

R Dustin Schaeffer

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

3,963
citations

567281

15
h-index

642732

23
g-index

25
all docs

25
docs citations

25
times ranked

3489
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Accurate prediction of protein structures and interactions using a three-track neural network. <i>Science</i> , 2021, 373, 871-876. | 12.6 | 2,843 |
| 2 | ECOD: An Evolutionary Classification of Protein Domains. <i>PLoS Computational Biology</i> , 2014, 10, e1003926. | 3.2 | 321 |
| 3 | Dynameomics: A Comprehensive Database of Protein Dynamics. <i>Structure</i> , 2010, 18, 423-435. | 3.3 | 131 |
| 4 | Combining experiment and simulation in protein folding: closing the gap for small model systems. <i>Current Opinion in Structural Biology</i> , 2008, 18, 4-9. | 5.7 | 98 |
| 5 | ECOD: new developments in the evolutionary classification of domains. <i>Nucleic Acids Research</i> , 2017, 45, D296-D302. | 14.5 | 68 |
| 6 | Manual classification strategies in the <scp>ECOD</scp> database. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1238-1251. | 2.6 | 64 |
| 7 | Dynameomics: mass annotation of protein dynamics and unfolding in water by high-throughput atomistic molecular dynamics simulations. <i>Protein Engineering, Design and Selection</i> , 2008, 21, 353-368. | 2.1 | 60 |
| 8 | Protein folds and protein folding. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 11-19. | 2.1 | 59 |
| 9 | Functional analysis of Rossmann-like domains reveals convergent evolution of topology and reaction pathways. <i>PLoS Computational Biology</i> , 2019, 15, e1007569. | 3.2 | 45 |
| 10 | Topology evaluation of models for difficult targets in the 14th round of the critical assessment of protein structure prediction (CASP14). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1673-1686. | 2.6 | 35 |
| 11 | Generation of a consensus protein domain dictionary. <i>Bioinformatics</i> , 2011, 27, 46-54. | 4.1 | 33 |
| 12 | Target classification in the 14th <scp>round</scp> of the <scp>critical assessment of protein structure prediction</scp> (<scp>CASP14</scp>). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1618-1632. | 2.6 | 32 |
| 13 | CASP 11 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 20-33. | 2.6 | 31 |
| 14 | A Fifth of the Protein World: Rossmann-like Proteins as an Evolutionarily Successful Structural unit. <i>Journal of Molecular Biology</i> , 2021, 433, 166788. | 4.2 | 26 |
| 15 | Classification of proteins with shared motifs and internal repeats in the <scp>ECOD</scp> database. <i>Protein Science</i> , 2016, 25, 1188-1203. | 7.6 | 23 |
| 16 | Manifestations of Native Topology in the Denatured State Ensemble of <i>Rhodospseudomonas palustris</i> Cytochrome <i>c</i>. <i>Biochemistry</i> , 2011, 50, 1029-1041. | 2.5 | 19 |
| 17 | ECOD: identification of distant homology among multidomain and transmembrane domain proteins. <i>BMC Molecular and Cell Biology</i> , 2019, 20, 18. | 2.0 | 12 |
| 18 | Completeness and Consistency in Structural Domain Classifications. <i>ACS Omega</i> , 2021, 6, 15698-15707. | 3.5 | 8 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Assessment of domain interactions in the fourteenth round of the Critical Assessment of Structure Prediction (CASP14). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1700-1710. | 2.6 | 8 |
| 20 | Estimation of Uncertainties in the Global Distance Test (GDT_TS) for CASP Models. <i>PLoS ONE</i> , 2016, 11, e0154786. | 2.5 | 8 |
| 21 | Searching ECOD for Homologous Domains by Sequence and Structure. <i>Current Protocols in Bioinformatics</i> , 2018, 61, e45. | 25.8 | 7 |
| 22 | A sequence family database built on ECOD structural domains. <i>Bioinformatics</i> , 2018, 34, 2997-3003. | 4.1 | 5 |
| 23 | Dynameomics: protein dynamics and unfolding across fold space. <i>Biomolecular Concepts</i> , 2010, 1, 335-344. | 2.2 | 1 |
| 24 | Identification of Multiple Folding Pathways Shared by Three-Helix Bundle Proteins. <i>Biophysical Journal</i> , 2010, 98, 636a. | 0.5 | 0 |