

# Nicolas Palopoli

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1401517/publications.pdf>

Version: 2024-02-01

26  
papers

1,003  
citations

687363

13  
h-index

610901

24  
g-index

39  
all docs

39  
docs citations

39  
times ranked

1880  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | ELMâ€”the eukaryotic linear motif resource in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D296-D306.  | 14.5 | 195       |
| 2  | The eukaryotic linear motif resource â€” 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D428-D434.  | 14.5 | 183       |
| 3  | DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.  | 14.5 | 141       |
| 4  | DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.  | 14.5 | 117       |
| 5  | Impact of protein conformational diversity on AlphaFold predictions. <i>Bioinformatics</i> , 2022, 38, 2742-2748.   | 4.1  | 57        |
| 6  | Functional and structural characterization of the catalytic domain of the starch synthase III from <i>Arabidopsis thaliana</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 31-40. | 2.6  | 42        |
| 7  | MetaBase--the wiki-database of biological databases. <i>Nucleic Acids Research</i> , 2012, 40, D1250-D1254.   | 14.5 | 40        |
| 8  | Computational Prediction of Short Linear Motifs from Protein Sequences. <i>Methods in Molecular Biology</i> , 2015, 1268, 89-141.   | 0.9  | 39        |
| 9  | Starch-synthase III family encodes a tandem of three starch-binding domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 27-31.   | 2.6  | 35        |
| 10 | Short linear motif core and flanking regions modulate retinoblastoma protein binding affinity and specificity. <i>Protein Engineering, Design and Selection</i> , 2018, 31, 69-77.                          | 2.1  | 33        |
| 11 | Protein Conformational Diversity Modulates Sequence Divergence. <i>Molecular Biology and Evolution</i> , 2013, 30, 79-87.   | 8.9  | 31        |
| 12 | QSLiMFinder: improved short linear motif prediction using specific query protein data. <i>Bioinformatics</i> , 2015, 31, 2284-2293.   | 4.1  | 19        |
| 13 | Addressing the Role of Conformational Diversity in Protein Structure Prediction. <i>PLoS ONE</i> , 2016, 11, e0154923.  | 2.5  | 14        |
| 14 | Starch Synthesis in <i>Ostreococcus tauri</i> : The Starch-Binding Domains of Starch Synthase III-B Are Essential for Catalytic Activity. <i>Frontiers in Plant Science</i> , 2018, 9, 1541.                | 3.6  | 9         |
| 15 | ProtMiscuity: a database of promiscuous proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .   | 3.0  | 7         |
| 16 | ISCB-Student Council Narratives: Strategic development of the ISCB-Regional Student Groups in 2016. <i>F1000Research</i> , 2016, 5, 2882.   | 1.6  | 6         |
| 17 | BeEP Server: using evolutionary information for quality assessment of protein structure models. <i>Nucleic Acids Research</i> , 2013, 41, W398-W405.  | 14.5 | 5         |
| 18 | Second ISCB Latin American Student Council Symposium (LA-SCS) 2016. <i>F1000Research</i> , 2017, 6, 1491.   | 1.6  | 5         |

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 19 | Intrinsically Disordered Protein Ensembles Shape Evolutionary Rates Revealing Conformational Patterns. Journal of Molecular Biology, 2021, 433, 166751.     | 4.2 | 3         |
| 20 | “Protein” no longer means what it used to. Current Research in Structural Biology, 2021, 3, 146-152.  | 2.2 | 3         |
| 21 | Bioinformatics calls the school: Use of smartphones to introduce Python for bioinformatics in high schools. PLoS Computational Biology, 2019, 15, e1006473. | 3.2 | 2         |
| 22 | SLiMScape 3.x: a Cytoscape 3 app for discovery of Short Linear Motifs in protein interaction networks. F1000Research, 2015, 4, 477.                         | 1.6 | 1         |
| 23 | A report on the “International Society for Computational Biology - Latin America (ISCB-LA)” Bioinformatics Conference 2016. EMBnet Journal, 2017, 23, 883.  | 0.6 | 1         |
| 24 | CoDNAS-RNA: a database of conformational diversity in the native state of RNA. Bioinformatics, 2022, 38, 1745-1748.   | 4.1 | 1         |
| 25 | Assessment of Structure Quality (RNA and Protein). , 2019, , 586-605.   |     | 0         |
| 26 | A report on the “International Society for Computational Biology - Latin America (ISCB-LA)” Bioinformatics Conference 2016. EMBnet Journal, 2016, 22, 883.  | 0.6 | 0         |