Jeffery G Saven

List of Publications by Year
in descending order

81 papers	3,414 citations	117625 34 h-index	149698 56 g-index
87 all docs	87 docs citations	87 times ranked	3692 citing authors

#	Article	IF	Citations
1	Colloid-like solution behavior of computationally designed coiled coil bundlemers. Journal of Colloid and Interface Science, 2022, 606, 1974-1982.	9.4	3
2	Computational Design of Single-Peptide Nanocages with Nanoparticle Templating. Molecules, 2022, 27, 1237.	3.8	5
3	Computational Design of Homotetrameric Peptide Bundle Variants Spanning a Wide Range of Charge States. Biomacromolecules, 2022, 23, 1652-1661.	5.4	3
4	The C-Terminus of the mu Opioid Receptor Is Critical in G-Protein Interaction as Demonstrated by a Novel Graphene Biosensor. IEEE Sensors Journal, 2021, 21, 5758-5762.	4.7	0
5	Recombinant expression of computationally designed peptide-bundlemers in Escherichia coli. Journal of Biotechnology, 2021, 330, 57-60.	3.8	5
6	Nanofibers Produced by Electrospinning of Ultrarigid Polymer Rods Made from Designed Peptide Bundlemers. ACS Applied Materials & Interfaces, 2021, 13, 26339-26351.	8.0	14
7	Novel variants of engineered water soluble mu opioid receptors with extensive mutations and removal of cysteines. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1386-1393.	2.6	0
8	Intramolecular structure and dynamics in computationally designed peptide-based polymers displaying tunable chain stiffness. Physical Review Materials, 2021, 5, .	2.4	1
9	Peptide Design and Self-assembly into Targeted Nanostructure and Functional Materials. Chemical Reviews, 2021, 121, 13915-13935.	47.7	116
10	Design of a Superpositively Charged Enzyme: Human Carbonic Anhydrase II Variant with Ferritin Encapsulation and Immobilization. Biochemistry, 2021, 60, 3596-3609.	2.5	8
11	Characterization of an engineered water-soluble variant of the full-length human mu opioid receptor. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4364-4370.	3.5	4
12	Polymers with controlled assembly and rigidity made with click-functional peptide bundles. Nature, 2019, 574, 658-662.	27.8	79
13	Polyelectrolyte character of rigid rod peptide bundlemer chains constructed via hierarchical self-assembly. Soft Matter, 2019, 15, 9858-9870.	2.7	15
14	Water Soluble G-protein Coupled Receptor Enabled Biosensors. Translational Perioperative and Pain Medicine, 2019, 6, 98-103.	0.1	4
15	All-Electronic Quantification of Neuropeptideâ€“Receptor Interaction Using a Bias-Free Functionalized Graphene Microelectrode. ACS Nano, 2018, 12, 4218-4223.	14.6	13
16	Fabrication of One- and Two-Dimensional Gold Nanoparticle Arrays on Computationally Designed Self-Assembled Peptide Templates. Chemistry of Materials, 2018, 30, 8510-8520.	6.7	17
17	Nanotubes, Plates, and Needles: Pathway-Dependent Self-Assembly of Computationally Designed Peptides. Biomacromolecules, 2018, 19, 4286-4298.	5.4	34
18	A proteinâ€“protein hostâ€“guest complex: Thermostable ferritin encapsulating positively supercharged green fluorescent protein. Protein Science, 2018, 27, 1755-1766.	7.6	17

