Bruno Correia

List of Publications by Year in Descending Order

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	RosettaSurf-A surface-centric computational design approach.. *PLoS Computational Biology*, **2022**, 18, e1009178	5	0
41	Computational design of novel protein-protein interactions - An overview on methodological approaches and applications.. *Current Opinion in Structural Biology*, **2022**, 74, 102370	8.1	2
40	Fast end-to-end learning on protein surfaces **2021**,		2
39	Modeling Immunity with Rosetta: Methods for Antibody and Antigen Design. *Biochemistry*, **2021**, 60, 825-846	3.2	6
38	Optimization of therapeutic antibodies by predicting antigen specificity from antibody sequence via deep learning. *Nature Biomedical Engineering*, **2021**, 5, 600-612	19	34
37	Optogenetic control of Neisseria meningitidis Cas9 genome editing using an engineered, light-switchable anti-CRISPR protein. *Nucleic Acids Research*, **2021**, 49, e29	20.1	8
36	Bottom-up de novo design of functional proteins with complex structural features. *Nature Chemical Biology*, **2021**, 17, 492-500	11.7	25
35	A Rosetta-based protein design protocol converging to natural sequences. *Journal of Chemical Physics*, **2021**, 154, 074114	3.9	1
34	A rational blueprint for the design of chemically-controlled protein switches. *Nature Communications*, **2021**, 12, 5754	17.4	6
33	Macromolecular modeling and design in Rosetta: recent methods and frameworks. *Nature Methods*, **2020**, 17, 665-680	21.6	165
32	De novo protein design enables the precise induction of RSV-neutralizing antibodies. *Science*, **2020**, 368,	33.3	69
31	Epitope Mapping and Fine Specificity of Human T and B Cell Responses for Novel Candidate Blood-Stage Malaria Vaccine P27A. *Frontiers in Immunology*, **2020**, 11, 412	8.4	
30	Computational design of anti-CRISPR proteins with improved inhibition potency. *Nature Chemical Biology*, **2020**, 16, 725-730	11.7	7
29	Cathepsin S Regulates Antigen Processing and T Cell Activity in Non-Hodgkin Lymphoma. *Cancer Cell*, **2020**, 37, 674-689.e12	24.3	23
28	A computationally designed chimeric antigen receptor provides a small-molecule safety switch for T-cell therapy. *Nature Biotechnology*, **2020**, 38, 426-432	44.5	42
27	Deciphering interaction fingerprints from protein molecular surfaces using geometric deep learning. *Nature Methods*, **2020**, 17, 184-192	21.6	112
26	rstoolbox - a Python library for large-scale analysis of computational protein design data and structural bioinformatics. *BMC Bioinformatics*, **2019**, 20, 240	3.6	11

25	Boosting subdominant neutralizing antibody responses with a computationally designed epitope-focused immunogen. *PLoS Biology*, **2019**, 17, e3000164	9.7	18
24	Rosetta FunFolDes - A general framework for the computational design of functional proteins. *PLoS Computational Biology*, **2018**, 14, e1006623	5	20
23	Engineered anti-CRISPR proteins for optogenetic control of CRISPR-Cas9. *Nature Methods*, **2018**, 15, 924-927	21.6	109
22	Structure-based immunogen design-leading the way to the new age of precision vaccines. *Current Opinion in Structural Biology*, **2018**, 51, 163-169	8.1	16
21	Chemoproteomic profiling and discovery of protein electrophiles in human cells. *Nature Chemistry*, **2017**, 9, 234-243	17.6	46
20	Proteome-wide covalent ligand discovery in native biological systems. *Nature*, **2016**, 534, 570-4	50.4	406
19	Protein-protein structure prediction by scoring molecular dynamics trajectories of putative poses. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84, 1312-20	4.2	9
18	Integrating gene synthesis and microfluidic protein analysis for rapid protein engineering. *Nucleic Acids Research*, **2016**, 44, e68	20.1	16
17	Motif-Driven Design of Protein-Protein Interfaces. *Methods in Molecular Biology*, **2016**, 1414, 285-304	1.4	26
16	A Global Map of Lipid-Binding Proteins and Their Ligandability in Cells. *Cell*, **2015**, 161, 1668-80	56.2	140
15	Proof of principle for epitope-focused vaccine design. *Nature*, **2014**, 507, 201-6	50.4	365
14	A computationally designed inhibitor of an Epstein-Barr viral Bcl-2 protein induces apoptosis in infected cells. *Cell*, **2014**, 157, 1644-1656	56.2	96
13	Computational protein design using flexible backbone remodeling and resurfacing: case studies in structure-based antigen design. *Journal of Molecular Biology*, **2011**, 405, 284-97	6.5	51
12	Design and characterization of epitope-scaffold immunogens that present the motavizumab epitope from respiratory syncytial virus. *Journal of Molecular Biology*, **2011**, 409, 853-66	6.5	90
11	High-resolution structure prediction of a circular permutation loop. *Protein Science*, **2011**, 20, 1929-34	6.3	3
10	Computation-guided backbone grafting of a discontinuous motif onto a protein scaffold. *Science*, **2011**, 334, 373-6	33.3	173
9	Computational design of epitope-scaffolds allows induction of antibodies specific for a poorly immunogenic HIV vaccine epitope. *Structure*, **2010**, 18, 1116-26	5.2	168
8	rstoolbox: management and analysis of computationally designed structural ensembles		1