

Trevor James Lithgow

List of Publications by Year in descending order

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237
papers

16,453
citations

12303

69
h-index

20900

115
g-index

256
all docs

256
docs citations

256
times ranked

15403
citing authors

#	ARTICLE	IF	CITATIONS
1	Importing Mitochondrial Proteins: Machineries and Mechanisms. <i>Cell</i> , 2009, 138, 628-644.	13.5	1,199
2	Evolution of the Molecular Machines for Protein Import into Mitochondria. <i>Science</i> , 2006, 313, 314-318.	6.0	487
3	The OXA1L protein family: modulating protein assembly, disassembly and translocation. <i>EMBO Reports</i> , 2004, 5, 567-571.	2.0	444
4	Structural insight into the biogenesis of β -barrel membrane proteins. <i>Nature</i> , 2013, 501, 385-390.	13.7	368
5	The Omp85 family of proteins is essential for outer membrane biogenesis in mitochondria and bacteria. <i>Journal of Cell Biology</i> , 2004, 164, 19-24.	2.3	335
6	Bacteriophage Transcytosis Provides a Mechanism To Cross Epithelial Cell Layers. <i>MBio</i> , 2017, 8, .	1.8	273
7	A protein complex containing Tho2, Hpr1, Mft1 and a novel protein, Thp2, connects transcription elongation with mitotic recombination in <i>Saccharomyces cerevisiae</i> . <i>EMBO Journal</i> , 2000, 19, 5824-5834.	3.5	267
8	PUF proteins: repression, activation and mRNA localization. <i>Trends in Cell Biology</i> , 2011, 21, 104-112.	3.6	263
9	Emerging rules for effective antimicrobial coatings. <i>Trends in Biotechnology</i> , 2014, 32, 82-90.	4.9	257
10	Molecular architecture and function of the Omp85 family of proteins. <i>Molecular Microbiology</i> , 2005, 58, 1216-1225.	1.2	204
11	Assembling the mitochondrial outer membrane. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 1044-1048.	3.6	196
12	MrkH, a Novel c-di-GMP-Dependent Transcriptional Activator, Controls <i>Klebsiella pneumoniae</i> Biofilm Formation by Regulating Type 3 Fimbriae Expression. <i>PLoS Pathogens</i> , 2011, 7, e1002204.	2.1	195
13	RAC, a stable ribosome-associated complex in yeast formed by the DnaK-DnaJ homologs Ssz1p and zuotin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 3762-3767.	3.3	194
14	Discovery of an archetypal protein transport system in bacterial outer membranes. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 506-510.	3.6	192
15	Role for yeast inhibitor of apoptosis (IAP)-like proteins in cell division. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 10170-10175.	3.3	186
16	Targeting of C-Terminal (Tail)-Anchored Proteins: Understanding how Cytoplasmic Activities are Anchored to Intracellular Membranes. <i>Traffic</i> , 2001, 2, 66-71.	1.3	178
17	Reconstitution of the initial steps of mitochondrial protein import. <i>Nature</i> , 1995, 376, 705-709.	13.7	176
18	Mas37p, a novel receptor subunit for protein import into mitochondria.. <i>Journal of Cell Biology</i> , 1995, 129, 25-34.	2.3	172

