

Erik Procko

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

2,983
citations

236925

25
h-index

265206

42
g-index

57
all docs

57
docs citations

57
times ranked

4510
citing authors

#	ARTICLE	IF	CITATIONS
1	Engineering human ACE2 to optimize binding to the spike protein of SARS coronavirus 2. <i>Science</i> , 2020, 369, 1261-1265.	12.6	520
2	The Ankyrin Repeats of TRPV1 Bind Multiple Ligands and Modulate Channel Sensitivity. <i>Neuron</i> , 2007, 54, 905-918.	8.1	377
3	Chromatin Remodeling, Measured by a Novel Real-Time Polymerase Chain Reaction Assay, Across the Proximal Promoter Region of the <i>IL-2</i> Gene. <i>Journal of Immunology</i> , 2001, 167, 4494-4503.	0.8	184
4	The mechanism of ABC transporters: general lessons from structural and functional studies of an antigenic peptide transporter. <i>FASEB Journal</i> , 2009, 23, 1287-1302.	0.5	155
5	Distinct Structural and Functional Properties of the ATPase Sites in an Asymmetric ABC Transporter. <i>Molecular Cell</i> , 2006, 24, 51-62.	9.7	134
6	A Computationally Designed Inhibitor of an Epstein-Barr Viral Bcl-2 Protein Induces Apoptosis in Infected Cells. <i>Cell</i> , 2014, 157, 1644-1656.	28.9	118
7	An engineered decoy receptor for SARS-CoV-2 broadly binds protein S sequence variants. <i>Science Advances</i> , 2021, 7, .	10.3	117
8	Distinct properties of Ca ²⁺ -calmodulin binding to N- and C-terminal regulatory regions of the TRPV1 channel. <i>Journal of General Physiology</i> , 2012, 140, 541-555.	1.9	94
9	Structural and energetic basis of folded-protein transport by the FimD usher. <i>Nature</i> , 2013, 496, 243-246.	27.8	88
10	Computational Design of a Protein-Based Enzyme Inhibitor. <i>Journal of Molecular Biology</i> , 2013, 425, 3563-3575.	4.2	85
11	Structural and Biochemical Consequences of Disease-Causing Mutations in the Ankyrin Repeat Domain of the Human TRPV4 Channel. <i>Biochemistry</i> , 2012, 51, 6195-6206.	2.5	84
12	Computationally designed high specificity inhibitors delineate the roles of BCL2 family proteins in cancer. <i>ELife</i> , 2016, 5, .	6.0	65
13	Engineered ACE2 decoy mitigates lung injury and death induced by SARS-CoV-2 variants. <i>Nature Chemical Biology</i> , 2022, 18, 342-351.	8.0	63
14	Mapping Interaction Sites on Human Chemokine Receptors by Deep Mutational Scanning. <i>Journal of Immunology</i> , 2018, 200, 3825-3839.	0.8	62
15	Structural architecture of a dimeric class C GPCR based on co-trafficking of sweet taste receptor subunits. <i>Journal of Biological Chemistry</i> , 2019, 294, 4759-4774.	3.4	48
16	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> , 2005, 83, 475-482.	2.3	47
17	Antigen processing and presentation: TAPping into ABC transporters. <i>Current Opinion in Immunology</i> , 2009, 21, 84-91.	5.5	44
18	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> , 2019, 116, 25602-25613.	7.1	43

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19	Stretch-activated ion channels identified in the touch-sensitive structures of carnivorous Droseraceae plants. <i>ELife</i> , 2021, 10, .	6.0	43
20	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> , 2016, 291, 24566-24578.	3.4	42
21	Identifying mutation hotspots reveals pathogenetic mechanisms of KCNQ2 epileptic encephalopathy. <i>Scientific Reports</i> , 2020, 10, 4756.	3.3	42
22	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> , 2022, 119, e2114397119.	7.1	38
23	Leukocytes on the move with phosphoinositide 3-kinase and its downstream effectors. <i>BioEssays</i> , 2005, 27, 153-163.	2.5	36
24	Motif-Driven Design of Protein-Protein Interfaces. <i>Methods in Molecular Biology</i> , 2016, 1414, 285-304.	0.9	34
25	Intracellular Delivery System for Antibody-Peptide Drug Conjugates. <i>Molecular Therapy</i> , 2015, 23, 907-917.	8.2	33
26	TAPBPR promotes antigen loading on MHC-I molecules using a peptide trap. <i>Nature Communications</i> , 2021, 12, 3174.	12.8	33
27	Computationally Designed ACE2 Decoy Receptor Binds SARS-CoV-2 Spike (S) Protein with Tight Nanomolar Affinity. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 4656-4669.	5.4	24
28	Insights into the Roles of Conserved and Divergent Residues in the Ankyrin Repeats of TRPV Ion Channels. <i>Channels</i> , 2007, 1, 148-151.	2.8	23
29	Reduced axonal surface expression and phosphoinositide sensitivity in Kv7 channels disrupts their function to inhibit neuronal excitability in Kcnq2 epileptic encephalopathy. <i>Neurobiology of Disease</i> , 2018, 118, 76-93.	4.4	23
30	ACE2-based decoy receptors for SARS coronavirus 2. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1065-1078.	2.6	23
31	An Engineered Switch in T Cell Receptor Specificity Leads to an Unusual but Functional Binding Geometry. <i>Structure</i> , 2016, 24, 1142-1154.	3.3	22
32	The substrate import mechanism of the human serotonin transporter. <i>Biophysical Journal</i> , 2022, 121, 715-730.	0.5	21
33	Functionally Important Interactions between the Nucleotide-Binding Domains of an Antigenic Peptide Transporter. <i>Biochemistry</i> , 2008, 47, 5699-5708.	2.5	15
34	TAPBPR employs a ligand-independent docking mechanism to chaperone MR1 molecules. <i>Nature Chemical Biology</i> , 2022, 18, 859-868.	8.0	15
35	Conformational Engineering of HIV-1 Env Based on Mutational Tolerance in the CD4 and PG16 Bound States. <i>Journal of Virology</i> , 2019, 93, .	3.4	14
36	Deep Mutational Scanning of Viral Glycoproteins and Their Host Receptors. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 636660.	3.5	12

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37	Engineered receptors for human cytomegalovirus that are orthogonal to normal human biology. PLoS Pathogens, 2020, 16, e1008647.	4.7	11
38	Structural Rearrangement of the Serotonin Transporter Intracellular Gate Induced by Thr276 Phosphorylation. ACS Chemical Neuroscience, 2022, 13, 933-945.	3.5	11
39	Deep mutagenesis in the study of COVID-19: a technical overview for the proteomics community. Expert Review of Proteomics, 2020, 17, 633-638.	3.0	10
40	The Ile191Val is a partial loss-of-function variant of the TAS1R2 sweet-taste receptor and is associated with reduced glucose excursions in humans. Molecular Metabolism, 2021, 54, 101339.	6.5	10
41	Engineering Proteins by Combining Deep Mutational Scanning and Yeast Display. Methods in Molecular Biology, 2022, 2491, 117-142.	0.9	2
42	Computationally engineered ACE2 decoy binds with nanomolar affinity with the SARS-CoV-2 spike protein. Biophysical Journal, 2022, 121, 422a.	0.5	1