# Sarah Cohen-Boulakia

## List of Publications by Year
in descending order

| 41 papers | 1,482 citations | 516710<br>16<br>h-index | 526287<br>27<br>g-index |
|---|---|---|---|
| 46 all docs | 46 docs citations | 46 times ranked | 2187 citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | FAIR Computational Workflows. Data Intelligence, 2020, 2, 108-121. | 1.5 | 97 |
| 2 | NGPhylogeny.fr: new generation phylogenetic services for non-specialists. Nucleic Acids Research, 2019, 47, W260-W265. | 14.5 | 489 |
| 3 | Reliability-Aware and Graph-Based Approach for Rank Aggregation of Biological Data. , 2019, , . | | 0 |
| 4 | The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. Frontiers in Physiology, 2018, 9, 680. | 2.8 | 67 |
| 5 | Biological Resource Discovery. , 2018, , 283-287. | | 0 |
| 6 | Biological Metadata Management. , 2018, , 277-283. | | 0 |
| 7 | Provenance in Scientific Databases. , 2018, , 2907-2912. | | 0 |
| 8 | Scientific workflows for computational reproducibility in the life sciences: Status, challenges and opportunities. Future Generation Computer Systems, 2017, 75, 284-298. | 7.5 | 104 |
| 9 | InfraPhenoGrid: A scientific workflow infrastructure for plant phenomics on the Grid. Future Generation Computer Systems, 2017, 67, 341-353. | 7.5 | 20 |
| 10 | Biological Metadata Management. , 2017, , 1-6. | | 1 |
| 11 | Provenance in Scientific Databases. , 2017, , 1-6. | | 0 |
| 12 | Biological Resource Discovery. , 2017, , 1-5. | | 1 |
| 13 | Effective and efficient similarity search in scientific workflow repositories. Future Generation Computer Systems, 2016, 56, 584-594. | 7.5 | 14 |
| 14 | Rank aggregation with ties. Proceedings of the VLDB Endowment, 2015, 8, 1202-1213. | 3.8 | 24 |
| 15 | OpenAlea. , 2015, , . | | 34 |
| 16 | Layer Decomposition: An Effective Structure-Based Approach for Scientific Workflow Similarity. , 2014, , . | | 11 |
| 17 | Distilling structure in Taverna scientific workflows: a refactoring approach. BMC Bioinformatics, 2014, 15, S12. | 2.6 | 13 |
| 18 | Similarity search for scientific workflows. Proceedings of the VLDB Endowment, 2014, 7, 1143-1154. | 3.8 | 33 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 19 | DistillFlow. , 2014, , . | | 0 |
| 20 | Scientific workflow rewriting while preserving provenance. , 2012, , . | | 2 |
| 21 | (Re)Use in Public Scientific Workflow Repositories. Lecture Notes in Computer Science, 2012, , 361-378. | 1.3 | 13 |
| 22 | Distilling structure in scientific workflows. EMBnet Journal, 2012, 18, 100. | 0.6 | 1 |
| 23 | Gene List significance at-a-glance with GeneValorization. Bioinformatics, 2011, 27, 1187-1189. | 4.1 | 14 |
| 24 | Next generation data integration for Life Sciences. , 2011, , . | | 5 |
| 25 | Search, adapt, and reuse. SIGMOD Record, 2011, 40, 6-16. | 1.2 | 39 |
| 26 | Using Medians to Generate Consensus Rankings for Biological Data. Lecture Notes in Computer Science, 2011, , 73-90. | 1.3 | 16 |
| 27 | PDiffView. Proceedings of the VLDB Endowment, 2009, 2, 1638-1641. | 3.8 | 11 |
| 28 | Differencing Provenance in Scientific Workflows. Proceedings - International Conference on Data Engineering, 2009, , . | 0.0 | 40 |
| 29 | Biological Resource Discovery. , 2009, , 220-223. | | 2 |
| 30 | BioBrowsing: Making the Most of the Data Available in Entrez. Lecture Notes in Computer Science, 2009, , 283-291. | 1.3 | 1 |
| 31 | Provenance in Scientific Databases. , 2009, , 2202-2207. | | 1 |
| 32 | Biological Metadata Management. , 2009, , 215-219. | | 1 |
| 33 | Addressing the provenance challenge using ZOOM. Concurrency Computation Practice and Experience, 2008, 20, 497-506. | 2.2 | 35 |
| 34 | Review of the selected proceedings of the Fifth International Workshop on Data Integration in the Life Sciences 2008. BMC Bioinformatics, 2008, 9, S1. | 2.6 | 1 |
| 35 | Querying and Managing Provenance through User Views in Scientific Workflows. , 2008, , . | | 94 |
| 36 | BioGuideSRS: querying multiple sources with a user-centric perspective. Bioinformatics, 2007, 23, 1301-1303. | 4.1 | 33 |

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|---|---------|-----|-----------|
| 37 | Proteome informatics II: Bioinformatics for comparative proteomics. Proteomics, 2006, 6, 5445-5466. | 2.2 | 34 |
| 38 | PATH-BASED SYSTEMS TO GUIDE SCIENTISTS IN THE MAZE OF BIOLOGICAL DATA SOURCES. Journal of Bioinformatics and Computational Biology, 2006, 04, 1069-1095. | 0.8 | 35 |
| 39 | Towards a Model of Provenance and User Views in Scientific Workflows. Lecture Notes in Computer Science, 2006, , 264-279. | 1.3 | 40 |
| 40 | SELECTING BIOLOGICAL DATA SOURCES AND TOOLS WITH XPR, A PATH LANGUAGE FOR RDF. , 2005, , 116-27. | | 1 |
| 41 | A User-Centric Framework for Accessing Biological Sources and Tools. Lecture Notes in Computer Science, 2005, , 3-18. | 1.3 | 8 |