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19	Mitochondrial FtsZ in a Chromophyte Alga. <i>Science</i> , 2000, 287, 1276-1279.	6.0	169
20	Molecular architecture of the active mitochondrial protein gate. <i>Science</i> , 2015, 349, 1544-1548.	6.0	169
21	Self-assembly of ciprofloxacin and a tripeptide into an antimicrobial nanostructured hydrogel. <i>Biomaterials</i> , 2013, 34, 3678-3687.	5.7	162
22	Bacteriophage-resistant <i>Acinetobacter baumannii</i> are resensitized to antimicrobials. <i>Nature Microbiology</i> , 2021, 6, 157-161.	5.9	159
23	The mitochondrial outer membrane protein Mas22p is essential for protein import and viability of yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 11973-11977.	3.3	158
24	The protein import receptor of mitochondria. <i>Trends in Biochemical Sciences</i> , 1995, 20, 98-101.	3.7	157
25	Bipartite Signals Mediate Subcellular Targeting of Tail-anchored Membrane Proteins in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 8219-8223.	1.6	156
26	Mitochondrial Release of Pro-apoptotic Proteins. <i>Journal of Biological Chemistry</i> , 2005, 280, 2266-2274.	1.6	154
27	<i>Quokka</i> : a comprehensive tool for rapid and accurate prediction of kinase family-specific phosphorylation sites in the human proteome. <i>Bioinformatics</i> , 2018, 34, 4223-4231.	1.8	151
28	Distinct Roles for the Hsp40 and Hsp90 Molecular Chaperones during Cystic Fibrosis Transmembrane Conductance Regulator Degradation in Yeast. <i>Molecular Biology of the Cell</i> , 2004, 15, 4787-4797.	0.9	149
29	Structure of the mitochondrial import gate reveals distinct preprotein paths. <i>Nature</i> , 2019, 575, 395-401.	13.7	146
30	POSSUM: a bioinformatics toolkit for generating numerical sequence feature descriptors based on PSSM profiles. <i>Bioinformatics</i> , 2017, 33, 2756-2758.	1.8	145
31	<i>Giardia</i> mitosomes and trichomonad hydrogenosomes share a common mode of protein targeting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10924-10929.	3.3	141
32	The yeast nascent polypeptide-associated complex initiates protein targeting to mitochondria in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 2296-2301.	3.3	140
33	Evolution of the β -barrel assembly machinery. <i>Trends in Microbiology</i> , 2012, 20, 612-620.	3.5	139
34	A Complete Set of SNAREs in Yeast. <i>Traffic</i> , 2004, 5, 45-52.	1.3	135
35	Filamentous phages: masters of a microbial sharing economy. <i>EMBO Reports</i> , 2019, 20, .	2.0	128
36	The Minimal Proteome in the Reduced Mitochondrion of the Parasitic Protist <i>Giardia intestinalis</i> . <i>PLoS ONE</i> , 2011, 6, e17285.	1.1	122

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37	Microsporidian mitosomes retain elements of the general mitochondrial targeting system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15916-15920.	3.3	121
38	Atlas of group A streptococcal vaccine candidates compiled using large-scale comparative genomics. <i>Nature Genetics</i> , 2019, 51, 1035-1043.	9.4	120
39	Convergent Evolution of Receptors for Protein Import into Mitochondria. <i>Current Biology</i> , 2006, 16, 221-229.	1.8	118
40	The mitochondrial import protein Mim1 promotes biogenesis of multispinning outer membrane proteins. <i>Journal of Cell Biology</i> , 2011, 194, 387-395.	2.3	117
41	The Peripheral Membrane Subunits of the SAM Complex Function Codependently in Mitochondrial Outer Membrane Biogenesis. <i>Molecular Biology of the Cell</i> , 2008, 19, 126-136.	0.9	115
42	Cell wall integrity is linked to mitochondria and phospholipid homeostasis in <i>Candida albicans</i> through the activity of the posttranscriptional regulator Ccr4 ^{Pop2} . <i>Molecular Microbiology</i> , 2011, 79, 968-989.	1.2	115
43	Targeting of proteins to mitochondria. <i>FEBS Letters</i> , 2000, 476, 22-26.	1.3	114
44	Formation and function of bacterial organelles. <i>Nature Reviews Microbiology</i> , 2020, 18, 677-689.	13.6	112
45	Bastion6: a bioinformatics approach for accurate prediction of type VI secreted effectors. <i>Bioinformatics</i> , 2018, 34, 2546-2555.	1.8	108
46	Outer membrane vesicles from <i>Neisseria gonorrhoeae</i> target PorB to mitochondria and induce apoptosis. <i>PLoS Pathogens</i> , 2018, 14, e1006945.	2.1	105
47	Proapoptotic BH3-only proteins trigger membrane integration of prosurvival Bcl-w and neutralize its activity. <i>Journal of Cell Biology</i> , 2003, 162, 877-888.	2.3	104
48	Mitochondrial Preprotein Translocase of Trypanosomatids Has a Bacterial Origin. <i>Current Biology</i> , 2011, 21, 1738-1743.	1.8	104
49	Tom22', an 8-kDa trans-Site Receptor in Plants and Protozoans, Is a Conserved Feature of the TOM Complex That Appeared Early in the Evolution of Eukaryotes. <i>Molecular Biology and Evolution</i> , 2004, 21, 1557-1564.	3.5	101
50	Evolution of macromolecular import pathways in mitochondria, hydrogenosomes and mitosomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 799-817.	1.8	101
51	The Yeast Mitochondrial Protein Import Receptor Mas20p Binds Precursor Proteins through Electrostatic Interaction with the Positively Charged Presequence. <i>Journal of Biological Chemistry</i> , 1995, 270, 5565-5570.	1.6	100
52	The C-terminal TPR Domain of Tom70 Defines a Family of Mitochondrial Protein Import Receptors Found only in Animals and Fungi. <i>Journal of Molecular Biology</i> , 2006, 358, 1010-1022.	2.0	97
53	Reconstitution of Membrane Proteins into Model Membranes: Seeking Better Ways to Retain Protein Activities. <i>International Journal of Molecular Sciences</i> , 2013, 14, 1589-1607.	1.8	95
54	The Single Mitochondrial Porin of <i>Trypanosoma brucei</i> is the Main Metabolite Transporter in the Outer Mitochondrial Membrane. <i>Molecular Biology and Evolution</i> , 2008, 26, 671-680.	3.5	94