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19	Self-assembly and soluble aggregate behavior of computationally designed coiled-coil peptide bundles. Soft Matter, 2018, 14, 5488-5496.	2.7	19
20	Quantifying the effect of ionic screening with protein-decorated graphene transistors. Biosensors and Bioelectronics, 2017, 89, 689-692.	10.1	35
21	Improving target amino acid selectivity in a permissive aminoacyl tRNA synthetase through counter-selection. Organic and Biomolecular Chemistry, 2017, 15, 3603-3610.	2.8	31
22	Transition from disordered aggregates to ordered lattices: kinetic control of the assembly of a computationally designed peptide. Organic and Biomolecular Chemistry, 2017, 15, 6109-6118.	2.8	18
23	Structural-functional analysis of engineered protein-nanoparticle assemblies using graphene microelectrodes. Chemical Science, 2017, 8, 5329-5334.	7.4	4
24	pH Sensing Properties of Flexible, Biasâ€Free Graphene Microelectrodes in Complex Fluids: From Phosphate Buffer Solution to Human Serum. Small, 2017, 13, 1700564.	10.0	5
25	Controlling Association and Separation of Gold Nanoparticles with Computationally Designed Zinc-Coordinating Proteins. Journal of the American Chemical Society, 2017, 139, 17811-17823.	13.7	18
26	Thermophilic Ferritin 24mer Assembly and Nanoparticle Encapsulation Modulated by Interdimer Electrostatic Repulsion. Biochemistry, 2017, 56, 3596-3606.	2.5	31
27	Scalable Production of Molybdenum Disulfide Based Biosensors. ACS Nano, 2016, 10, 6173-6179.	14.6	68
28	Computationally designed peptides for self-assembly of nanostructured lattices. Science Advances, 2016, 2, e1600307.	10.3	58
29	Photoinduced Electron Transfer Elicits a Change in the Static Dielectric Constant of a de Novo Designed Protein. Journal of the American Chemical Society, 2016, 138, 2130-2133.	13.7	22
30	Molecular recognition of ketamine by a subset of olfactory G proteinâ€“coupled receptors. Science Signaling, 2015, 8, ra33.	3.6	14
31	Xe affinities of water-soluble cryptophanes and the role of confined water. Chemical Science, 2015, 6, 7238-7248.	7.4	21
32	Observing Changes in the Structure and Oligomerization State of a Helical Protein Dimer Using Solid-State Nanopores. ACS Nano, 2015, 9, 8907-8915.	14.6	32
33	Scalable Production of Highly Sensitive Nanosensors Based on Graphene Functionalized with a Designed G Protein-Coupled Receptor. Nano Letters, 2014, 14, 2709-2714.	9.1	105
34	Engineering Complementary Hydrophobic Interactions to Control Î²-Hairpin Peptide Self-Assembly, Network Branching, and Hydrogel Properties. Biomacromolecules, 2014, 15, 3891-3900.	5.4	51
35	Characterization of a Computationally Designed Water-soluble Human Î¼-Opioid Receptor Variant Using Available Structural Information. Anesthesiology, 2014, 121, 866-875.	2.5	13
36	Computational de Novo Design and Characterization of a Protein That Selectively Binds a Highly Hyperpolarizable Abiological Chromophore. Journal of the American Chemical Society, 2013, 135, 13914-13926.	13.7	55

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37	A Computationally Designed Water-Soluble Variant of a G-Protein-Coupled Receptor: The Human Mu Opioid Receptor. PLoS ONE, 2013, 8, e66009.	2.5	34
38	NMR structure and dynamics of a designed water-soluble transmembrane domain of nicotinic acetylcholine receptor. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 617-626.	2.6	25
39	Computational design of a protein crystal. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7304-7309.	7.1	157
40	Computational Design of Membrane Proteins. Structure, 2012, 20, 5-14.	3.3	32
41	Human Î¼ Opioid Receptor Models with Evaluation of the Accuracy Using the Crystal Structure of the Murine Î¼ Opioid Receptor. Journal of Anesthesia & Clinical Research, 2012, 03, 218.	0.1	5
42	An induced fit mechanism regulates p53 DNA binding kinetics to confer sequence specificity. EMBO Journal, 2011, 30, 2167-2176.	7.8	95
43	Theoretical and Computational Protein Design. Annual Review of Physical Chemistry, 2011, 62, 129-149.	10.8	125
44	Computational design and selections for an engineered, thermostable terpene synthase. Protein Science, 2011, 20, 1597-1606.	7.6	53
45	Computational protein design: engineering molecular diversity, nonnatural enzymes, nonbiological cofactor complexes, and membrane proteins. Current Opinion in Chemical Biology, 2011, 15, 452-457.	6.1	45
46	Computational protein design: Advances in the design and redesign of biomolecular nanostructures. Current Opinion in Colloid and Interface Science, 2010, 15, 13-17.	7.4	25
47	Computational Design and Elaboration of a de Novo Heterotetrameric Î±-Helical Protein That Selectively Binds an Emissive Abiological (Porphinato)zinc Chromophore. Journal of the American Chemical Society, 2010, 132, 3997-4005.	13.7	54
48	Structural coupling between FKBP12 and buried water. Proteins: Structure, Function and Bioinformatics, 2009, 74, 603-611.	2.6	63
49	Characterization of the Cofactor-Induced Folding Mechanism of a Zinc-Binding Peptide Using Computationally Designed Mutants. Journal of Molecular Biology, 2009, 389, 90-102.	4.2	19
50	Computational Design of Four-Helix Bundle Proteins That Bind Nonbiological Cofactors. Biotechnology Progress, 2008, 24, 74-79.	2.6	8
51	Directing Noble Metal Ion Chemistry within a Designed Ferritin Protein[,]. Biochemistry, 2008, 47, 12729-12739.	2.5	84
52	Using Î±-Helical Coiled-Coils to Design Nanostructured Metalloporphyrin Arrays. Journal of the American Chemical Society, 2008, 130, 11921-11927.	13.7	63
53	Combinatorial Protein Design Strategies Using Computational Methods. , 2007, 352, 3-22.		3
54	Computational protein design: structure, function and combinatorial diversity. Current Opinion in Chemical Biology, 2007, 11, 329-334.	6.1	42

