

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