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55	A SNARE required for retrograde transport to the endoplasmic reticulum. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9873-9877.	3.3	91
56	Tom40, the import channel of the mitochondrial outer membrane, plays an active role in sorting imported proteins. EMBO Journal, 2003, 22, 2380-2386.	3.5	89
57	Mature DIABLO/Smac Is Produced by the IMP Protease Complex on the Mitochondrial Inner Membrane. Molecular Biology of the Cell, 2005, 16, 2926-2933.	0.9	89
58	The Transmembrane Segment of Tom20 Is Recognized by Mim1 for Docking to the Mitochondrial TOM Complex. Journal of Molecular Biology, 2008, 376, 694-704.	2.0	88
59	The nascent polypeptide-associated complex (NAC) promotes interaction of ribosomes with the mitochondrial surface in vivo. FEBS Letters, 2002, 516, 213-216.	1.3	87
60	Bacterial Proteins Predisposed for Targeting to Mitochondria. Molecular Biology and Evolution, 2004, 21, 652-658.	3.5	86
61	Conserved Motifs Reveal Details of Ancestry and Structure in the Small TIM Chaperones of the Mitochondrial Intermembrane Space. Molecular Biology and Evolution, 2007, 24, 1149-1160.	3.5	86
62	Dynamic Association of BAM Complex Modules Includes Surface Exposure of the Lipoprotein BamC. Journal of Molecular Biology, 2012, 422, 545-555.	2.0	79
63	How Do Plant Mitochondria Avoid Importing Chloroplast Proteins? Components of the Import Apparatus Tom20 and Tom22 from Arabidopsis Differ from Their Fungal Counterparts1. Plant Physiology, 2000, 123, 811-816.	2.3	78
64	The alpha and the beta: protein translocation across mitochondrial and plastid outer membranes. Trends in Biochemical Sciences, 2001, 26, 36-40.	3.7	78
65	The Type II Secretion System and Its Ubiquitous Lipoprotein Substrate, SslE, Are Required for Biofilm Formation and Virulence of Enteropathogenic Escherichia coli. Infection and Immunity, 2012, 80, 2042-2052.	1.0	78
66	A comprehensive analysis of the Omp85/TpsB protein superfamily structural diversity, taxonomic occurrence, and evolution. Frontiers in Microbiology, 2014, 5, 370.	1.5	78
67	Protein import into mitochondria: origins and functions today (Review). Molecular Membrane Biology, 2005, 22, 87-100.	2.0	76
68	Protein secretion and outer membrane assembly in <i>Alphaproteobacteria</i> . FEMS Microbiology Reviews, 2008, 32, 995-1009.	3.9	76
69	Eliminating Legionella by inhibiting BCL-XL to induce macrophage apoptosis. Nature Microbiology, 2016, 1, 15034.	5.9	75
70	The direct route: a simplified pathway for protein import into the mitochondrion of trypanosomes. Trends in Cell Biology, 2008, 18, 12-18.	3.6	73
71	The Major Surface-Associated Saccharides of Klebsiella pneumoniae Contribute to Host Cell Association. PLoS ONE, 2008, 3, e3817.	1.1	72
72	The WD40 Protein BamB Mediates Coupling of BAM Complexes into Assembly Precincts in the Bacterial Outer Membrane. Cell Reports, 2018, 23, 2782-2794.	2.9	72

