

Jessica Andreani

List of Publications by Year in descending order

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32
papers

1,030
citations

566801

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docs citations

37
times ranked

1639
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide Analysis of RNA Polymerase II Termination at Protein-Coding Genes. <i>Molecular Cell</i> , 2017, 66, 38-49.e6.	4.5	100
2	A meiotic XPF-ERCC1-like complex recognizes joint molecule recombination intermediates to promote crossover formation. <i>Genes and Development</i> , 2018, 32, 283-296.	2.7	98
3	InterEvScore: a novel coarse-grained interface scoring function using a multi-body statistical potential coupled to evolution. <i>Bioinformatics</i> , 2013, 29, 1742-1749.	1.8	79
4	A structural model of the active ribosome-bound membrane protein insertase YidC. <i>ELife</i> , 2014, 3, e03035.	2.8	69
5	InterEvDock: a docking server to predict the structure of protein-protein interactions using evolutionary information. <i>Nucleic Acids Research</i> , 2016, 44, W542-W549.	6.5	67
6	The COMA complex interacts with Cse4 and positions Sli15/Ipl1 at the budding yeast inner kinetochore. <i>ELife</i> , 2019, 8, .	2.8	64
7	Evolution of protein interactions: From interactomes to interfaces. <i>Archives of Biochemistry and Biophysics</i> , 2014, 554, 65-75.	1.4	49
8	Mutations in the netrin-1 gene cause congenital mirror movements. <i>Journal of Clinical Investigation</i> , 2017, 127, 3923-3936.	3.9	48
9	InterEvol database: exploring the structure and evolution of protein complex interfaces. <i>Nucleic Acids Research</i> , 2012, 40, D847-D856.	6.5	47
10	InterEvDock2: an expanded server for protein docking using evolutionary and biological information from homology models and multimeric inputs. <i>Nucleic Acids Research</i> , 2018, 46, W408-W416.	6.5	47
11	Versatility and Invariance in the Evolution of Homologous Heteromeric Interfaces. <i>PLoS Computational Biology</i> , 2012, 8, e1002677.	1.5	42
12	Lessons from (co-)evolution in the docking of proteins and peptides for CAPRI Rounds 28-35. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 378-390.	1.5	39
13	bbcontacts: prediction of β -strand pairing from direct coupling patterns. <i>Bioinformatics</i> , 2015, 31, 1729-1737.	1.8	34
14	A Compact Viral Processing Proteinase/Ubiquitin Hydrolase from the OTU Family. <i>PLoS Pathogens</i> , 2013, 9, e1003560.	2.1	28
15	Molecular determinants of the DprA-RecA interaction for nucleation on ssDNA. <i>Nucleic Acids Research</i> , 2014, 42, 7395-7408.	6.5	26
16	Structural characterization of the RH1-LZI tandem of JIP3/4 highlights RH1 domains as a cytoskeletal motor-binding motif. <i>Scientific Reports</i> , 2019, 9, 16036.	1.6	22
17	The Zip4 protein directly couples meiotic crossover formation to synaptonemal complex assembly. <i>Genes and Development</i> , 2022, 36, 53-69.	2.7	22
18	Genetic evidence for the involvement of mismatch repair proteins, PMS2 and MLH3, in a late step of homologous recombination. <i>Journal of Biological Chemistry</i> , 2020, 295, 17460-17475.	1.6	18

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19	Study of the DnaB:DciA interplay reveals insights into the primary mode of loading of the bacterial replicative helicase. <i>Nucleic Acids Research</i> , 2021, 49, 6569-6586.	6.5	18
20	Molecular basis of the dual role of the Mlh1-Mlh3 endonuclease in MMR and in meiotic crossover formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	18
21	InterEvDock3: a combined template-based and free docking server with increased performance through explicit modeling of complex homologs and integration of covariation-based contact maps. <i>Nucleic Acids Research</i> , 2021, 49, W277-W284.	6.5	14
22	Structural prediction of protein interactions and docking using conservation and coevolution. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2020, 10, e1470.	6.2	13
23	Protein-Protein Docking Using Evolutionary Information. <i>Methods in Molecular Biology</i> , 2018, 1764, 429-447.	0.4	11
24	Design on a Rational Basis of High-Affinity Peptides Inhibiting the Histone Chaperone ASF1. <i>Cell Chemical Biology</i> , 2019, 26, 1573-1585.e10.	2.5	11
25	Characterization of the binding mode of JNK-interacting protein 1 (JIP1) to kinesin-light chain 1 (KLC1). <i>Journal of Biological Chemistry</i> , 2018, 293, 13946-13960.	1.6	10
26	Structural plasticity of the N-terminal capping helix of the TPR domain of kinesin light chain. <i>PLoS ONE</i> , 2017, 12, e0186354.	1.1	9
27	Docking proteins and peptides under evolutionary constraints in Critical Assessment of PRediction of Interactions rounds 38 to 45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 986-998.	1.5	8
28	Probing Protein Interaction Networks by Combining MS-Based Proteomics and Structural Data Integration. <i>Journal of Proteome Research</i> , 2020, 19, 2807-2820.	1.8	6
29	Proteo3Dnet: a web server for the integration of structural information with interactomics data. <i>Nucleic Acids Research</i> , 2021, 49, W567-W572.	6.5	5
30	Editorial: Web Tools for Modeling and Analysis of Biomolecular Interactions. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 875859.	1.6	3
31	Atomic-level evolutionary information improves proteinâ€“protein interface scoring. <i>Bioinformatics</i> , 2021, 37, 3175-3181.	1.8	2
32	The C-terminal domain of HpDprA is a DNA-binding winged helix domain that does not bind double-stranded DNA. <i>FEBS Journal</i> , 2019, 286, 1941-1958.	2.2	1