

Vijayalakshmi Chelliah

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

1,642
citations

687363

13
h-index

1058476

14
g-index

17
all docs

17
docs citations

17
times ranked

3078
citing authors

#	ARTICLE	IF	CITATIONS
1	BioModels Database: A Public Repository for Sharing Models of Biological Processes. , 2022, , 463-467.		0
2	Harmonizing semantic annotations for computational models in biology. Briefings in Bioinformatics, 2019, 20, 540-550.	6.5	52
3	BioModels: expanding horizons to include more modelling approaches and formats. Nucleic Acids Research, 2018, 46, D1248-D1253.	14.5	80
4	BioModels: ten-year anniversary. Nucleic Acids Research, 2015, 43, D542-D548.	14.5	334
5	BioModels Database: A Repository of Mathematical Models of Biological Processes. , 2013, , 134-138.		2
6	BioModels Database: A Repository of Mathematical Models of Biological Processes. Methods in Molecular Biology, 2013, 1021, 189-199.	0.9	102
7	BioModels Database: a public repository for sharing models of biological processes. , 2013, , 1-5.		0
8	Minimum Information About a Simulation Experiment (MIASE). PLoS Computational Biology, 2011, 7, e1001122.	3.2	133
9	BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models. BMC Systems Biology, 2010, 4, 92.	3.0	467
10	Designing and encoding models for synthetic biology. Journal of the Royal Society Interface, 2009, 6, S405-17.	3.4	51
11	Probing the "Dark Matter" of Protein Fold Space. Structure, 2009, 17, 1244-1252.	3.3	85
12	Prediction of protein structure from ideal forms. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1610-1619.	2.6	32
13	Functional site prediction selects correct protein models. BMC Bioinformatics, 2008, 9, S13.	2.6	4
14	Efficient Restraints for Protein-Protein Docking by Comparison of Observed Amino Acid Substitution Patterns with those Predicted from Local Environment. Journal of Molecular Biology, 2006, 357, 1669-1682.	4.2	58
15	Structural biology and bioinformatics in drug design: opportunities and challenges for target identification and lead discovery. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 413-423.	4.0	140
16	Functional restraints on the patterns of amino acid substitutions: Application to sequence-structure homology recognition. Proteins: Structure, Function and Bioinformatics, 2005, 61, 722-731.	2.6	13
17	Distinguishing Structural and Functional Restraints in Evolution in Order to Identify Interaction Sites. Journal of Molecular Biology, 2004, 342, 1487-1504.	4.2	89