Carles Pons

List of Publications by Year
in descending order

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41 papers	3,871 citations	257101 24 h-index	301761 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. Science, 2016, 353, .	6.0	979
2	A reference map of the human binary protein interactome. Nature, 2020, 580, 402-408.	13.7	724
3	pyDockWEB: a web server for rigid-body proteinâ€“protein docking using electrostatics and desolvation scoring. Bioinformatics, 2013, 29, 1698-1699.	1.8	214
4	Systematic analysis of complex genetic interactions. Science, 2018, 360, .	6.0	201
5	Exploring genetic suppression interactions on a global scale. Science, 2016, 354, .	6.0	157
6	A framework for exhaustively mapping functional missense variants. Molecular Systems Biology, 2017, 13, 957.	3.2	146
7	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	2.0	131
8	FRODOCK: a new approach for fast rotational proteinâ€“protein docking. Bioinformatics, 2009, 25, 2544-2551.	1.8	126
9	Towards the prediction of protein interaction partners using physical docking. Molecular Systems Biology, 2011, 7, 469.	3.2	102
10	Extensive Rewiring and Complex Evolutionary Dynamics in a C.Âelegans Multiparameter Transcription Factor Network. Molecular Cell, 2013, 51, 116-127.	4.5	83
11	Present and future challenges and limitations in proteinâ€“protein docking. Proteins: Structure, Function and Bioinformatics, 2010, 78, 95-108.	1.5	76
12	A geneâ€centered C.Âelegans proteinâ€“ <scp>DNA</scp> interaction network provides a framework for functional predictions. Molecular Systems Biology, 2016, 12, 884.	3.2	71
13	Scoring by Intermolecular Pairwise Propensities of Exposed Residues (SIPPER): A New Efficient Potential for Proteinâ^'Protein Docking. Journal of Chemical Information and Modeling, 2011, 51, 370-377.	2.5	70
14	Pushing Structural Information into the Yeast Interactome by High-Throughput Protein Docking Experiments. PLoS Computational Biology, 2009, 5, e1000490.	1.5	67
15	Structural Characterization of Proteinâ€“Protein Complexes by Integrating Computational Docking with Small-angle Scattering Data. Journal of Molecular Biology, 2010, 403, 217-230.	2.0	64
16	Transcription Factor Activity Mapping of a Tissue-Specific InÂVivo Gene Regulatory Network. Cell Systems, 2015, 1, 152-162.	2.9	64
17	pyDockSAXS: proteinâ€“protein complex structure by SAXS and computational docking. Nucleic Acids Research, 2015, 43, W356-W361.	6.5	61
18	Features of the Chaperone Cellular Network Revealed through Systematic Interaction Mapping. Cell Reports, 2017, 20, 2735-2748.	2.9	47

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19	Prediction of protein-binding areas by small-world residue networks and application to docking. BMC Bioinformatics, 2011, 12, 378.	1.2	46
20	Systematic analysis of bypass suppression of essential genes. Molecular Systems Biology, 2020, 16, e9828.	3.2	45
21	Prediction and scoring of docking poses with pyDock. Proteins: Structure, Function and Bioinformatics, 2007, 69, 852-858.	1.5	40
22	Environmental robustness of the global yeast genetic interaction network. Science, 2021, 372, .	6.0	40
23	Systematic genetics and singleâ€cell imaging reveal widespread morphological pleiotropy and cellâ€toâ€cell variability. Molecular Systems Biology, 2020, 16, e9243.	3.2	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.	1.2	31
26	TSEMA: interactive prediction of protein pairings between interacting families. Nucleic Acids Research, 2006, 34, W315-W319.	6.5	25
27	Optimization of pyDock for the new CAPRI challenges: Docking of homologyâ€based models, domainâ€“domain assembly and proteinâ€RNA binding. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3182-3188.	1.5	25
28	Genetic Interactions Implicating Postreplicative Repair in Okazaki Fragment Processing. PLoS Genetics, 2015, 11, e1005659.	1.5	24
29	Enhancing the prediction of protein pairings between interacting families using orthology information. BMC Bioinformatics, 2008, 9, 35.	1.2	21
30	Expanding the frontiers of proteinâ€“protein modeling: From docking and scoring to binding affinity predictions and other challenges. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2192-2200.	1.5	20
31	Cell-Dock: high-performance proteinâ€“protein docking. Bioinformatics, 2012, 28, 2394-2396.	1.8	14
32	Efficient Relaxation of Proteinâ€“Protein Interfaces by Discrete Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2013, 9, 1222-1229.	2.3	13
33	Natural variants suppress mutations in hundreds of essential genes. Molecular Systems Biology, 2021, 17, e10138.	3.2	13
34	Hâ€bond network optimization in proteinâ€“protein complexes: Are allâ€atom force field scores enough?. Proteins: Structure, Function and Bioinformatics, 2012, 80, 818-824.	1.5	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.	2.3	7
36	A PanorOmic view of personal cancer genomes. Nucleic Acids Research, 2017, 45, W195-W200.	6.5	6

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37	Analysing the yeast complexomeâ€"the Complex Portal rising to the challenge. Nucleic Acids Research, 2021, 49, 3156-3167.	6.5	5
38	Validated Conformational Ensembles Are Key for the Successful Prediction of Protein Complexes. Journal of Chemical Theory and Computation, 2013, 9, 1830-1837.	2.3	4
39	Bioactivity Profile Similarities to Expand the Repertoire of COVID-19 Drugs. Journal of Chemical Information and Modeling, 2020, 60, 5730-5734.	2.5	3
40	Linking Genetics to Structural Biology: Complex Heterozygosity Screening with Actin Alanine Scan Alleles Identifies Functionally Related Surfaces on Yeast Actin. G3: Genes, Genomes, Genetics, 2014, 4, 1491-1501.	0.8	1
41	Computational paradigms for analyzing genetic interaction networks. , 0, , 12-35.		0