

# Erik Procko

## List of Publications by Citations

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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.

46  
papers

2,041  
citations

22  
h-index

45  
g-index

57  
ext. papers

2,590  
ext. citations

9.4  
avg, IF

5.52  
L-index

#	Paper	IF	Citations
46	The ankyrin repeats of TRPV1 bind multiple ligands and modulate channel sensitivity. <i>Neuron</i> , <b>2007</b> , 54, 905-18	13.9	314
45	Engineering human ACE2 to optimize binding to the spike protein of SARS coronavirus 2. <i>Science</i> , <b>2020</b> , 369, 1261-1265	33.3	269
44	Chromatin remodeling, measured by a novel real-time polymerase chain reaction assay, across the proximal promoter region of the IL-2 gene. <i>Journal of Immunology</i> , <b>2001</b> , 167, 4494-503	5.3	176
43	The mechanism of ABC transporters: general lessons from structural and functional studies of an antigenic peptide transporter. <i>FASEB Journal</i> , <b>2009</b> , 23, 1287-302	0.9	135
42	Distinct structural and functional properties of the ATPase sites in an asymmetric ABC transporter. <i>Molecular Cell</i> , <b>2006</b> , 24, 51-62	17.6	128
41	A computationally designed inhibitor of an Epstein-Barr viral Bcl-2 protein induces apoptosis in infected cells. <i>Cell</i> , <b>2014</b> , 157, 1644-1656	56.2	96
40	Distinct properties of Ca <sup>2+</sup> -calmodulin binding to N- and C-terminal regulatory regions of the TRPV1 channel. <i>Journal of General Physiology</i> , <b>2012</b> , 140, 541-55	3.4	81
39	Structural and energetic basis of folded-protein transport by the FimD usher. <i>Nature</i> , <b>2013</b> , 496, 243-6	50.4	78
38	Computational design of a protein-based enzyme inhibitor. <i>Journal of Molecular Biology</i> , <b>2013</b> , 425, 3563-75	37.5	71
37	Structural and biochemical consequences of disease-causing mutations in the ankyrin repeat domain of the human TRPV4 channel. <i>Biochemistry</i> , <b>2012</b> , 51, 6195-206	3.2	63
36	An engineered decoy receptor for SARS-CoV-2 broadly binds protein S sequence variants. <i>Science Advances</i> , <b>2021</b> , 7,	14.3	58
35	Computationally designed high specificity inhibitors delineate the roles of BCL2 family proteins in cancer. <i>ELife</i> , <b>2016</b> , 5,	8.9	52
34	Identification of domain boundaries within the N-termini of TAP1 and TAP2 and their importance in tapasin binding and tapasin-mediated increase in peptide loading of MHC class I. <i>Immunology and Cell Biology</i> , <b>2005</b> , 83, 475-82	5	45
33	The sequence of human ACE2 is suboptimal for binding the S spike protein of SARS coronavirus 2 <b>2020</b> ,		43
32	Antigen processing and presentation: TAPPING into ABC transporters. <i>Current Opinion in Immunology</i> , <b>2009</b> , 21, 84-91	7.8	40
31	Mapping Interaction Sites on Human Chemokine Receptors by Deep Mutational Scanning. <i>Journal of Immunology</i> , <b>2018</b> , 200, 3825-3839	5.3	38
30	Deep Mutational Scans as a Guide to Engineering High Affinity T Cell Receptor Interactions with Peptide-bound Major Histocompatibility Complex. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 24566-24578	5.4	36

