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	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
2	Protein sequence design with a learned potential. Nature Communications, 2022, 13, 746.	12.8	85
3	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
4	Ig-VAE: Generative modeling of protein structure by direct 3D coordinate generation. PLoS Computational Biology, 2022, 18, e1010271.	3.2	51
5	Identification of N-Terminally Diversified GLP-1R Agonists Using Saturation Mutagenesis and Chemical Design. ACS Chemical Biology, 2021, 16, 58-66.	3.4	5
6	Optical control of fast and processive engineered myosins in vitro and in living cells. Nature Chemical Biology, 2021, 17, 540-548.	8.0	17
7	Theoretical basis for stabilizing messenger RNA through secondary structure design. Nucleic Acids Research, 2021, 49, 10604-10617.	14.5	67
8	Structure-based protein design with deep learning. Current Opinion in Chemical Biology, 2021, 65, 136-144.	6.1	53
9	Multi-scale structural analysis of proteins by deep semantic segmentation. Bioinformatics, 2020, 36, 1740-1749.	4.1	10
10	HIV-1 VRC01 Germline-Targeting Immunogens Select Distinct Epitope-Specific B Cell Receptors. Immunity, 2020, 53, 840-851.e6.	14.3	27
11	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
12	Computational design of transmembrane pores. Nature, 2020, 585, 129-134.	27.8	120
13	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
14	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
15	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
16	Structure and Functional Binding Epitope of V-domain Ig Suppressor of T Cell Activation. Cell Reports, 2019, 28, 2509-2516.e5.	6.4	61
17	The molecular basis of chaperone-mediated interleukin 23 assembly control. Nature Communications, 2019, 10, 4121.	12.8	18
18	Harnessing Human Neural Networks for Protein Design. Biochemistry, 2019, 58, 5100-5101.	2.5	0

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19	De novo design of a fluorescence-activating Î²-barrel. Nature, 2018, 561, 485-491.	27.8	269
20	Protein structure determination using metagenome sequence data. Science, 2017, 355, 294-298.	12.6	456
21	Designing repeat proteins: a modular approach to protein design. Current Opinion in Structural Biology, 2017, 45, 116-123.	5.7	40
22	A computationally engineered RAS rheostat reveals RASâ€“ERK signaling dynamics. Nature Chemical Biology, 2017, 13, 119-126.	8.0	21
23	Accurate de novo design of hyperstable constrained peptides. Nature, 2016, 538, 329-335.	27.8	327
24	The coming of age of de novo protein design. Nature, 2016, 537, 320-327.	27.8	1,069
25	Design of a hyperstable 60-subunit protein icosahedron. Nature, 2016, 535, 136-139.	27.8	373
26	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
27	Exploring the repeat protein universe through computational protein design. Nature, 2015, 528, 580-584.	27.8	227
28	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
29	Control of repeat-protein curvature by computational protein design. Nature Structural and Molecular Biology, 2015, 22, 167-174.	8.2	84
30	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
31	Computational De Novo Design of a Self-Assembling Peptide with Predefined Structure. Journal of Molecular Biology, 2015, 427, 550-562.	4.2	20
32	A General Computational Approach for Repeat Protein Design. Journal of Molecular Biology, 2015, 427, 563-575.	4.2	72
33	High thermodynamic stability of parametrically designed helical bundles. Science, 2014, 346, 481-485.	12.6	264
34	Refocussing Antibody Responses by Chemical Modification of Vaccine Antigens. AIDS Research and Human Retroviruses, 2014, 30, A66-A67.	1.1	0
35	Rational HIV Immunogen Design to Target Specific Germline B Cell Receptors. Science, 2013, 340, 711-716.	12.6	680
36	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

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37	Immune Focusing and Enhanced Neutralization Induced by HIV-1 gp140 Chemical Cross-Linking. Journal of Virology, 2013, 87, 10163-10172.	3.4	43
38	Computation-Guided Backbone Grafting of a Discontinuous Motif onto a Protein Scaffold. Science, 2011, 334, 373-376.	12.6	212
39	A Potent and Broad Neutralizing Antibody Recognizes and Penetrates the HIV Glycan Shield. Science, 2011, 334, 1097-1103.	12.6	644
40	Highâ€resolution structure prediction of a circular permutation loop. Protein Science, 2011, 20, 1929-1934.	7.6	3
41	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
42	RosettaRemodel: A Generalized Framework for Flexible Backbone Protein Design. PLoS ONE, 2011, 6, e24109.	2.5	310
43	Modulation of Integrin Activation by an Entropic Spring in the Î²-Knee. Journal of Biological Chemistry, 2010, 285, 32954-32966.	3.4	32
44	A de novo designed proteinâ€“protein interface. Protein Science, 2007, 16, 2770-2774.	7.6	83
45	Adaptation of a fast Fourier transform-based docking algorithm for protein design. Journal of Computational Chemistry, 2005, 26, 1222-1232.	3.3	27
46	A Designed Protein Interface That Blocks Fibril Formation. Journal of the American Chemical Society, 2004, 126, 13914-13915.	13.7	12