

# Carles Pons

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

3,871  
citations

257450

24  
h-index

302126

39  
g-index

45  
all docs

45  
docs citations

45  
times ranked

5893  
citing authors

#	ARTICLE	IF	CITATIONS
1	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016, 353, .	12.6	979
2	A reference map of the human binary protein interactome. <i>Nature</i> , 2020, 580, 402-408.	27.8	724
3	pyDockWEB: a web server for rigid-body protein-protein docking using electrostatics and desolvation scoring. <i>Bioinformatics</i> , 2013, 29, 1698-1699.	4.1	214
4	Systematic analysis of complex genetic interactions. <i>Science</i> , 2018, 360, .	12.6	201
5	Exploring genetic suppression interactions on a global scale. <i>Science</i> , 2016, 354, .	12.6	157
6	A framework for exhaustively mapping functional missense variants. <i>Molecular Systems Biology</i> , 2017, 13, 957.	7.2	146
7	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. <i>Journal of Molecular Biology</i> , 2011, 414, 289-302.	4.2	131
8	FRODOCK: a new approach for fast rotational protein-protein docking. <i>Bioinformatics</i> , 2009, 25, 2544-2551.	4.1	126
9	Towards the prediction of protein interaction partners using physical docking. <i>Molecular Systems Biology</i> , 2011, 7, 469.	7.2	102
10	Extensive Rewiring and Complex Evolutionary Dynamics in a <i>C.Âlegans</i> Multiparameter Transcription Factor Network. <i>Molecular Cell</i> , 2013, 51, 116-127.	9.7	83
11	Present and future challenges and limitations in protein-protein docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 95-108.	2.6	76
12	A gene-centered <i>C.Âlegans</i> protein-DNA interaction network provides a framework for functional predictions. <i>Molecular Systems Biology</i> , 2016, 12, 884.	7.2	71
13	Scoring by Intermolecular Pairwise Propensities of Exposed Residues (SIPPER): A New Efficient Potential for Protein-Protein Docking. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 370-377.	5.4	70
14	Pushing Structural Information into the Yeast Interactome by High-Throughput Protein Docking Experiments. <i>PLoS Computational Biology</i> , 2009, 5, e1000490.	3.2	67
15	Structural Characterization of Protein-Protein Complexes by Integrating Computational Docking with Small-angle Scattering Data. <i>Journal of Molecular Biology</i> , 2010, 403, 217-230.	4.2	64
16	Transcription Factor Activity Mapping of a Tissue-Specific In Vivo Gene Regulatory Network. <i>Cell Systems</i> , 2015, 1, 152-162.	6.2	64
17	pyDockSAXS: protein-protein complex structure by SAXS and computational docking. <i>Nucleic Acids Research</i> , 2015, 43, W356-W361.	14.5	61
18	Features of the Chaperone Cellular Network Revealed through Systematic Interaction Mapping. <i>Cell Reports</i> , 2017, 20, 2735-2748.	6.4	47

#	ARTICLE	IF	CITATIONS
19	Prediction of protein-binding areas by small-world residue networks and application to docking. BMC Bioinformatics, 2011, 12, 378.	2.6	46
20	Systematic analysis of bypass suppression of essential genes. Molecular Systems Biology, 2020, 16, e9828.	7.2	45
21	Prediction and scoring of docking poses with pyDock. Proteins: Structure, Function and Bioinformatics, 2007, 69, 852-858.	2.6	40
22	Environmental robustness of the global yeast genetic interaction network. Science, 2021, 372, .	12.6	40
23	Systematic genetics and single-cell imaging reveal widespread morphological pleiotropy and cell-to-cell variability. Molecular Systems Biology, 2020, 16, e9243.	7.2	37
24	STRUCTURAL PREDICTION OF PROTEIN-RNA INTERACTION BY COMPUTATIONAL DOCKING WITH PROPENSITY-BASED STATISTICAL POTENTIALS. , 2009, , 293-301.		33
25	Mechanisms of suppression: The wiring of genetic resilience. BioEssays, 2017, 39, 1700042.	2.5	31
26	TSEMA: interactive prediction of protein pairings between interacting families. Nucleic Acids Research, 2006, 34, W315-W319.	14.5	25
27	Optimization of pyDock for the new CAPRI challenges: Docking of homology-based models, domain-domain assembly and protein-RNA binding. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3182-3188.	2.6	25
28	Genetic Interactions Implicating Postreplicative Repair in Okazaki Fragment Processing. PLoS Genetics, 2015, 11, e1005659.	3.5	24
29	Enhancing the prediction of protein pairings between interacting families using orthology information. BMC Bioinformatics, 2008, 9, 35.	2.6	21
30	Expanding the frontiers of protein-protein modeling: From docking and scoring to binding affinity predictions and other challenges. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2192-2200.	2.6	20
31	Cell-Dock: high-performance protein-protein docking. Bioinformatics, 2012, 28, 2394-2396.	4.1	14
32	Efficient Relaxation of Protein-Protein Interfaces by Discrete Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2013, 9, 1222-1229.	5.3	13
33	Natural variants suppress mutations in hundreds of essential genes. Molecular Systems Biology, 2021, 17, e10138.	7.2	13
34	Hydrogen bond network optimization in protein-protein complexes: Are all atom force field scores enough?. Proteins: Structure, Function and Bioinformatics, 2012, 80, 818-824.	2.6	12
35	On the Use of low-resolution Data to Improve Structure Prediction of Proteins and Protein Complexes. Journal of Chemical Theory and Computation, 2009, 5, 3129-3137.	5.3	7
36	A PanorOmic view of personal cancer genomes. Nucleic Acids Research, 2017, 45, W195-W200.	14.5	6

#	ARTICLE	IF	CITATIONS
37	Analysing the yeast complexome—the Complex Portal rising to the challenge. <i>Nucleic Acids Research</i> , 2021, 49, 3156-3167.	14.5	5
38	Validated Conformational Ensembles Are Key for the Successful Prediction of Protein Complexes. <i>Journal of Chemical Theory and Computation</i> , 2013, 9, 1830-1837.	5.3	4
39	Bioactivity Profile Similarities to Expand the Repertoire of COVID-19 Drugs. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 5730-5734.	5.4	3
40	Linking Genetics to Structural Biology: Complex Heterozygosity Screening with Actin Alanine Scan Alleles Identifies Functionally Related Surfaces on Yeast Actin. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1491-1501.	1.8	1
41	Computational paradigms for analyzing genetic interaction networks. , 0, , 12-35.		0