29	Leukocytes on the move with phosphoinositide 3-kinase and its downstream effectors. <i>BioEssays</i> , <b>2005</b> , 27, 153-63	4.1	35
28	Structural architecture of a dimeric class C GPCR based on co-trafficking of sweet taste receptor subunits. <i>Journal of Biological Chemistry</i> , <b>2019</b> , 294, 4759-4774	5.4	30
27	Intracellular delivery system for antibody-Peptide drug conjugates. <i>Molecular Therapy</i> , <b>2015</b> , 23, 907-917	11.7	28
26	Motif-Driven Design of Protein-Protein Interfaces. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1414, 285-304	1.4	26
25	Molecular determinants of chaperone interactions on MHC-I for folding and antigen repertoire selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 25602-25613	11.5	24
24	Insights into the roles of conserved and divergent residues in the ankyrin repeats of TRPV ion channels. <i>Channels</i> , <b>2007</b> , 1, 148-51	3	20
23	An Engineered Switch in T Cell Receptor Specificity Leads to an Unusual but Functional Binding Geometry. <i>Structure</i> , <b>2016</b> , 24, 1142-1154	5.2	19
22	Identifying mutation hotspots reveals pathogenetic mechanisms of KCNQ2 epileptic encephalopathy. <i>Scientific Reports</i> , <b>2020</b> , 10, 4756	4.9	18
21	Functionally important interactions between the nucleotide-binding domains of an antigenic peptide transporter. <i>Biochemistry</i> , <b>2008</b> , 47, 5699-708	3.2	15
20	An engineered decoy receptor for SARS-CoV-2 broadly binds protein S sequence variants <b>2020</b> ,		15
19	Reduced axonal surface expression and phosphoinositide sensitivity in K7 channels disrupts their function to inhibit neuronal excitability in Kcnq2 epileptic encephalopathy. <i>Neurobiology of Disease</i> , <b>2018</b> , 118, 76-93	7.5	13
18	Stretch-activated ion channels identified in the touch-sensitive structures of carnivorous Droseraceae plants. <i>ELife</i> , <b>2021</b> , 10,	8.9	11
17	Engineered ACE2 decoy mitigates lung injury and death induced by SARS-CoV-2 variants.. <i>Nature Chemical Biology</i> , <b>2022</b> ,	11.7	10
16	TAPBPR promotes antigen loading on MHC-I molecules using a peptide trap. <i>Nature Communications</i> , <b>2021</b> , 12, 3174	17.4	9
15	Conformational Engineering of HIV-1 Env Based on Mutational Tolerance in the CD4 and PG16 Bound States. <i>Journal of Virology</i> , <b>2019</b> , 93,	6.6	7
14	Engineered receptors for human cytomegalovirus that are orthogonal to normal human biology. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008647	7.6	7
13	Deep mutagenesis in the study of COVID-19: a technical overview for the proteomics community. <i>Expert Review of Proteomics</i> , <b>2020</b> , 17, 633-638	4.2	5
12	Computationally Designed ACE2 Decoy Receptor Binds SARS-CoV-2 Spike (S) Protein with Tight Nanomolar Affinity. <i>Journal of Chemical Information and Modeling</i> , <b>2021</b> , 61, 4656-4669	6.1	5

11	ACE2-based decoy receptors for SARS coronavirus 2. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2021</b> , 89, 1065-1078	4.2	4
10	Deep Mutational Scanning of Viral Glycoproteins and Their Host Receptors. <i>Frontiers in Molecular Biosciences</i> , <b>2021</b> , 8, 636660	5.6	3
9	The Substrate Import Mechanism of the Human Serotonin Transporter		2
8	Stretch-activated ion channels identified in the touch-sensitive structures of carnivorous Droseraceae plants		1
7	TAPBPR Promotes Antigen Loading on MHC-I Molecules Using a Peptide Trap		1
6	Deep Mutagenesis of a Transporter for Uptake of a Non-Native Substrate Identifies Conformationally Dynamic Regions		1
5	The Ile191Val is a partial loss-of-function variant of the TAS1R2 sweet-taste receptor and is associated with reduced glucose excursions in humans. <i>Molecular Metabolism</i> , <b>2021</b> , 54, 101339	8.8	1
4	Engineered High-Affinity ACE2 Peptide Mitigates ARDS and Death Induced by Multiple SARS-CoV-2 Variants. <b>2021</b> ,		1
3	Machine learning guided design of high affinity ACE2 decoys for SARS-CoV-2 neutralization. <b>2021</b> ,		1
2	A tethered ligand assay to probe SARS-CoV-2:ACE2 interactions.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2022</b> , 119, e2114397119	11.5	0
1	Engineering Proteins by Combining Deep Mutational Scanning and Yeast Display.. <i>Methods in Molecular Biology</i> , <b>2022</b> , 2491, 117-142	1.4	0