Jaume Bonet

List of Publications by Year in descending order

45 papers	2,310 citations	331670 21 h-index	254184 43 g-index
59 all docs	59 docs citations	59 times ranked	3973 citing authors

#	Article	IF	Citations
1	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
2	Inferring causal molecular networks: empirical assessment through a community-based effort. Nature Methods, 2016, 13, 310-318.	19.0	209
3	Multivalent antibodies: when design surpasses evolution. Trends in Biotechnology, 2010, 28, 355-362.	9.3	172
4	ADP-riboseâ€“derived nuclear ATP synthesis by NUDIX5 is required for chromatin remodeling. Science, 2016, 352, 1221-1225.	12.6	141
5	De novo protein design enables the precise induction of RSV-neutralizing antibodies. Science, 2020, 368, .	12.6	137
6	CDK2-dependent activation of PARP-1 is required for hormonal gene regulation in breast cancer cells. Genes and Development, 2012, 26, 1972-1983.	5.9	107
7	A computationally designed chimeric antigen receptor provides a small-molecule safety switch for T-cell therapy. Nature Biotechnology, 2020, 38, 426-432.	17.5	100
8	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. Nature Communications, 2016, 7, 12460.	12.8	73
9	Bottom-up de novo design of functional proteins with complex structural features. Nature Chemical Biology, 2021, 17, 492-500.	8.0	65
10	In Vivo Tumor Targeting and Imaging with Engineered Trivalent Antibody Fragments Containing Collagen-Derived Sequences. PLoS ONE, 2009, 4, e5381.	2.5	56
11	ATTACK, a novel bispecific T cell-recruiting antibody with trivalent EGFR binding and monovalent CD3 binding for cancer immunotherapy. Oncolmmunology, 2018, 7, e1377874.	4.6	56
12	Characterization of Protein Hubs by Inferring Interacting Motifs from Protein Interactions. PLoS Computational Biology, 2007, 3, e178.	3.2	51
13	Amyloid-Î² Peptide Nitrotyrosination Stabilizes Oligomers and Enhances NMDAR-Mediated Toxicity. Journal of Neuroscience, 2016, 36, 11693-11703.	3.6	50
14	iLoops: a proteinâ€“protein interaction prediction server based on structural features. Bioinformatics, 2013, 29, 2360-2362.	4.1	47
15	Understanding Proteinâ€“Protein Interactions Using Local Structural Features. Journal of Molecular Biology, 2013, 425, 1210-1224.	4.2	46
16	ArchDB 2014: structural classification of loops in proteins. Nucleic Acids Research, 2014, 42, D315-D319.	14.5	38
17	On the Use of Knowledge-Based Potentials for the Evaluation of Models of Proteinâ€“Protein, Proteinâ€“DNA, and Proteinâ€“RNA Interactions. Advances in Protein Chemistry and Structural Biology, 2014, 94, 77-120.	2.3	32
18	Rosetta FunFolDes â€“ A general framework for the computational design of functional proteins. PLoS Computational Biology, 2018, 14, e1006623.	3.2	32

