Carles Pons

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6765334/publications.pdf

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	Analysing the yeast complexomeâ€"the Complex Portal rising to the challenge. Nucleic Acids Research, 2021, 49, 3156-3167.	14.5	5
2	Environmental robustness of the global yeast genetic interaction network. Science, 2021, 372, .	12.6	40
3	Natural variants suppress mutations in hundreds of essential genes. Molecular Systems Biology, 2021, 17, e10138.	7.2	13
4	Bioactivity Profile Similarities to Expand the Repertoire of COVID-19 Drugs. Journal of Chemical Information and Modeling, 2020, 60, 5730-5734.	5.4	3
5	A reference map of the human binary protein interactome. Nature, 2020, 580, 402-408.	27.8	724
6	Systematic genetics and singleâ€cell imaging reveal widespread morphological pleiotropy and cellâ€toâ€cell variability. Molecular Systems Biology, 2020, 16, e9243.	7.2	37
7	Systematic analysis of bypass suppression of essential genes. Molecular Systems Biology, 2020, 16, e9828.	7.2	45
8	Systematic analysis of complex genetic interactions. Science, 2018, 360, .	12.6	201
9	A PanorOmic view of personal cancer genomes. Nucleic Acids Research, 2017, 45, W195-W200.	14.5	6
10	Features of the Chaperone Cellular Network Revealed through Systematic Interaction Mapping. Cell Reports, 2017, 20, 2735-2748.	6.4	47
11	A framework for exhaustively mapping functional missense variants. Molecular Systems Biology, 2017, 13, 957.	7.2	146
12	Mechanisms of suppression: The wiring of genetic resilience. BioEssays, 2017, 39, 1700042.	2.5	31
13	A geneâ€centered C.Âelegans proteinâ€“ <scp>DNA</scp> interaction network provides a framework for functional predictions. Molecular Systems Biology, 2016, 12, 884.	7.2	71
14	A global genetic interaction network maps a wiring diagram of cellular function. Science, 2016, 353, .	12.6	979
15	Exploring genetic suppression interactions on a global scale. Science, 2016, 354, .	12.6	157
16	Genetic Interactions Implicating Postreplicative Repair in Okazaki Fragment Processing. PLoS Genetics, 2015, 11, e1005659.	3.5	24
17	pyDockSAXS: proteinâ€“protein complex structure by SAXS and computational docking. Nucleic Acids Research, 2015, 43, W356-W361.	14.5	61
18	Transcription Factor Activity Mapping of a Tissue-Specific InÂVivo Gene Regulatory Network. Cell Systems, 2015, 1, 152-162.	6.2	64

#	Article	IF	Citations
19	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.	1.8	1
20	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.	2.6	20
21	pyDockWEB: a web server for rigid-body proteinâ€“protein docking using electrostatics and desolvation scoring. Bioinformatics, 2013, 29, 1698-1699.	4.1	214
22	Efficient Relaxation of Proteinâ€“Protein Interfaces by Discrete Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2013, 9, 1222-1229.	5.3	13
23	Extensive Rewiring and Complex Evolutionary Dynamics in a C.Âelegans Multiparameter Transcription Factor Network. Molecular Cell, 2013, 51, 116-127.	9.7	83
24	Validated Conformational Ensembles Are Key for the Successful Prediction of Protein Complexes. Journal of Chemical Theory and Computation, 2013, 9, 1830-1837.	5.3	4
25	Cell-Dock: high-performance proteinâ€“protein docking. Bioinformatics, 2012, 28, 2394-2396.	4.1	14
26	Hâ€bond network optimization in proteinâ€“protein complexes: Are allâ€atom force field scores enough?. Proteins: Structure, Function and Bioinformatics, 2012, 80, 818-824.	2.6	12
27	Towards the prediction of protein interaction partners using physical docking. Molecular Systems Biology, 2011, 7, 469.	7.2	102
28	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.	5.4	70
29	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
30	Prediction of protein-binding areas by small-world residue networks and application to docking. BMC Bioinformatics, 2011, 12, 378.	2.6	46
31	Present and future challenges and limitations in proteinâ€“protein docking. Proteins: Structure, Function and Bioinformatics, 2010, 78, 95-108.	2.6	76
32	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.	2.6	25
33	Structural Characterization of Proteinâ€“Protein Complexes by Integrating Computational Docking with Small-angle Scattering Data. Journal of Molecular Biology, 2010, 403, 217-230.	4.2	64
34	STRUCTURAL PREDICTION OF PROTEIN-RNA INTERACTION BY COMPUTATIONAL DOCKING WITH PROPENSITY-BASED STATISTICAL POTENTIALS. , 2009, , 293-301.		33
35	Pushing Structural Information into the Yeast Interactome by High-Throughput Protein Docking Experiments. PLoS Computational Biology, 2009, 5, e1000490.	3.2	67
36	FRODOCK: a new approach for fast rotational proteinâ€“protein docking. Bioinformatics, 2009, 25, 2544-2551.	4.1	126

#	Article	IF	Citations
37	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
38	Enhancing the prediction of protein pairings between interacting families using orthology information. BMC Bioinformatics, 2008, 9, 35.	2.6	21
39	Prediction and scoring of docking poses with pyDock. Proteins: Structure, Function and Bioinformatics, 2007, 69, 852-858.	2.6	40
40	TSEMA: interactive prediction of protein pairings between interacting families. Nucleic Acids Research, 2006, 34, W315-W319.	14.5	25
41	Computational paradigms for analyzing genetic interaction networks. , 0, , 12-35.		0