

# Scott E Boyken

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

34  
papers

2,207  
citations

20  
h-index

42  
g-index

42  
ext. papers

3,099  
ext. citations

22  
avg, IF

5.23  
L-index

#	Paper	IF	Citations
34	Multivalent designed proteins neutralize SARS-CoV-2 variants of concern and confer protection against infection in mice.. <i>Science Translational Medicine</i> , <b>2022</b> , 14, eabn1252	17.5	3
33	Computational design of mechanically coupled axle-rotor protein assemblies.. <i>Science</i> , <b>2022</b> , 376, 383-390	39.3	2
32	De novo design of modular and tunable protein biosensors. <i>Nature</i> , <b>2021</b> , 591, 482-487	50.4	53
31	Multivalent designed proteins protect against SARS-CoV-2 variants of concern <b>2021</b> ,		4
30	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , <b>2020</b> , 17, 665-680	21.6	165
29	De novo design of protein logic gates. <i>Science</i> , <b>2020</b> , 368, 78-84	33.3	88
28	Rapid online buffer exchange for screening of proteins, protein complexes and cell lysates by native mass spectrometry. <i>Nature Protocols</i> , <b>2020</b> , 15, 1132-1157	18.8	46
27	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> , <b>2020</b> , 117, 7208-7215	11.5	27
26	design of modular and tunable allosteric biosensors <b>2020</b> ,		6
25	Design and structure of two new protein cages illustrate successes and ongoing challenges in protein engineering. <i>Protein Science</i> , <b>2020</b> , 29, 919-929	6.3	9
24	Computational design of transmembrane pores. <i>Nature</i> , <b>2020</b> , 585, 129-134	50.4	56
23	Conditional Recruitment to a DNA-Bound CRISPR-Cas Complex Using a Colocalization-Dependent Protein Switch. <i>ACS Synthetic Biology</i> , <b>2020</b> , 9, 2316-2323	5.7	1
22	Designed protein logic to target cells with precise combinations of surface antigens. <i>Science</i> , <b>2020</b> , 369, 1637-1643	33.3	48
21	De novo design of tunable, pH-driven conformational changes. <i>Science</i> , <b>2019</b> , 364, 658-664	33.3	60
20	Self-Assembling 2D Arrays with de Novo Protein Building Blocks. <i>Journal of the American Chemical Society</i> , <b>2019</b> , 141, 8891-8895	16.4	24
19	Modular and tunable biological feedback control using a de novo protein switch. <i>Nature</i> , <b>2019</b> , 572, 265-269	36.9	58
18	De novo design of bioactive protein switches. <i>Nature</i> , <b>2019</b> , 572, 205-210	50.4	113

17	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> , <b>2019</b> , 294, 15480-15494	5.4	5
16	De novo design of a homo-trimeric amantadine-binding protein. <i>ELife</i> , <b>2019</b> , 8,	8.9	10
15	Programmable design of orthogonal protein heterodimers. <i>Nature</i> , <b>2019</b> , 565, 106-111	50.4	87
14	Accurate computational design of multipass transmembrane proteins. <i>Science</i> , <b>2018</b> , 359, 1042-1046	33.3	93
13	Rapid Sampling of Hydrogen Bond Networks for Computational Protein Design. <i>Journal of Chemical Theory and Computation</i> , <b>2018</b> , 14, 2751-2760	6.4	24
12	An Autoinhibitory Role for the Pleckstrin Homology Domain of Interleukin-2-Inducible Tyrosine Kinase and Its Interplay with Canonical Phospholipid Recognition. <i>Biochemistry</i> , <b>2017</b> , 56, 2938-2949	3.2	10
11	Modeling oblong proteins and water-mediated interfaces with RosettaDock in CAPRI rounds 28-35. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2017</b> , 85, 479-486	4.2	14
10	The coming of age of de novo protein design. <i>Nature</i> , <b>2016</b> , 537, 320-7	50.4	697
9	Dynamic Allostery Mediated by a Conserved Tryptophan in the Tec Family Kinases. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1004826	5	30
8	De novo design of protein homo-oligomers with modular hydrogen-bond network-mediated specificity. <i>Science</i> , <b>2016</b> , 352, 680-7	33.3	194
7	A conserved isoleucine maintains the inactive state of Bruton's tyrosine kinase. <i>Journal of Molecular Biology</i> , <b>2014</b> , 426, 3656-69	6.5	10
6	Calmodulin and PI(3,4,5)P <sub>3</sub> cooperatively bind to the Itk pleckstrin homology domain to promote efficient calcium signaling and IL-17A production. <i>Science Signaling</i> , <b>2014</b> , 7, ra74	8.8	18
5	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> , <b>2012</b> , 178, 164-73	3	25
4	Rescue of the aggregation prone Itk Pleckstrin Homology domain by two mutations derived from the related kinases, Btk and Tec. <i>Protein Science</i> , <b>2012</b> , 21, 1288-97	6.3	11
3	Crystal structures of the CusA efflux pump suggest methionine-mediated metal transport. <i>Nature</i> , <b>2010</b> , 467, 484-8	50.4	177
2	Proline isomerization preorganizes the Itk SH2 domain for binding to the Itk SH3 domain. <i>Journal of Molecular Biology</i> , <b>2009</b> , 387, 726-43	6.5	33
1	Rapid Online Buffer Exchange: A Method for Screening of Proteins, Protein Complexes, and Cell Lysates by Native Mass Spectrometry		4