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73	Reconstitution of a nanomachine driving the assembly of proteins into bacterial outer membranes. <i>Nature Communications</i> , 2014, 5, 5078.	5.8	71
74	Twenty years of bioinformatics research for protease-specific substrate and cleavage site prediction: a comprehensive revisit and benchmarking of existing methods. <i>Briefings in Bioinformatics</i> , 2019, 20, 2150-2166.	3.2	70
75	The Core Components of Organelle Biogenesis and Membrane Transport in the Hydrogenosomes of <i>Trichomonas vaginalis</i> . <i>PLoS ONE</i> , 2011, 6, e24428.	1.1	69
76	GlycoMinestruct: a new bioinformatics tool for highly accurate mapping of the human N-linked and O-linked glycoproteomes by incorporating structural features. <i>Scientific Reports</i> , 2016, 6, 34595.	1.6	69
77	Bastion3: a two-layer ensemble predictor of type III secreted effectors. <i>Bioinformatics</i> , 2019, 35, 2017-2028.	1.8	69
78	An Outbreak of Carbapenem-Resistant and Hypervirulent <i>Klebsiella pneumoniae</i> in an Intensive Care Unit of a Major Teaching Hospital in Wenzhou, China. <i>Frontiers in Public Health</i> , 2019, 7, 229.	1.3	67
79	Targeting of tail-anchored proteins to yeast mitochondria in vivo. <i>FEBS Letters</i> , 1999, 451, 243-248.	1.3	66
80	A Bioinformatic Strategy for the Detection, Classification and Analysis of Bacterial Autotransporters. <i>PLoS ONE</i> , 2012, 7, e43245.	1.1	65
81	The evolution of new lipoprotein subunits of the bacterial outer membrane BAM complex. <i>Molecular Microbiology</i> , 2012, 84, 832-844.	1.2	65
82	Assembly of β -barrel proteins into bacterial outer membranes. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 1542-1550.	1.9	65
83	Systematic analysis and prediction of type IV secreted effector proteins by machine learning approaches. <i>Briefings in Bioinformatics</i> , 2019, 20, 931-951.	3.2	65
84	The Twists and Turns of Maurer's Cleft Trafficking in <i>P. falciparum</i> -Infected Erythrocytes. <i>Traffic</i> , 2008, 9, 187-197.	1.3	64
85	The reducible complexity of a mitochondrial molecular machine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15791-15795.	3.3	64
86	The Essentials of Protein Import in the Degenerate Mitochondrion of <i>Entamoeba histolytica</i> . <i>PLoS Pathogens</i> , 2010, 6, e1000812.	2.1	64
87	<i>Legionella pneumophila</i> Secretes a Mitochondrial Carrier Protein during Infection. <i>PLoS Pathogens</i> , 2012, 8, e1002459.	2.1	64
88	A Modular BAM Complex in the Outer Membrane of the β -Proteobacterium <i>Caulobacter crescentus</i> . <i>PLoS ONE</i> , 2010, 5, e8619.	1.1	62
89	Evolution of the Translocation and Assembly Module (TAM). <i>Genome Biology and Evolution</i> , 2015, 7, 1628-1643.	1.1	62
90	Extensively Drug-Resistant <i>Klebsiella pneumoniae</i> Causing Nosocomial Bloodstream Infections in China: Molecular Investigation of Antibiotic Resistance Determinants, Informing Therapy, and Clinical Outcomes. <i>Frontiers in Microbiology</i> , 2017, 8, 1230.	1.5	61

