolomics, 2015, 11, 1587-1597.	1.4	140
44	The center for expanded data annotation and retrieval. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1148-1152.	2.2	74
45	Modeling a microbial community and biodiversity assay with OBO Foundry ontologies: the interoperability gains of a modular approach. Database: the Journal of Biological Databases and Curation, 2015, 2015, bau132-bau132.	1.4	5
46	From Peer-Reviewed to Peer-Reproduced in Scholarly Publishing: The Complementary Roles of Data Models and Workflows in Bioinformatics. PLoS ONE, 2015, 10, e0127612.	1.1	27
47	A sea of standards for omics data: sink or swim?. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 200-203.	2.2	52
48	The founding charter of the Genomic Observatories Network. GigaScience, 2014, 3, 2.	3.3	51
49	The Risa R/Bioconductor package: integrative data analysis from experimental metadata and back again. BMC Bioinformatics, 2014, 15, S11.	1.2	22
50	EBI metagenomicsâ€”a new resource for the analysis and archiving of metagenomic data. Nucleic Acids Research, 2014, 42, D600-D606.	6.5	127
51	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	9.4	883
52	linkedISA: semantic representation of ISA-Tab experimental metadata. BMC Bioinformatics, 2014, 15, S4.	1.2	49
53	Selected papers from the 15th Annual Bio-Ontologies Special Interest Group Meeting. Journal of Biomedical Semantics, 2013, 4, 11.	0.9	0
54	Visual Compression of Workflow Visualizations with Automated Detection of Macro Motifs. IEEE Transactions on Visualization and Computer Graphics, 2013, 19, 2576-2585.	2.9	19

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55	OntoMaton: a Bioportal powered ontology widget for Google Spreadsheets. <i>Bioinformatics</i> , 2013, 29, 525-527.	1.8	49
56	MetaboLights“an open-access general-purpose repository for metabolomics studies and associated meta-data. <i>Nucleic Acids Research</i> , 2013, 41, D781-D786.	6.5	578
57	The MetaboLights repository: curation challenges in metabolomics. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat029.	1.4	46
58	Standardizing data. <i>Nature Nanotechnology</i> , 2013, 8, 73-74.	15.6	19
59	Bio-Graphlln: a graph-based, integrative and semantically-enabled repository for life science experimental data. <i>EMBnet Journal</i> , 2013, 19, 46.	0.2	9
60	The Stem Cell Discovery Engine: an integrated repository and analysis system for cancer stem cell comparisons. <i>Nucleic Acids Research</i> , 2012, 40, D984-D991.	6.5	29
61	Toward interoperable bioscience data. <i>Nature Genetics</i> , 2012, 44, 121-126.	9.4	362
62	Investigation-Study-Assay, a toolkit for standardizing data capture and sharing. , 2012, , 173-188.		1
63	The Metadata Coverage Index (MCI): A standardized metric for quantifying database metadata richness. <i>Standards in Genomic Sciences</i> , 2012, 6, 444-453.	1.5	8
64	Conceptualizing a Genomics Software Institute (GSI). <i>Standards in Genomic Sciences</i> , 2012, 6, 136-144.	1.5	1
65	Report of the 13th Genomic Standards Consortium Meeting, Shenzhen, China, March 4“7, 2012.. <i>Standards in Genomic Sciences</i> , 2012, 6, 276-286.	1.5	3
66	MetaboLights: towards a new COSMOS of metabolomics data management. <i>Metabolomics</i> , 2012, 8, 757-760.	1.4	79
67	Taxonomy-Based Glyph Design“with a Case Study on Visualizing Workflows of Biological Experiments. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2012, 18, 2603-2612.	2.9	51
68	On the evolving portfolio of community-standards and data sharing policies: turning challenges into new opportunities. <i>GigaScience</i> , 2012, 1, 10.	3.3	11
69	Data Standards for Omics Data: The Basis of Data Sharing and Reuse. <i>Methods in Molecular Biology</i> , 2011, 719, 31-69.	0.4	73
70	The genomic standards consortium: bringing standards to life for microbial ecology. <i>ISME Journal</i> , 2011, 5, 1565-1567.	4.4	59
71	Empowering industrial research with shared biomedical vocabularies. <i>Drug Discovery Today</i> , 2011, 16, 940-947.	3.2	20
72	Towards BioDBcore: a community-defined information specification for biological databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, baq027-baq027.	1.4	30

