

Scott E Boyken

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

3,880
citations

304368

22
h-index

414034

32
g-index

42
all docs

42
docs citations

42
times ranked

4943
citing authors

#	ARTICLE	IF	CITATIONS
1	The coming of age of de novo protein design. <i>Nature</i> , 2016, 537, 320-327.	13.7	1,069
2	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	9.0	513
3	De novo design of protein homo-oligomers with modular hydrogen-bond network-mediated specificity. <i>Science</i> , 2016, 352, 680-687.	6.0	262
4	Crystal structures of the CusA efflux pump suggest methionine-mediated metal transport. <i>Nature</i> , 2010, 467, 484-488.	13.7	223
5	De novo design of bioactive protein switches. <i>Nature</i> , 2019, 572, 205-210.	13.7	190
6	De novo design of modular and tunable protein biosensors. <i>Nature</i> , 2021, 591, 482-487.	13.7	153
7	De novo design of protein logic gates. <i>Science</i> , 2020, 368, 78-84.	6.0	151
8	Accurate computational design of multipass transmembrane proteins. <i>Science</i> , 2018, 359, 1042-1046.	6.0	149
9	Programmable design of orthogonal protein heterodimers. <i>Nature</i> , 2019, 565, 106-111.	13.7	139
10	Computational design of transmembrane pores. <i>Nature</i> , 2020, 585, 129-134.	13.7	120
11	Designed protein logic to target cells with precise combinations of surface antigens. <i>Science</i> , 2020, 369, 1637-1643.	6.0	117
12	De novo design of tunable, pH-driven conformational changes. <i>Science</i> , 2019, 364, 658-664.	6.0	109
13	Modular and tunable biological feedback control using a de novo protein switch. <i>Nature</i> , 2019, 572, 265-269.	13.7	96
14	Rapid online buffer exchange for screening of proteins, protein complexes and cell lysates by native mass spectrometry. <i>Nature Protocols</i> , 2020, 15, 1132-1157.	5.5	88
15	Multivalent designed proteins neutralize SARS-CoV-2 variants of concern and confer protection against infection in mice. <i>Science Translational Medicine</i> , 2022, 14, eabn1252.	5.8	68
16	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.	3.3	48
17	Dynamic Allostery Mediated by a Conserved Tryptophan in the Tec Family Kinases. <i>PLoS Computational Biology</i> , 2016, 12, e1004826.	1.5	40
18	Proline Isomerization Preorganizes the Itk SH2 Domain for Binding to the Itk SH3 Domain. <i>Journal of Molecular Biology</i> , 2009, 387, 726-743.	2.0	37

#	ARTICLE	IF	CITATIONS
19	Self-Assembling 2D Arrays with <i>de Novo</i> Protein Building Blocks. <i>Journal of the American Chemical Society</i> , 2019, 141, 8891-8895.	6.6	37
20	Rapid Sampling of Hydrogen Bond Networks for Computational Protein Design. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 2751-2760.	2.3	36
21	Computational design of mechanically coupled axle-rotor protein assemblies. <i>Science</i> , 2022, 376, 383-390.	6.0	33
22	Design and structure of two new protein cages illustrate successes and ongoing challenges in protein engineering. <i>Protein Science</i> , 2020, 29, 919-929.	3.1	32
23	Rates of molecular evolution vary in vertebrates for insulin-like growth factor-1 (IGF-1), a pleiotropic locus that regulates life history traits. <i>General and Comparative Endocrinology</i> , 2012, 178, 164-173.	0.8	29
24	Calmodulin and PI(3,4,5)P ₃ cooperatively bind to the Itk pleckstrin homology domain to promote efficient calcium signaling and IL-17A production. <i>Science Signaling</i> , 2014, 7, ra74.	1.6	22
25	An Autoinhibitory Role for the Pleckstrin Homology Domain of Interleukin-2-Inducible Tyrosine Kinase and Its Interplay with Canonical Phospholipid Recognition. <i>Biochemistry</i> , 2017, 56, 2938-2949.	1.2	18
26	Modeling oblong proteins and water-mediated interfaces with RosettaDock in CAPRI rounds 28-35. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 479-486.	1.5	18
27	De novo design of a homo-trimeric amantadine-binding protein. <i>ELife</i> , 2019, 8, .	2.8	18
28	Rescue of the aggregation prone Itk Pleckstrin Homology domain by two mutations derived from the related kinases, Btk and Tec. <i>Protein Science</i> , 2012, 21, 1288-1297.	3.1	12
29	A Conserved Isoleucine Maintains the Inactive State of Bruton's Tyrosine Kinase. <i>Journal of Molecular Biology</i> , 2014, 426, 3656-3669.	2.0	10
30	The SH3 domains of the protein kinases ITK and LCK compete for adjacent sites on T cell-specific adapter protein. <i>Journal of Biological Chemistry</i> , 2019, 294, 15480-15494.	1.6	9
31	Conditional Recruitment to a DNA-Bound CRISPR-Cas Complex Using a Colocalization-Dependent Protein Switch. <i>ACS Synthetic Biology</i> , 2020, 9, 2316-2323.	1.9	4