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91	Positive-unlabelled learning of glycosylation sites in the human proteome. BMC Bioinformatics, 2019, 20, 112.	1.2	60
92	Structure, topology and function of the translocase of the outer membrane of mitochondria. Plant Physiology and Biochemistry, 2008, 46, 265-274.	2.8	59
93	The Protein Import Channel in the Outer Mitosomal Membrane of Giardia intestinalis. Molecular Biology and Evolution, 2009, 26, 1941-1947.	3.5	59
94	Assembly of the Type II Secretion System such as Found in Vibrio cholerae Depends on the Novel Pilotin AspS. PLoS Pathogens, 2013, 9, e1003117.	2.1	59
95	Delivery of nascent polypeptides to the mitochondrial surface. Biochimica Et Biophysica Acta - Molecular Cell Research, 2002, 1592, 35-39.	1.9	58
96	Structural Basis of Type 2 Secretion System Engagement between the Inner and Outer Bacterial Membranes. MBio, 2017, 8, .	1.8	58
97	Mitochondrial Sorting and Assembly Machinery Subunit Sam37 in Candida albicans: Insight into the Roles of Mitochondria in Fitness, Cell Wall Integrity, and Virulence. Eukaryotic Cell, 2012, 11, 532-544.	3.4	57
98	Zim17, a Novel Zinc Finger Protein Essential for Protein Import into Mitochondria. Journal of Biological Chemistry, 2004, 279, 50243-50249.	1.6	54
99	Minor modifications and major adaptations: The evolution of molecular machines driving mitochondrial protein import. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 947-954.	1.4	54
100	Highways for protein delivery to the mitochondria. Trends in Biochemical Sciences, 1997, 22, 110-113.	3.7	53
101	Patterns that Define the Four Domains Conserved in Known and Novel Isoforms of the Protein Import Receptor Tom20. Journal of Molecular Biology, 2005, 347, 81-93.	2.0	53
102	Both the p33 and p55 Subunits of the Helicobacter pylori VacA Toxin Are Targeted to Mammalian Mitochondria. Journal of Molecular Biology, 2010, 401, 792-798.	2.0	53
103	Effective assembly of fimbriae in Escherichia coli depends on the translocation assembly module nanomachine. Nature Microbiology, 2016, 1, 16064.	5.9	52
104	Systems Biology: The Next Frontier for Bioinformatics. Advances in Bioinformatics, 2010, 2010, 1-10.	5.7	51
105	Comprehensive assessment and performance improvement of effector protein predictors for bacterial secretion systems III, IV and VI. Briefings in Bioinformatics, 2018, 19, bbw100.	3.2	51
106	Integral membrane proteins in the mitochondrial outer membrane of Saccharomyces cerevisiae. FEBS Journal, 2006, 273, 1507-1515.	2.2	50
107	Environmental stresses inhibit and stimulate different protein import pathways in plant mitochondria. FEBS Letters, 2003, 547, 125-130.	1.3	47
108	Evidence of a Reduced and Modified Mitochondrial Protein Import Apparatus in Microsporidian Mitosomes. Eukaryotic Cell, 2009, 8, 19-26.	3.4	47