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73	Towards BioDBcore: a community-defined information specification for biological databases. <i>Nucleic Acids Research</i> , 2011, 39, D7-D10.	6.5	32
74	Overcoming the ontology enrichment bottleneck with Quick Term Templates. <i>Applied Ontology</i> , 2011, 6, 13-22.	1.0	7
75	The Genomic Standards Consortium. <i>PLoS Biology</i> , 2011, 9, e1001088.	2.6	180
76	Meeting Report from the Second "Minimum Information for Biological and Biomedical Investigations" (MIBBI) workshop. <i>Standards in Genomic Sciences</i> , 2010, 3, 259-266.	1.5	32
77	Meeting Report: "Metagenomics, Metadata and Meta-analysis" (M3) Workshop at the Pacific Symposium on Biocomputing 2010. <i>Standards in Genomic Sciences</i> , 2010, 2, 357-360.	1.5	2
78	Modeling biomedical experimental processes with OBI. <i>Journal of Biomedical Semantics</i> , 2010, 1, S7.	0.9	207
79	ISA software suite: supporting standards-compliant experimental annotation and enabling curation at the community level. <i>Bioinformatics</i> , 2010, 26, 2354-2356.	1.8	247
80	ArrayExpress update—from an archive of functional genomics experiments to the atlas of gene expression. <i>Nucleic Acids Research</i> , 2009, 37, D868-D872.	6.5	380
81	Survey-based naming conventions for use in OBO Foundry ontology development. <i>BMC Bioinformatics</i> , 2009, 10, 125.	1.2	50
82	'Omics Data Sharing. <i>Science</i> , 2009, 326, 234-236.	6.0	136
83	Towards interoperable reporting standards for omics data: hopes and hurdles. <i>Summit on Translational Bioinformatics</i> , 2009, 2009, 112-5.	0.7	1
84	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896.	9.4	506
85	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008, 26, 541-547.	9.4	1,069
86	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). <i>Nature Biotechnology</i> , 2008, 26, 305-312.	9.4	111
87	The carcinoGENOMICS project: Critical selection of model compounds for the development of omics-based in vitro carcinogenicity screening assays. <i>Mutation Research - Reviews in Mutation Research</i> , 2008, 659, 202-210.	2.4	60
88	Toward a Standards-Compliant Genomic and Metagenomic Publication Record. <i>OMICS A Journal of Integrative Biology</i> , 2008, 12, 157-160.	1.0	33
89	Foreword to the Special Issue on the Fifth Genomic Standards Consortium Workshop. <i>OMICS A Journal of Integrative Biology</i> , 2008, 12, 99-99.	1.0	3
90	The Metabolomics Standards Initiative. <i>Nature Biotechnology</i> , 2007, 25, 846-848.	9.4	328

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91	The OBO Foundry: coordinated evolution of ontologies to support biomedical data integration. <i>Nature Biotechnology</i> , 2007, 25, 1251-1255.	9.4	1,955
92	The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics. <i>Nature Biotechnology</i> , 2007, 25, 1127-1133.	9.4	96
93	Standard reporting requirements for biological samples in metabolomics experiments: environmental context. <i>Metabolomics</i> , 2007, 3, 203-210.	1.4	93
94	Metabolomics standards initiative: ontology working group work in progress. <i>Metabolomics</i> , 2007, 3, 249-256.	1.4	52
95	The metabolomics standards initiative (MSI). <i>Metabolomics</i> , 2007, 3, 175-178.	1.4	396
96	Standard Annotation of Environmental OMICS Data: Application to the Transcriptomics Domain. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 172-178.	1.0	21
97	A Strategy Capitalizing on Synergies: The Reporting Structure for Biological Investigation (RSBI) Working Group. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 164-171.	1.0	33
98	A Special Issue on Data Standards. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 84-93.	1.0	46
99	Wrestling with SUMO and bio-ontologies. <i>Nature Biotechnology</i> , 2006, 24, 21-21.	9.4	8
100	The MGED Ontology: a resource for semantics-based description of microarray experiments. <i>Bioinformatics</i> , 2006, 22, 866-873.	1.8	190
101	Development of FuGO: An Ontology for Functional Genomics Investigations. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 199-204.	1.0	56
102	Establishing Reporting Standards for Metabolomic and Metabonomic Studies: A Call for Participation. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 158-163.	1.0	100
103	Defining best practice for microarray analyses in nutrigenomic studies. <i>British Journal of Nutrition</i> , 2005, 93, 425-432.	1.2	39
104	Summary recommendations for standardization and reporting of metabolic analyses. <i>Nature Biotechnology</i> , 2005, 23, 833-838.	9.4	261
105	Microarray Data Standards: An Open Letter. <i>Environmental Health Perspectives</i> , 2004, 112, A666-7.	2.8	23
106	Database development in toxicogenomics: issues and efforts.. <i>Environmental Health Perspectives</i> , 2004, 112, 495-505.	2.8	112
107	Standardization Initiatives in the (eco)toxicogenomics Domain: A Review. <i>Comparative and Functional Genomics</i> , 2004, 5, 633-641.	2.0	17
108	ArrayExpress: a public database of gene expression data at EBI. <i>Comptes Rendus - Biologies</i> , 2003, 326, 1075-1078.	0.1	69

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109	ArrayExpress—a public repository for microarray gene expression data at the EBI. <i>Nucleic Acids Research</i> , 2003, 31, 68-71.	6.5	727
110	Overcoming the Ontology Enrichment Bottleneck with Quick Term Templates. <i>Nature Precedings</i> , 0, , .	0.1	6
111	COPO: a metadata platform for brokering FAIR data in the life sciences. <i>F1000Research</i> , 0, 9, 495.	0.8	27
112	ELIXIR and Toxicology: a community in development. <i>F1000Research</i> , 0, 10, 1129.	0.8	3