

Bruno Correia

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

42
papers

2,310
citations

20
h-index

48
g-index

51
ext. papers

3,204
ext. citations

19.3
avg, IF

4.64
L-index

#	Paper	IF	Citations
42	Proteome-wide covalent ligand discovery in native biological systems. <i>Nature</i> , 2016 , 534, 570-4	50.4	406
41	Proof of principle for epitope-focused vaccine design. <i>Nature</i> , 2014 , 507, 201-6	50.4	365
40	Computation-guided backbone grafting of a discontinuous motif onto a protein scaffold. <i>Science</i> , 2011 , 334, 373-6	33.3	173
39	Computational design of epitope-scaffolds allows induction of antibodies specific for a poorly immunogenic HIV vaccine epitope. <i>Structure</i> , 2010 , 18, 1116-26	5.2	168
38	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020 , 17, 665-680	21.6	165
37	A Global Map of Lipid-Binding Proteins and Their Ligandability in Cells. <i>Cell</i> , 2015 , 161, 1668-80	56.2	140
36	Deciphering interaction fingerprints from protein molecular surfaces using geometric deep learning. <i>Nature Methods</i> , 2020 , 17, 184-192	21.6	112
35	Engineered anti-CRISPR proteins for optogenetic control of CRISPR-Cas9. <i>Nature Methods</i> , 2018 , 15, 924-927	21.6	109
34	A computationally designed inhibitor of an Epstein-Barr viral Bcl-2 protein induces apoptosis in infected cells. <i>Cell</i> , 2014 , 157, 1644-1656	56.2	96
33	Design and characterization of epitope-scaffold immunogens that present the motavizumab epitope from respiratory syncytial virus. <i>Journal of Molecular Biology</i> , 2011 , 409, 853-66	6.5	90
32	De novo protein design enables the precise induction of RSV-neutralizing antibodies. <i>Science</i> , 2020 , 368,	33.3	69
31	Computational protein design using flexible backbone remodeling and resurfacing: case studies in structure-based antigen design. <i>Journal of Molecular Biology</i> , 2011 , 405, 284-97	6.5	51
30	Chemoproteomic profiling and discovery of protein electrophiles in human cells. <i>Nature Chemistry</i> , 2017 , 9, 234-243	17.6	46
29	A computationally designed chimeric antigen receptor provides a small-molecule safety switch for T-cell therapy. <i>Nature Biotechnology</i> , 2020 , 38, 426-432	44.5	42
28	Optimization of therapeutic antibodies by predicting antigen specificity from antibody sequence via deep learning. <i>Nature Biomedical Engineering</i> , 2021 , 5, 600-612	19	34
27	Motif-Driven Design of Protein-Protein Interfaces. <i>Methods in Molecular Biology</i> , 2016 , 1414, 285-304	1.4	26
26	Bottom-up de novo design of functional proteins with complex structural features. <i>Nature Chemical Biology</i> , 2021 , 17, 492-500	11.7	25

25	Cathepsin S Regulates Antigen Processing and T Cell Activity in Non-Hodgkin Lymphoma. <i>Cancer Cell</i> , 2020 , 37, 674-689.e12	24.3	23
24	Deep learning enables therapeutic antibody optimization in mammalian cells by deciphering high-dimensional protein sequence space		23
23	Rosetta FunFoldDes - A general framework for the computational design of functional proteins. <i>PLoS Computational Biology</i> , 2018 , 14, e1006623	5	20
22	Boosting subdominant neutralizing antibody responses with a computationally designed epitope-focused immunogen. <i>PLoS Biology</i> , 2019 , 17, e3000164	9.7	18
21	Integrating gene synthesis and microfluidic protein analysis for rapid protein engineering. <i>Nucleic Acids Research</i> , 2016 , 44, e68	20.1	16
20	Structure-based immunogen design-leading the way to the new age of precision vaccines. <i>Current Opinion in Structural Biology</i> , 2018 , 51, 163-169	8.1	16
19	rstoolbox - a Python library for large-scale analysis of computational protein design data and structural bioinformatics. <i>BMC Bioinformatics</i> , 2019 , 20, 240	3.6	11
18	Protein-protein structure prediction by scoring molecular dynamics trajectories of putative poses. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84, 1312-20	4.2	9
17	Optogenetic control of <i>Neisseria meningitidis</i> Cas9 genome editing using an engineered, light-switchable anti-CRISPR protein. <i>Nucleic Acids Research</i> , 2021 , 49, e29	20.1	8
16	Computational design of anti-CRISPR proteins with improved inhibition potency. <i>Nature Chemical Biology</i> , 2020 , 16, 725-730	11.7	7
15	Modeling Immunity with Rosetta: Methods for Antibody and Antigen Design. <i>Biochemistry</i> , 2021 , 60, 825-846	3.2	6
14	A rational blueprint for the design of chemically-controlled protein switches. <i>Nature Communications</i> , 2021 , 12, 5754	17.4	6
13	De novo protein design enables precise induction of functional antibodies in vivo		4
12	High-resolution structure prediction of a circular permutation loop. <i>Protein Science</i> , 2011 , 20, 1929-34	6.3	3
11	A bottom-up approach for the de novo design of functional proteins		3
10	Fast end-to-end learning on protein surfaces		3
9	Fast end-to-end learning on protein surfaces 2021 ,		2
8	Computational design of anti-CRISPR proteins with improved inhibition potency and expanded specificity		2

7	Computational design of novel protein-protein interactions - An overview on methodological approaches and applications.. <i>Current Opinion in Structural Biology</i> , 2022 , 74, 102370	8.1	2
6	rstoolbox: management and analysis of computationally designed structural ensembles		1
5	Optogenetic control of <i>Neisseria meningitidis</i> Cas9 genome editing using an engineered, light-switchable anti-CRISPR protein		1
4	A Rosetta-based protein design protocol converging to natural sequences. <i>Journal of Chemical Physics</i> , 2021 , 154, 074114	3.9	1
3	The Physiological Landscape and Specificity of Antibody Repertoires		1
2	RosettaSurf-A surface-centric computational design approach.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009178	5	0
1	Epitope Mapping and Fine Specificity of Human T and B Cell Responses for Novel Candidate Blood-Stage Malaria Vaccine P27A. <i>Frontiers in Immunology</i> , 2020 , 11, 412	8.4	