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109	Assembly of the secretion pores <i>GspD</i> , <i>Wza</i> and <i>CsgG</i> into bacterial outer membranes does not require the <i>Omp85</i> proteins <i>BamA</i> or <i>TamA</i> . <i>Molecular Microbiology</i> , 2015, 97, 616-629.	1.2	47
110	Porin Associates with Tom22 to Regulate the Mitochondrial Protein Gate Assembly. <i>Molecular Cell</i> , 2019, 73, 1044-1055.e8.	4.5	47
111	A mortise-tenon joint in the transmembrane domain modulates autotransporter assembly into bacterial outer membranes. <i>Nature Communications</i> , 2014, 5, 4239.	5.8	46
112	Light-triggered release of ciprofloxacin from an in situ forming click hydrogel for antibacterial wound dressings. <i>Journal of Materials Chemistry B</i> , 2015, 3, 8771-8774.	2.9	46
113	A conserved proline residue is present in the transmembrane-spanning domain of Tom7 and other tail-anchored protein subunits of the TOM translocase. <i>FEBS Letters</i> , 2002, 514, 347-350.	1.3	44
114	Genome-scale metabolic modeling of responses to polymyxins in <i>Pseudomonas aeruginosa</i> . <i>GigaScience</i> , 2018, 7, .	3.3	44
115	Recognition of Mitochondrial Targeting Sequences by the Import Receptors Tom20 and Tom22. <i>Journal of Molecular Biology</i> , 2011, 405, 804-818.	2.0	43
116	Prebiotic-chemistry inspired polymer coatings for biomedical and material science applications. <i>NPG Asia Materials</i> , 2015, 7, e225-e225.	3.8	41
117	Global Trends in Proteome Remodeling of the Outer Membrane Modulate Antimicrobial Permeability in <i>Klebsiella pneumoniae</i> . <i>MBio</i> , 2020, 11, .	1.8	41
118	Tinkering Inside the Organelle. <i>Science</i> , 2010, 327, 649-650.	6.0	40
119	Nanomechanics measurements of live bacteria reveal a mechanism for bacterial cell protection: the polysaccharide capsule in <i>Klebsiella</i> is a responsive polymer hydrogel that adapts to osmotic stress. <i>Soft Matter</i> , 2013, 9, 7560.	1.2	40
120	Conserved Features in the Structure, Mechanism, and Biogenesis of the Inverse Autotransporter Protein Family. <i>Genome Biology and Evolution</i> , 2016, 8, 1690-1705.	1.1	40
121	DeepVF: a deep learning-based hybrid framework for identifying virulence factors using the stacking strategy. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	40
122	Domain Organization of the Monomeric Form of the Tom70 Mitochondrial Import Receptor. <i>Journal of Molecular Biology</i> , 2009, 388, 1043-1058.	2.0	38
123	SecretEPDB: a comprehensive web-based resource for secreted effector proteins of the bacterial types III, IV and VI secretion systems. <i>Scientific Reports</i> , 2017, 7, 41031.	1.6	38
124	Re-assessing the locations of components of the classical vesicle-mediated trafficking machinery in transfected <i>Plasmodium falciparum</i> . <i>International Journal for Parasitology</i> , 2007, 37, 1127-1141.	1.3	37
125	Structural Basis for Linezolid Binding Site Rearrangement in the <i>Staphylococcus aureus</i> Ribosome. <i>MBio</i> , 2017, 8, .	1.8	37
126	PaCRISPR: a server for predicting and visualizing anti-CRISPR proteins. <i>Nucleic Acids Research</i> , 2020, 48, W348-W357.	6.5	37

