Pilar Cossio

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4983474/publications.pdf

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41	922	516710 16	477307 29
papers	citations	h-index	g-index

42	42	42	1140
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Molecular Mechanism of Substrate Engagement and Immunosuppressant Inhibition of Calcineurin. PLoS Biology, 2013, 11, e1001492.	5.6	123
2	On artifacts in single-molecule force spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14248-14253.	7.1	89
3	Exponential consensus ranking improves the outcome in docking and receptor ensemble docking. Scientific Reports, 2019, 9, 5142.	3.3	89
4	Bayesian analysis of individual electron microscopy images: Towards structures of dynamic and heterogeneous biomolecular assemblies. Journal of Structural Biology, 2013, 184, 427-437.	2.8	66
5	Exploring the Universe of Protein Structures beyond the Protein Data Bank. PLoS Computational Biology, 2010, 6, e1000957.	3.2	62
6	A simple and efficient statistical potential for scoring ensembles of protein structures. Scientific Reports, 2012, 2, .	3.3	48
7	Transition paths in single-molecule force spectroscopy. Journal of Chemical Physics, 2018, 148, 123309.	3.0	47
8	Optimizing the Performance of Bias-Exchange Metadynamics: Folding a 48-Residue LysM Domain Using a Coarse-Grained Model. Journal of Physical Chemistry B, 2010, 114, 3259-3265.	2.6	40
9	Predicting the Affinity of Peptides to Major Histocompatibility Complex Class II by Scoring Molecular Dynamics Simulations. Journal of Chemical Information and Modeling, 2019, 59, 3464-3473.	5.4	34
10	Kinetic Ductility and Force-Spike Resistance of Proteins from Single-Molecule Force Spectroscopy. Biophysical Journal, 2016, 111, 832-840.	0.5	27
11	BioEM: GPU-accelerated computing of Bayesian inference of electron microscopy images. Computer Physics Communications, 2017, 210, 163-171.	7.5	27
12	A Bayesian approach to extracting free-energy profiles from cryo-electron microscopy experiments. Scientific Reports, 2021, 11, 13657.	3.3	27
13	Which similarity measure is better for analyzing protein structures in a molecular dynamics trajectory?. Physical Chemistry Chemical Physics, 2011, 13, 10421.	2.8	25
14	Conformations of the Huntingtin N-term in aqueous solution from atomistic simulations. FEBS Letters, 2011, 585, 3086-3089.	2.8	24
15	Discovery of antimicrobial compounds targeting bacterial type FAD synthetases. Journal of Enzyme Inhibition and Medicinal Chemistry, 2018, 33, 241-254.	5.2	23
16	Assessing the capability ofin silicomutation protocols for predicting the finite temperature conformation of amino acids. Physical Chemistry Chemical Physics, 2018, 20, 25901-25909.	2.8	18
17	Likelihood-based structural analysis of electron microscopy images. Current Opinion in Structural Biology, 2018, 49, 162-168.	5.7	15
18	Molecular free energy profiles from force spectroscopy experiments by inversion of observed committors. Journal of Chemical Physics, 2019, 151, 154115.	3.0	14

#	Article	IF	Citations
19	Application of ensemble pharmacophore-based virtual screening to the discovery of novel antimitotic tubulin inhibitors. Computational and Structural Biotechnology Journal, 2021, 19, 4360-4372.	4.1	14
20	PARCE: Protocol for Amino acid Refinement through Computational Evolution. Computer Physics Communications, 2021, 260, 107716.	7.5	12
21	The Dimer-of-Trimers Assembly Prevents Catalysis at the Transferase Site of Prokaryotic FAD Synthase. Biophysical Journal, 2018, 115, 988-995.	0.5	11
22	In silico discovery and biological validation of ligands of FAD synthase, a promising new antimicrobial target. PLoS Computational Biology, 2020, 16, e1007898.	3.2	11
23	PepFun: Open Source Protocols for Peptide-Related Computational Analysis. Molecules, 2021, 26, 1664.	3.8	11
24	Flexi-pharma: a molecule-ranking strategy for virtual screening using pharmacophores from ligand-free conformational ensembles. Journal of Computer-Aided Molecular Design, 2020, 34, 1063-1077.	2.9	9
25	Cardiolipin prevents pore formation in phosphatidylglycerol bacterial membrane models. FEBS Letters, 2021, 595, 2701-2714.	2.8	9
26	Bayesian inference of rotor ring stoichiometry from electron microscopy images of archaeal ATP synthase. Microscopy (Oxford, England), 2018, 67, 266-273.	1.5	8
27	An automated protocol for modelling peptide substrates to proteases. BMC Bioinformatics, 2020, 21, 586.	2.6	7
28	Multiple-Allele MHC Class II Epitope Engineering by a Molecular Dynamics-Based Evolution Protocol. Frontiers in Immunology, 2022, 13, 862851.	4.8	7
29	Protein Folding and Ligand-Enzyme Binding from Bias-Exchange Metadynamics Simulations. Current Physical Chemistry, 2012, 2, 79-91.	0.2	6
30	Need for Cross-Validation of Single Particle Cryo-EM. Journal of Chemical Information and Modeling, 2020, 60, 2413-2418.	5.4	5
31	Ab initio metadynamics determination of temperature-dependent free-energy landscape in ultrasmall silver clusters. Journal of Chemical Physics, 2022, 156, 154301.	3.0	4
32	Effects of a disulfide bridge prior to amyloid formation of the ABRI peptide. RSC Advances, 2014, 4, 36923-36928.	3.6	3
33	Impact of Structural Observables From Simulations to Predict the Effect of Single-Point Mutations in MHC Class II Peptide Binders. Frontiers in Molecular Biosciences, 2021, 8, 636562.	3.5	3
34	Computational Evolution Protocol for Peptide Design. Methods in Molecular Biology, 2022, 2405, 335-359.	0.9	3
35	Validation tests for cryo-EM maps using an independent particle set. Journal of Structural Biology: X, 2020, 4, 100032.	1.3	1
36	Computational Design of Peptides Bound to the Major Histocompatibility Complex Class II. Biophysical Journal, 2020, 118, 359a.	0.5	0

#	Article	IF	Citations
37	Editorial: Integrating Timescales From Molecules Up. Frontiers in Chemistry, 2021, 9, 680533.	3.6	0
38	Title is missing!. , 2020, 16, e1007898.		0
39	Title is missing!. , 2020, 16, e1007898.		0
40	Title is missing!. , 2020, 16, e1007898.		0
41	Title is missing!. , 2020, 16, e1007898.		0