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55	Molecular Dynamics Simulation of WSK-3, a Computationally Designed, Water-Soluble Variant of the Integral Membrane Protein KcsA. Biophysical Journal, 2006, 90, 1156-1163.	0.5	14
56	Design of Functional Ferritin-Like Proteins with Hydrophobic Cavities. Journal of the American Chemical Society, 2006, 128, 6611-6619.	13.7	55
57	Ultrafast Folding of a Computationally Designed Trp-Cage Mutant:Â Trp2-Cageâ€. Journal of Physical Chemistry B, 2006, 110, 3759-3763.	2.6	85
58	Simulation of pH-dependent edge strand rearrangement in human Â-2 microglobulin. Protein Science, 2006, 15, 200-207.	7.6	18
59	Limitations of yeast surface display in engineering proteins of high thermostability. Protein Engineering, Design and Selection, 2006, 19, 211-217.	2.1	51
60	Functional modification of phosphatidylinositolâ€specific phospholipase C from Bacillus cereus by computer modeling and siteâ€directed mutagenesis. FASEB Journal, 2006, 20, A900.	0.5	0
61	Chapter 18 Computationally Assisted Protein Design. Annual Reports in Computational Chemistry, 2005, , 245-253.	1.7	1
62	Progress in the development and application of computational methods for probabilistic protein design. Computers and Chemical Engineering, 2005, 29, 407-421.	3.8	22
63	Computational methods for protein design and protein sequence variability: biased Monte Carlo and replica exchange. Chemical Physics Letters, 2005, 401, 205-210.	2.6	37
64	Statistical and molecular dynamics studies of buried waters in globular proteins. Proteins: Structure, Function and Bioinformatics, 2005, 60, 450-463.	2.6	100
65	Statistical theory for protein ensembles with designed energy landscapes. Journal of Chemical Physics, 2005, 123, 154908.	3.0	21
66	De Novo Design of a Redox-Active Minimal Rubredoxin Mimic. Journal of the American Chemical Society, 2005, 127, 5804-5805.	13.7	126
67	Computational De Novo Design and Characterization of a Four-Helix Bundle Protein that Selectively Binds a Nonbiological Cofactor. Journal of the American Chemical Society, 2005, 127, 1346-1347.	13.7	167
68	Modulating the DNA Affinity of Elk-1 with Computationally Selected Mutations. Journal of Molecular Biology, 2005, 348, 75-83.	4.2	7
69	Advances in computational protein design. Current Opinion in Structural Biology, 2004, 14, 487-494.	5.7	90
70	Guiding the search for a protein's maximum rate of folding. Chemical Physics, 2004, 307, 99-109.	1.9	52
71	7ÂÂComputational protein design and discovery. Annual Reports on the Progress of Chemistry Section C, 2004, 100, 195-236.	4.4	8
72	Computational design of water-soluble analogues of the potassium channel KcsA. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1828-1833.	7.1	106

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73	Computational Design and Characterization of a Monomeric Helical Dinuclear Metalloprotein. Journal of Molecular Biology, 2003, 334, 1101-1115.	4.2	138
74	Using self-consistent fields to bias Monte Carlo methods with applications to designing and sampling protein sequences. Journal of Chemical Physics, 2003, 118, 3843-3854.	3.0	40
75	Connecting statistical and optimized potentials in protein folding via a generalized foldability criterion. Journal of Chemical Physics, 2003, 118, 6133-6136.	3.0	15
76	Probabilistic approach to the design of symmetric protein quaternary structures. Protein Engineering, Design and Selection, 2003, 16, 971-977.	2.1	18
77	Combinatorial protein design. Current Opinion in Structural Biology, 2002, 12, 453-458.	5.7	60
78	Statistical theory for protein combinatorial libraries. packing interactions, backbone flexibility, and the sequence variability of a main-chain structure11Edited by J. Thornton. Journal of Molecular Biology, 2001, 306, 607-628.	4.2	130
79	Designing Protein Energy Landscapes. Chemical Reviews, 2001, 101, 3113-3130.	47.7	49
80	Statistical theory of combinatorial libraries of folding proteins: energetic discrimination of a target structure 1 1Edited by J. Thornton. Journal of Molecular Biology, 2000, 296, 281-294.	4.2	80
81	Statistical Mechanics of the Combinatorial Synthesis and Analysis of Folding Macromolecules. Journal of Physical Chemistry B, 1997, 101, 8375-8389.	2.6	54