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19	Generation and characterization of monospecific and bispecific hexavalent trimerbodies. MAbs, 2013, 5, 70-79.	5.2	30
20	Intramolecular trimerization, a novel strategy for making multispecific antibodies with controlled orientation of the antigen binding domains. Scientific Reports, 2016, 6, 28643.	3.3	26
21	Boosting subdominant neutralizing antibody responses with a computationally designed epitope-focused immunogen. PLoS Biology, 2019, 17, e3000164.	5.6	26
22	Preclinical development of a humanized chimeric antigen receptor against B cell maturation antigen for multiple myeloma. Haematologica, 2020, 106, 173-184.	3.5	25
23	Modeling Immunity with Rosetta: Methods for Antibody and Antigen Design. Biochemistry, 2021, 60, 825-846.	2.5	24
24	Networks of Proteinï£¿Protein Interactions: From Uncertainty to Molecular Details. Molecular Informatics, 2012, 31, 342-362.	2.5	22
25	Structure-based immunogen design â€" leading the way to the new age of precision vaccines. Current Opinion in Structural Biology, 2018, 51, 163-169.	5.7	22
26	Targeting Importin-Î±7 as a Therapeutic Approach against Pandemic Influenza Viruses. Journal of Virology, 2015, 89, 9010-9020.	3.4	20
27	Bispecific light T-cell engagers for gene-based immunotherapy of epidermal growth factor receptor (EGFR)-positive malignancies. Cancer Immunology, Immunotherapy, 2018, 67, 1251-1260.	4.2	20
28	Human Albumin Impairs Amyloid Î²-peptide Fibrillation Through its C-terminus: From docking Modeling to Protection Against Neurotoxicity in Alzheimer's disease. Computational and Structural Biotechnology Journal, 2019, 17, 963-971.	4.1	19
29	Elongation of the C-terminal domain of an anti-amyloid Î² single-chain variable fragment increases its thermodynamic stability and decreases its aggregation tendency. MAbs, 2013, 5, 678-689.	5.2	16
30	Fragâ€™râ€™Us: knowledge-based sampling of protein backbone conformations for de novo structure-based protein design. Bioinformatics, 2014, 30, 1935-1936.	4.1	15
31	rstoolbox - a Python library for large-scale analysis of computational protein design data and structural bioinformatics. BMC Bioinformatics, 2019, 20, 240.	2.6	15
32	Using collections of structural models to predict changes of binding affinity caused by mutations in proteinâ€“protein interactions. Protein Science, 2020, 29, 2112-2130.	7.6	14
33	The role of residue stability in transient protein-protein interactions involved in enzymatic phosphate hydrolysis. A computational study. Proteins: Structure, Function and Bioinformatics, 2005, 63, 65-77.	2.6	13
34	On the mechanisms of protein interactions: predicting their affinity from unbound tertiary structures. Bioinformatics, 2018, 34, 592-598.	4.1	12
35	SPServer: split-statistical potentials for the analysis of protein structures and proteinâ€“protein interactions. BMC Bioinformatics, 2021, 22, 4.	2.6	8
36	The antigen-binding fragment of human gamma immunoglobulin prevents amyloid Î²-peptide folding into Î²-sheet to form oligomers. Oncotarget, 2017, 8, 41154-41165.	1.8	7

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37	On the prediction of DNA-binding preferences of C2H2-ZF domains using structural models: application on human CTCF. NAR Genomics and Bioinformatics, 2020, 2, lqaa046.	3.2	6
38	RosettaSurfâ€"A surface-centric computational design approach. PLoS Computational Biology, 2022, 18, e1009178.	3.2	5
39	Alternative interaction sites in the influenza A virus nucleoprotein mediate viral escape from the importinâ€‡7 mediated nuclear import pathway. FEBS Journal, 2019, 286, 3374-3388.	4.7	4
40	InteractoMIX: a suite of computational tools to exploit interactomes in biological and clinical research. Biochemical Society Transactions, 2016, 44, 917-924.	3.4	3
41	Smotifs as structural local descriptors of supersecondary elements: classification, completeness and applications. Bio-Algorithms and Med-Systems, 2014, 10, 195-212.	2.4	2
42	Prediction of a new class of RNA recognition motif. Journal of Molecular Modeling, 2011, 17, 1863-1875.	1.8	1
43	Structural Bioinformatics of Proteins: Predicting the Tertiary and Quaternary Structure of Proteins from Sequence. , 2012, , .		1
44	On the use of direct-coupling analysis with a reduced alphabet of amino acids combined with super-secondary structure motifs for protein fold prediction. NAR Genomics and Bioinformatics, 2021, 3, lqab027.	3.2	0
45	Characterization of Protein Hubs by Inferring Interacting Motifs from Protein Interactions. PLoS Computational Biology, 2005, preprint, e178.	3.2	0