

# Peter Li

## List of Publications by Year in descending order

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Version: 2024-02-01

26  
papers

4,097  
citations

516710

16  
h-index

552781

26  
g-index

27  
all docs

27  
docs citations

27  
times ranked

4826  
citing authors

#	ARTICLE	IF	CITATIONS
1	Increased interactivity and improvements to the GigaScience database, GigaDB. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	9
2	Experiences in integrated data and research object publishing using GigaDB. International Journal on Digital Libraries, 2017, 18, 99-111.	1.5	14
3	Looking back: forward looking. GigaScience, 2017, 6, 1-3.	6.4	2
4	From Peer-Reviewed to Peer-Reproduced in Scholarly Publishing: The Complementary Roles of Data Models and Workflows in Bioinformatics. PLoS ONE, 2015, 10, e0127612.	2.5	27
5	GigaDB: promoting data dissemination and reproducibility. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau018-bau018.	3.0	20
6	Turning pipe dreams into reality. Genome Biology, 2012, 13, 318.	9.6	1
7	GigaDB: announcing the GigaScience database. GigaScience, 2012, 1, 11.	6.4	58
8	Workflows for Information Integration in the Life Sciences. Lecture Notes in Computer Science, 2011, , 215-225.	1.3	1
9	Systematic integration of experimental data and models in systems biology. BMC Bioinformatics, 2010, 11, 582.	2.6	28
10	myExperiment: a repository and social network for the sharing of bioinformatics workflows. Nucleic Acids Research, 2010, 38, W677-W682.	14.5	246
11	Integrative Information Management for Systems Biology. Lecture Notes in Computer Science, 2010, , 164-178.	1.3	6
12	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. Nature Biotechnology, 2008, 26, 1155-1160.	17.5	530
13	Performing statistical analyses on quantitative data in Taverna workflows: An example using R and maxdBrowse to identify differentially-expressed genes from microarray data. BMC Bioinformatics, 2008, 9, 334.	2.6	38
14	Automated manipulation of systems biology models using libSBML within Taverna workflows. Bioinformatics, 2008, 24, 287-289.	4.1	28
15	Growth control of the eukaryote cell: a systems biology study in yeast. Journal of Biology, 2007, 6, 4.	2.7	234
16	Bridging the gap between in silico and cell-based analysis of the nuclear factor- $\kappa$ B signaling pathway by in vitro studies of IKK2. FEBS Journal, 2007, 274, 1678-1690.	4.7	20
17	Taverna: a tool for building and running workflows of services. Nucleic Acids Research, 2006, 34, W729-W732.	14.5	758
18	Taverna: lessons in creating a workflow environment for the life sciences. Concurrency Computation Practice and Experience, 2006, 18, 1067-1100.	2.2	485

#	ARTICLE	IF	CITATIONS
19	Measuring the Dependability of Web Services for Use in e-Science Experiments. Lecture Notes in Computer Science, 2006, , 193-205.	1.3	3
20	Expression, location, and interactions of ErbB2 and its intramembrane ligand Muc4 (sialomucin) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70	4.1	32
21	Taverna: a tool for the composition and enactment of bioinformatics workflows. Bioinformatics, 2004, 20, 3045-3054.	4.1	1,303
22	Biosphere. Applied Bioinformatics, 2004, 3, 253-256.	1.6	9
23	Rat Muc4 (sialomucin complex) reduces binding of anti-ErbB2 antibodies to tumor cell surfaces, a potential mechanism for herceptin resistance. International Journal of Cancer, 2002, 99, 783-791.	5.1	180
24	Expression and localization of immunoreactive-sialomucin complex (Muc4) in salivary glands. Tissue and Cell, 2001, 33, 111-118.	2.2	15
25	Sialomucin complex (rat Muc4) transmembrane subunit binds the differentiation marker peanut lectin in the normal rat mammary gland. Journal of Cellular Physiology, 2001, 186, 397-405.	4.1	6
26	Identification of cell types in the developing goat mammary gland. The Histochemical Journal, 1999, 31, 379-393.	0.6	44