Robert J Keenan

List of Publications by Year
in descending order

36 papers	3,869 citations	218677 26 h-index	345221 36 g-index
39 all docs	39 docs citations	39 times ranked	5820 citing authors

#	Article	IF	Citations
1	The mechanisms of integral membrane protein biogenesis. Nature Reviews Molecular Cell Biology, 2022, 23, 107-124.	37.0	100
2	An ER translocon for multi-pass membrane protein biogenesis. ELife, 2020, 9, .	6.0	85
3	The architecture of EMC reveals a path for membrane protein insertion. ELife, 2020, 9, .	6.0	81
4	A structural perspective on tail-anchored protein biogenesis by the GET pathway. Current Opinion in Structural Biology, 2018, 51, 195-202.	5.7	31
5	The GET System Inserts the Tail-Anchored Protein, SYP72, into Endoplasmic Reticulum Membranes. Plant Physiology, 2017, 173, 1137-1145.	4.8	24
6	Tail-Anchored Protein Insertion by a Single Get1/2 Heterodimer. Cell Reports, 2017, 20, 2287-2293.	6.4	24
7	Msp1 Is a Membrane Protein Dislocase for Tail-Anchored Proteins. Molecular Cell, 2017, 67, 194-202.e6.	9.7	90
8	Identification of Oxa1 Homologs Operating in the Eukaryotic Endoplasmic Reticulum. Cell Reports, 2017, 21, 3708-3716.	6.4	107
9	Data publication with the structural biology data grid supports live analysis. Nature Communications, 2016, 7, 10882.	12.8	113
10	Ubiquilins Chaperone and Triage Mitochondrial Membrane Proteins for Degradation. Molecular Cell, 2016, 63, 21-33.	9.7	203
11	A dual fluorescent reporter for the investigation of methionine mistranslation in live cells. Rna, 2016, 22, 467-476.	3.5	14
12	Conformational Chaperones for Structural Studies of Membrane Proteins Using Antibody Phage Display with Nanodiscs. Structure, 2016, 24, 300-309.	3.3	57
13	Structure of the Get3 targeting factor in complex with its membrane protein cargo. Science, 2015, 347, 1152-1155.	12.6	100
14	Fission yeast profilin is tailored to facilitate actin assembly by the cytokinesis formin Cdc12. Molecular Biology of the Cell, 2015, 26, 283-293.	2.1	9
15	A YidC-like Protein in the Archaeal Plasma Membrane. Structure, 2015, 23, 1715-1724.	3.3	65
16	A Conserved Archaeal Pathway for Tailâ€Anchored Membrane Protein Insertion. Traffic, 2011, 12, 1119-1123.	2.7	13
17	Tail-anchored membrane protein insertion into the endoplasmic reticulum. Nature Reviews Molecular Cell Biology, 2011, 12, 787-798.	37.0	257
18	Noncytotoxic DsRed Derivatives for Whole-Cell Labeling. Methods in Molecular Biology, 2011, 699, 355-370.	0.9	15

#	Article	IF	Citations
19	The mechanism of membrane-associated steps in tail-anchored protein insertion. Nature, 2011, 477, 61-66.	27.8	144
20	A ribosome-associating factor chaperones tail-anchored membrane proteins. Nature, 2010, 466, 1120-1124.	27.8	246
21	Chromophore Formation in DsRed Occurs by a Branched Pathway. Journal of the American Chemical Society, 2010, 132, 8496-8505.	13.7	70
22	A noncytotoxic DsRed variant for whole-cell labeling. Proceedings of SPIE, 2009, , .	0.8	1
23	Noncytotoxic orange and red/green derivatives of DsRed-Express2 for whole-cell labeling. BMC Biotechnology, 2009, 9, 32.	3.3	28
24	A Rapidly Maturing Far-Red Derivative of DsRed-Express2 for Whole-Cell Labeling. Biochemistry, 2009, 48, 8279-8281.	2.5	167
25	The structural basis of tail-anchored membrane protein recognition by Get3. Nature, 2009, 461, 361-366.	27.8	162
26	Spectral Diversity of Fluorescent Proteins from the Anthozoan Corynactis californica. Marine Biotechnology, 2008, 10, 328-342.	2.4	20
27	A noncytotoxic DsRed variant for whole-cell labeling. Nature Methods, 2008, 5, 955-957.	19.0	171
28	The Molecular Basis of Glyphosate Resistance by an Optimized Microbial Acetyltransferase. Journal of Biological Chemistry, 2007, 282, 11446-11455.	3.4	59
29	Structural rearrangements near the chromophore influence the maturation speed and brightness of DsRed variants. Protein Engineering, Design and Selection, 2007, 20, 525-534.	2.1	49
30	DNA shuffling as a tool for protein crystallization. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 8887-8892.	7.1	26
31	Laboratory-Directed Protein Evolution. Microbiology and Molecular Biology Reviews, 2005, 69, 373-392.	6.6	161
32	The Signal Recognition Particle. Annual Review of Biochemistry, 2001, 70, 755-775.	11.1	541
33	Structure of the phylogenetically most conserved domain of SRP RNA. Rna, 1999, 5, 1419-1429.	3.5	47
34	Functional changes in the structure of the SRP GTPase on binding GDP and Mg2+GDP. Nature Structural Biology, 1999, 6, 793-801.	9.7	83
35	Crystal Structure of the Signal Sequence Binding Subunit of the Signal Recognition Particle. Cell, 1998, 94, 181-191.	28.9	277
36	Structure of the conserved GTPase domain of the signal recognition particle. Nature, 1997, 385, 361-364.	27.8	228