

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	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
2	The substrate import mechanism of the human serotonin transporter. <i>Biophysical Journal</i> , 2022, 121, 715-730.	0.5	21
3	Computationally engineered ACE2 decoy binds with nanomolar affinity with the SARS-CoV-2 spike protein. <i>Biophysical Journal</i> , 2022, 121, 422a.	0.5	1
4	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
5	Structural Rearrangement of the Serotonin Transporter Intracellular Gate Induced by Thr276 Phosphorylation. <i>ACS Chemical Neuroscience</i> , 2022, 13, 933-945.	3.5	11
6	Engineering Proteins by Combining Deep Mutational Scanning and Yeast Display. <i>Methods in Molecular Biology</i> , 2022, 2491, 117-142.	0.9	2
7	TAPBPR employs a ligand-independent docking mechanism to chaperone MR1 molecules. <i>Nature Chemical Biology</i> , 2022, 18, 859-868.	8.0	15
8	An engineered decoy receptor for SARS-CoV-2 broadly binds protein S sequence variants. <i>Science Advances</i> , 2021, 7, .	10.3	117
9	Stretch-activated ion channels identified in the touch-sensitive structures of carnivorous Droseraceae plants. <i>ELife</i> , 2021, 10, .	6.0	43
10	Deep Mutational Scanning of Viral Glycoproteins and Their Host Receptors. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 636660.	3.5	12
11	<scp>ACE2-based</scp> decoy receptors for <scp>SARS</scp> coronavirus 2. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1065-1078.	2.6	23
12	TAPBPR promotes antigen loading on MHC-I molecules using a peptide trap. <i>Nature Communications</i> , 2021, 12, 3174.	12.8	33
13	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
14	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> , 2021, 54, 101339.	6.5	10
15	Engineering human ACE2 to optimize binding to the spike protein of SARS coronavirus 2. <i>Science</i> , 2020, 369, 1261-1265.	12.6	520
16	Deep mutagenesis in the study of COVID-19: a technical overview for the proteomics community. <i>Expert Review of Proteomics</i> , 2020, 17, 633-638.	3.0	10
17	Engineered receptors for human cytomegalovirus that are orthogonal to normal human biology. <i>PLoS Pathogens</i> , 2020, 16, e1008647.	4.7	11
18	Identifying mutation hotspots reveals pathogenetic mechanisms of KCNQ2 epileptic encephalopathy. <i>Scientific Reports</i> , 2020, 10, 4756.	3.3	42

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19	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
20	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
21	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
22	Mapping Interaction Sites on Human Chemokine Receptors by Deep Mutational Scanning. <i>Journal of Immunology</i> , 2018, 200, 3825-3839.	0.8	62
23	Reduced axonal surface expression and phosphoinositide sensitivity in K v 7 channels disrupts their function to inhibit neuronal excitability in Kcnq2 epileptic encephalopathy. <i>Neurobiology of Disease</i> , 2018, 118, 76-93.	4.4	23
24	Computationally designed high specificity inhibitors delineate the roles of BCL2 family proteins in cancer. <i>ELife</i> , 2016, 5, .	6.0	65
25	Motif-Driven Design of Protein-Protein Interfaces. <i>Methods in Molecular Biology</i> , 2016, 1414, 285-304.	0.9	34
26	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
27	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
28	Intracellular Delivery System for Antibody-Peptide Drug Conjugates. <i>Molecular Therapy</i> , 2015, 23, 907-917.	8.2	33
29	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
30	Computational Design of a Protein-Based Enzyme Inhibitor. <i>Journal of Molecular Biology</i> , 2013, 425, 3563-3575.	4.2	85
31	Structural and energetic basis of folded-protein transport by the FimD usher. <i>Nature</i> , 2013, 496, 243-246.	27.8	88
32	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
33	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
34	Antigen processing and presentation: TAPping into ABC transporters. <i>Current Opinion in Immunology</i> , 2009, 21, 84-91.	5.5	44
35	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
36	Functionally Important Interactions between the Nucleotide-Binding Domains of an Antigenic Peptide Transporter. <i>Biochemistry</i> , 2008, 47, 5699-5708.	2.5	15

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37	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
38	The Ankyrin Repeats of TRPV1 Bind Multiple Ligands and Modulate Channel Sensitivity. <i>Neuron</i> , 2007, 54, 905-918.	8.1	377
39	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
40	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
41	Leukocytes on the move with phosphoinositide 3-kinase and its downstream effectors. <i>BioEssays</i> , 2005, 27, 153-163.	2.5	36
42	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