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127	PeNGaRoo, a combined gradient boosting and ensemble learning framework for predicting non-classical secreted proteins. <i>Bioinformatics</i> , 2020, 36, 704-712.	1.8	36
128	Isolation and Characterization of <i>Klebsiella</i> Phages for Phage Therapy. <i>Phage</i> , 2021, 2, 26-42.	0.8	36
129	Conserved features in TamA enable interaction with TamB to drive the activity of the translocation and assembly module. <i>Scientific Reports</i> , 2015, 5, 12905.	1.6	35
130	Of linkers and autochaperones: an unambiguous nomenclature to identify common and uncommon themes for autotransporter secretion. <i>Molecular Microbiology</i> , 2015, 95, 1-16.	1.2	34
131	BastionHub: a universal platform for integrating and analyzing substrates secreted by Gram-negative bacteria. <i>Nucleic Acids Research</i> , 2021, 49, D651-D659.	6.5	34
132	The Structure of a Conserved Domain of TamB Reveals a Hydrophobic β^2 Taco Fold. <i>Structure</i> , 2017, 25, 1898-1906.e5.	1.6	33
133	Structure and Membrane Topography of the Vibrio-Type Secretin Complex from the Type 2 Secretion System of Enteropathogenic <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	33
134	Phylogenetic Analysis of <i>Klebsiella pneumoniae</i> from Hospitalized Children, Pakistan. <i>Emerging Infectious Diseases</i> , 2017, 23, 1872-1875.	2.0	32
135	Mft52, an Acid-bristle Protein in the Cytosol That Delivers Precursor Proteins to Yeast Mitochondria. <i>Journal of Biological Chemistry</i> , 1997, 272, 5320-5325.	1.6	31
136	Conserved substrate binding by chaperones in the bacterial periplasm and the mitochondrial intermembrane space. <i>Biochemical Journal</i> , 2008, 409, 377-387.	1.7	31
137	Antibacterial poly(ethylene glycol) hydrogels from combined epoxy-amine and thiol-ene click reaction. <i>Journal of Polymer Science Part A</i> , 2016, 54, 656-667.	2.5	31
138	Antibiotic regimen based on population analysis of residing persister cells eradicates <i>Staphylococcus epidermidis</i> biofilms. <i>Scientific Reports</i> , 2016, 5, 18578.	1.6	31
139	Polymyxins Bind to the Cell Surface of Unculturable <i>Acinetobacter baumannii</i> and Cause Unique Dependent Resistance. <i>Advanced Science</i> , 2020, 7, 2000704.	5.6	31
140	AcrDB: a database of anti-CRISPR operons in prokaryotes and viruses. <i>Nucleic Acids Research</i> , 2021, 49, D622-D629.	6.5	31
141	Targeting bacterial outer-membrane remodelling to impact antimicrobial drug resistance. <i>Trends in Microbiology</i> , 2022, 30, 544-552.	3.5	31
142	A model system for mitochondrial biogenesis reveals evolutionary rewiring of protein import and membrane assembly pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3358-66.	3.3	30
143	Evidence of Distinct Channel Conformations and Substrate Binding Affinities for the Mitochondrial Outer Membrane Protein Translocase Pore Tom40. <i>Journal of Biological Chemistry</i> , 2015, 290, 26204-26217.	1.6	30
144	Structural basis for substrate selection by the translocation and assembly module of the β -barrel assembly machinery. <i>Molecular Microbiology</i> , 2017, 106, 142-156.	1.2	29

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145	Investigation of LuxS-mediated quorum sensing in <i>Klebsiella pneumoniae</i> . <i>Journal of Medical Microbiology</i> , 2020, 69, 402-413.	0.7	29
146	The three domains of the mitochondrial outer membrane protein Mim1 have discrete functions in assembly of the TOM complex. <i>FEBS Letters</i> , 2009, 583, 1475-1480.	1.3	28
147	The architecture and stabilisation of flagellotropic tailed bacteriophages. <i>Nature Communications</i> , 2020, 11, 3748.	5.8	28
148	Mechanistic Insights into the Capsule-Targeting Depolymerase from a <i>Klebsiella pneumoniae</i> Bacteriophage. <i>Microbiology Spectrum</i> , 2021, 9, e0102321.	1.2	28
149	Do cytosolic factors prevent promiscuity at the membrane surface?. <i>FEBS Letters</i> , 1993, 329, 1-4.	1.3	27
150	Using Hidden Markov Models to Discover New Protein Transport Machines. <i>Methods in Molecular Biology</i> , 2010, 619, 271-284.	0.4	27
151	Prechaperonin 60 and preornithine transcarbamylase share components of the import apparatus but have distinct maturation pathways in rat liver mitochondria. <i>FEBS Journal</i> , 1993, 211, 881-889.	0.2	26
152	A constitutive form of heat-shock protein 70 is located in the outer membranes of mitochondria from rat liver. <i>FEBS Letters</i> , 1993, 332, 277-281.	1.3	26
153	Ancestral and Derived Protein Import Pathways in the Mitochondrion of <i>Reclinomonas americana</i> . <i>Molecular Biology and Evolution</i> , 2011, 28, 1581-1591.	3.5	26
154	An essential novel component of the noncanonical mitochondrial outer membrane protein import system of trypanosomatids. <i>Molecular Biology of the Cell</i> , 2012, 23, 3420-3428.	0.9	26
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