Po-Ssu Huang

List of Publications by Year
in descending order

46 papers	6,900 citations	201674 27 h-index	223800 46 g-index
54 all docs	54 docs citations	54 times ranked	8565 citing authors

#	Article	IF	Citations
1	The coming of age of de novo protein design. Nature, 2016, 537, 320-327.	27.8	1,069
2	Rational HIV Immunogen Design to Target Specific Germline B Cell Receptors. Science, 2013, 340, 711-716.	12.6	680
3	A Potent and Broad Neutralizing Antibody Recognizes and Penetrates the HIV Glycan Shield. Science, 2011, 334, 1097-1103.	12.6	644
4	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
5	Protein structure determination using metagenome sequence data. Science, 2017, 355, 294-298.	12.6	456
6	Design of a hyperstable 60-subunit protein icosahedron. Nature, 2016, 535, 136-139.	27.8	373
7	Accurate de novo design of hyperstable constrained peptides. Nature, 2016, 538, 329-335.	27.8	327
8	RosettaRemodel: A Generalized Framework for Flexible Backbone Protein Design. PLoS ONE, 2011, 6, e24109.	2.5	310
9	De novo design of a fluorescence-activating Î²-barrel. Nature, 2018, 561, 485-491.	27.8	269
10	High thermodynamic stability of parametrically designed helical bundles. Science, 2014, 346, 481-485.	12.6	264
11	Exploring the repeat protein universe through computational protein design. Nature, 2015, 528, 580-584.	27.8	227
12	De novo design of a four-fold symmetric TIM-barrel protein with atomic-level accuracy. Nature Chemical Biology, 2016, 12, 29-34.	8.0	214
13	Computation-Guided Backbone Grafting of a Discontinuous Motif onto a Protein Scaffold. Science, 2011, 334, 373-376.	12.6	212
14	Computational design of transmembrane pores. Nature, 2020, 585, 129-134.	27.8	120
15	Protein sequence design with a learned potential. Nature Communications, 2022, 13, 746.	12.8	85
16	Control of repeat-protein curvature by computational protein design. Nature Structural and Molecular Biology, 2015, 22, 167-174.	8.2	84
17	A de novo designed proteinâ€“protein interface. Protein Science, 2007, 16, 2770-2774.	7.6	83
18	A General Computational Approach for Repeat Protein Design. Journal of Molecular Biology, 2015, 427, 563-575.	4.2	72

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19	Theoretical basis for stabilizing messenger RNA through secondary structure design. Nucleic Acids Research, 2021, 49, 10604-10617.	14.5	67
20	Structure and Functional Binding Epitope of V-domain Ig Suppressor of T Cell Activation. Cell Reports, 2019, 28, 2509-2516.e5.	6.4	61
21	Structure-based protein design with deep learning. Current Opinion in Chemical Biology, 2021, 65, 136-144.	6.1	53
22	Ig-VAE: Generative modeling of protein structure by direct 3D coordinate generation. PLoS Computational Biology, 2022, 18, e1010271.	3.2	51
23	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.	7.1	48
24	Immune Focusing and Enhanced Neutralization Induced by HIV-1 gp140 Chemical Cross-Linking. Journal of Virology, 2013, 87, 10163-10172.	3.4	43
25	Designing repeat proteins: a modular approach to protein design. Current Opinion in Structural Biology, 2017, 45, 116-123.	5.7	40
26	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, 10714-10719.	7.1	34
27	Modulation of Integrin Activation by an Entropic Spring in the Î²-Knee. Journal of Biological Chemistry, 2010, 285, 32954-32966.	3.4	32
28	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.	7.1	31
29	Adaptation of a fast Fourier transform-based docking algorithm for protein design. Journal of Computational Chemistry, 2005, 26, 1222-1232.	3.3	27
30	HIV-1 VRC01 Germline-Targeting Immunogens Select Distinct Epitope-Specific B Cell Receptors. Immunity, 2020, 53, 840-851.e6.	14.3	27
31	A computationally engineered RAS rheostat reveals RASâ€“ERK signaling dynamics. Nature Chemical Biology, 2017, 13, 119-126.	8.0	21
32	Computational De Novo Design of a Self-Assembling Peptide with Predefined Structure. Journal of Molecular Biology, 2015, 427, 550-562.	4.2	20
33	The molecular basis of chaperone-mediated interleukin 23 assembly control. Nature Communications, 2019, 10, 4121.	12.8	18
34	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.	7.1	17
35	Optical control of fast and processive engineered myosins in vitro and in living cells. Nature Chemical Biology, 2021, 17, 540-548.	8.0	17
36	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, 22250-22261.	3.4	15

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37	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, 6284-6294.	3.4	13
38	A Designed Protein Interface That Blocks Fibril Formation. Journal of the American Chemical Society, 2004, 126, 13914-13915.	13.7	12
39	Interleukin-2 superkines by computational design. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2117401119.	7.1	12
40	Using Molecular Dynamics Simulations as an Aid in the Prediction of Domain Swapping of Computationally Designed Protein Variants. Journal of Molecular Biology, 2015, 427, 2697-2706.	4.2	11
41	Multi-scale structural analysis of proteins by deep semantic segmentation. Bioinformatics, 2020, 36, 1740-1749.	4.1	10
42	Identification of N-Terminally Diversified GLP-1R Agonists Using Saturation Mutagenesis and Chemical Design. ACS Chemical Biology, 2021, 16, 58-66.	3.4	5
43	Highâ€resolution structure prediction of a circular permutation loop. Protein Science, 2011, 20, 1929-1934.	7.6	3
44	Chimeric mutants of staphylococcal hemolysin, which act as both oneâ€component and twoâ€component hemolysin, created by grafting the stem domain. FEBS Journal, 2022, 289, 3505-3520.	4.7	1
45	Refocussing Antibody Responses by Chemical Modification of Vaccine Antigens. AIDS Research and Human Retroviruses, 2014, 30, A66-A67.	1.1	0
46	Harnessing Human Neural Networks for Protein Design. Biochemistry, 2019, 58, 5100-5101.	2.5	0