

Po-Ssu Huang

List of Publications by Year in Descending Order

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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.

47 papers	4,529 citations	25 h-index	54 g-index
54 ext. papers	5,858 ext. citations	17.1 avg, IF	5.5 L-index

#	Paper	IF	Citations
47	Protein sequence design with a learned potential.. <i>Nature Communications</i> , 2022 , 13, 746	17.4	3
46	Interleukin-2 superkines by computational design.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2117401119	11.5	1
45	Theoretical basis for stabilizing messenger RNA through secondary structure design 2021 ,		8
44	Identification of N-Terminally Diversified GLP-1R Agonists Using Saturation Mutagenesis and Chemical Design. <i>ACS Chemical Biology</i> , 2021 , 16, 58-66	4.9	1
43	Optical control of fast and processive engineered myosins in vitro and in living cells. <i>Nature Chemical Biology</i> , 2021 , 17, 540-548	11.7	5
42	Theoretical basis for stabilizing messenger RNA through secondary structure design. <i>Nucleic Acids Research</i> , 2021 , 49, 10604-10617	20.1	15
41	Structure-based protein design with deep learning. <i>Current Opinion in Chemical Biology</i> , 2021 , 65, 136-144	4.7	3
40	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020 , 17, 665-680	21.6	165
39	Engineering a potent receptor superagonist or antagonist from a novel IL-6 family cytokine ligand. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 14110-14118	11.5	7
38	Computational design of closely related proteins that adopt two well-defined but structurally divergent folds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 7208-7215	11.5	27
37	HIV-1 VRC01 Germline-Targeting Immunogens Select Distinct Epitope-Specific B Cell Receptors. <i>Immunity</i> , 2020 , 53, 840-851.e6	32.3	8
36	Tight and specific lanthanide binding in a de novo TIM barrel with a large internal cavity designed by symmetric domain fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 30362-30369	11.5	17
35	Computational design of transmembrane pores. <i>Nature</i> , 2020 , 585, 129-134	50.4	56
34	Multi-scale structural analysis of proteins by deep semantic segmentation. <i>Bioinformatics</i> , 2020 , 36, 1740-1749	9.1	496
33	Structure and Functional Binding Epitope of V-domain Ig Suppressor of T Cell Activation. <i>Cell Reports</i> , 2019 , 28, 2509-2516.e5	10.6	35
32	The molecular basis of chaperone-mediated interleukin 23 assembly control. <i>Nature Communications</i> , 2019 , 10, 4121	17.4	12
31	De novo design of a fluorescence-activating E-barrel. <i>Nature</i> , 2018 , 561, 485-491	50.4	156

30	Protein structure determination using metagenome sequence data. <i>Science</i> , 2017 , 355, 294-298	33.3	346
29	Designing repeat proteins: a modular approach to protein design. <i>Current Opinion in Structural Biology</i> , 2017 , 45, 116-123	8.1	27
28	A computationally engineered RAS rheostat reveals RAS-ERK signaling dynamics. <i>Nature Chemical Biology</i> , 2017 , 13, 119-126	11.7	15
27	Accurate de novo design of hyperstable constrained peptides. <i>Nature</i> , 2016 , 538, 329-335	50.4	231
26	The coming of age of de novo protein design. <i>Nature</i> , 2016 , 537, 320-7	50.4	697
25	Design of a hyperstable 60-subunit protein dodecahedron. [corrected]. <i>Nature</i> , 2016 , 535, 136-9	50.4	243
24	De novo design of a four-fold symmetric TIM-barrel protein with atomic-level accuracy. <i>Nature Chemical Biology</i> , 2016 , 12, 29-34	11.7	151
23	Using Molecular Dynamics Simulations as an Aid in the Prediction of Domain Swapping of Computationally Designed Protein Variants. <i>Journal of Molecular Biology</i> , 2015 , 427, 2697-706	6.5	10
22	Computational de novo design of a self-assembling peptide with predefined structure. <i>Journal of Molecular Biology</i> , 2015 , 427, 550-62	6.5	15
21	A general computational approach for repeat protein design. <i>Journal of Molecular Biology</i> , 2015 , 427, 563-75	6.5	63
20	Exploring the repeat protein universe through computational protein design. <i>Nature</i> , 2015 , 528, 580-4	50.4	156
19	Computational design and experimental verification of a symmetric protein homodimer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 10714-9	11.5	29
18	Control of repeat-protein curvature by computational protein design. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 167-74	17.6	69
17	Refocussing Antibody Responses by Chemical Modification of Vaccine Antigens. <i>AIDS Research and Human Retroviruses</i> , 2014 , 30, A66-A67	1.6	
16	High thermodynamic stability of parametrically designed helical bundles. <i>Science</i> , 2014 , 346, 481-485	33.3	196
15	Rational HIV immunogen design to target specific germline B cell receptors. <i>Science</i> , 2013 , 340, 711-6	33.3	519
14	Domain 1 of mucosal addressin cell adhesion molecule has an I1-set fold and a flexible integrin-binding loop. <i>Journal of Biological Chemistry</i> , 2013 , 288, 6284-94	5.4	5
13	Immune focusing and enhanced neutralization induced by HIV-1 gp140 chemical cross-linking. <i>Journal of Virology</i> , 2013 , 87, 10163-72	6.6	39

12	A potent and broad neutralizing antibody recognizes and penetrates the HIV glycan shield. <i>Science</i> , 2011 , 334, 1097-103	33.3	576
11	High-resolution structure prediction of a circular permutation loop. <i>Protein Science</i> , 2011 , 20, 1929-34	6.3	3
10	Computation-guided backbone grafting of a discontinuous motif onto a protein scaffold. <i>Science</i> , 2011 , 334, 373-6	33.3	173
9	A chimeric HIV-1 envelope glycoprotein trimer with an embedded granulocyte-macrophage colony-stimulating factor (GM-CSF) domain induces enhanced antibody and T cell responses. <i>Journal of Biological Chemistry</i> , 2011 , 286, 22250-61	5.4	13
8	RosettaRemodel: a generalized framework for flexible backbone protein design. <i>PLoS ONE</i> , 2011 , 6, e24109	3.7	200
7	Modulation of integrin activation by an entropic spring in the {beta}-knee. <i>Journal of Biological Chemistry</i> , 2010 , 285, 32954-32966	5.4	26
6	A de novo designed protein protein interface. <i>Protein Science</i> , 2007 , 16, 2770-4	6.3	81
5	Adaptation of a fast Fourier transform-based docking algorithm for protein design. <i>Journal of Computational Chemistry</i> , 2005 , 26, 1222-32	3.5	26
4	A designed protein interface that blocks fibril formation. <i>Journal of the American Chemical Society</i> , 2004 , 126, 13914-5	16.4	11
3	Protein Sequence Design with a Learned Potential		11
2	ProGen: Language Modeling for Protein Generation		39
1	IG-VAE: Generative Modeling of Immunoglobulin Proteins by Direct 3D Coordinate Generation		13