Po-Ssu Huang

List of Publications by Citations

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	The coming of age of de novo protein design. *Nature*, **2016**, 537, 320-7	50.4	697
46	A potent and broad neutralizing antibody recognizes and penetrates the HIV glycan shield. *Science*, **2011**, 334, 1097-103	33.3	576
45	Rational HIV immunogen design to target specific germline B cell receptors. *Science*, **2013**, 340, 711-6	33.3	519
44	Protein structure determination using metagenome sequence data. *Science*, **2017**, 355, 294-298	33.3	346
43	Design of a hyperstable 60-subunit protein dodecahedron. [corrected]. *Nature*, **2016**, 535, 136-9	50.4	243
42	Accurate de novo design of hyperstable constrained peptides. *Nature*, **2016**, 538, 329-335	50.4	231
41	RosettaRemodel: a generalized framework for flexible backbone protein design. *PLoS ONE*, **2011**, 6, e24109	3.7	200
40	High thermodynamic stability of parametrically designed helical bundles. *Science*, **2014**, 346, 481-485	33.3	196
39	Computation-guided backbone grafting of a discontinuous motif onto a protein scaffold. *Science*, **2011**, 334, 373-6	33.3	173
38	Macromolecular modeling and design in Rosetta: recent methods and frameworks. *Nature Methods*, **2020**, 17, 665-680	21.6	165
37	Exploring the repeat protein universe through computational protein design. *Nature*, **2015**, 528, 580-4	50.4	156
36	De novo design of a fluorescence-activating β-barrel. *Nature*, **2018**, 561, 485-491	50.4	156
35	De novo design of a four-fold symmetric TIM-barrel protein with atomic-level accuracy. *Nature Chemical Biology*, **2016**, 12, 29-34	11.7	151
34	A de novo designed protein protein interface. *Protein Science*, **2007**, 16, 2770-4	6.3	81
33	Control of repeat-protein curvature by computational protein design. *Nature Structural and Molecular Biology*, **2015**, 22, 167-74	17.6	69
32	A general computational approach for repeat protein design. *Journal of Molecular Biology*, **2015**, 427, 563-75	6.5	63
31	Computational design of transmembrane pores. *Nature*, **2020**, 585, 129-134	50.4	56

30	Immune focusing and enhanced neutralization induced by HIV-1 gp140 chemical cross-linking. *Journal of Virology*, **2013**, 87, 10163-72	6.6	39
29	ProGen: Language Modeling for Protein Generation		39
28	Structure and Functional Binding Epitope of V-domain Ig Suppressor of T Cell Activation. *Cell Reports*, **2019**, 28, 2509-2516.e5	10.6	35
27	Computational design and experimental verification of a symmetric protein homodimer. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 10714-9	11.5	29
26	Designing repeat proteins: a modular approach to protein design. *Current Opinion in Structural Biology*, **2017**, 45, 116-123	8.1	27
25	Computational design of closely related proteins that adopt two well-defined but structurally divergent folds. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 7208-7215	11.5	27
24	Modulation of integrin activation by an entropic spring in the {beta}-knee. *Journal of Biological Chemistry*, **2010**, 285, 32954-32966	5.4	26
23	Adaptation of a fast Fourier transform-based docking algorithm for protein design. *Journal of Computational Chemistry*, **2005**, 26, 1222-32	3.5	26
22	Tight and specific lanthanide binding in a de novo TIM barrel with a large internal cavity designed by symmetric domain fusion. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 30362-30369	11.5	17
21	Computational de novo design of a self-assembling peptide with predefined structure. *Journal of Molecular Biology*, **2015**, 427, 550-62	6.5	15
20	A computationally engineered RAS rheostat reveals RAS-ERK signaling dynamics. *Nature Chemical Biology*, **2017**, 13, 119-126	11.7	15
19	Theoretical basis for stabilizing messenger RNA through secondary structure design. *Nucleic Acids Research*, **2021**, 49, 10604-10617	20.1	15
18	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. *Journal of Biological Chemistry*, **2011**, 286, 22250-61	5.4	13
17	IG-VAE: Generative Modeling of Immunoglobulin Proteins by Direct 3D Coordinate Generation		13
16	The molecular basis of chaperone-mediated interleukin 23 assembly control. *Nature Communications*, **2019**, 10, 4121	17.4	12
15	A designed protein interface that blocks fibril formation. *Journal of the American Chemical Society*, **2004**, 126, 13914-5	16.4	11
14	Protein Sequence Design with a Learned Potential		11
13	Using Molecular Dynamics Simulations as an Aid in the Prediction of Domain Swapping of Computationally Designed Protein Variants. *Journal of Molecular Biology*, **2015**, 427, 2697-706	6.5	10

12	Theoretical basis for stabilizing messenger RNA through secondary structure design **2021**,		8
11	HIV-1 VRC01 Germline-Targeting Immunogens Select Distinct Epitope-Specific B Cell Receptors. *Immunity*, **2020**, 53, 840-851.e6	32.3	8
10	Engineering a potent receptor superagonist or antagonist from a novel IL-6 family cytokine ligand. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 14110-14118	11.5	7
9	Multi-scale structural analysis of proteins by deep semantic segmentation. *Bioinformatics*, **2020**, 36, 1740-1749	7.1	6
8	Domain 1 of mucosal addressin cell adhesion molecule has an I1-set fold and a flexible integrin-binding loop. *Journal of Biological Chemistry*, **2013**, 288, 6284-94	5.4	5
7	Optical control of fast and processive engineered myosins in vitro and in living cells. *Nature Chemical Biology*, **2021**, 17, 540-548	11.7	5
6	High-resolution structure prediction of a circular permutation loop. *Protein Science*, **2011**, 20, 1929-34	6.3	3
5	Protein sequence design with a learned potential.. *Nature Communications*, **2022**, 13, 746	17.4	3
4	Structure-based protein design with deep learning. *Current Opinion in Chemical Biology*, **2021**, 65, 136-144	9.7	3
3	Identification of N-Terminally Diversified GLP-1R Agonists Using Saturation Mutagenesis and Chemical Design. *ACS Chemical Biology*, **2021**, 16, 58-66	4.9	1
2	Interleukin-2 superkines by computational design.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119, e2117401119	11.5	1
1	Refocussing Antibody Responses by Chemical Modification of Vaccine Antigens. *AIDS Research and Human Retroviruses*, **2014**, 30, A66-A67	1.6	