

# 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	Targeting bacterial outer-membrane remodelling to impact antimicrobial drug resistance. Trends in Microbiology, 2022, 30, 544-552.	3.5	31
2	A noncanonical chaperone interacts with drug efflux pumps during their assembly into bacterial outer membranes. PLoS Biology, 2022, 20, e3001523.	2.6	6
3	Adaptation of the periplasm to maintain spatial constraints essential for cell envelope processes and cell viability. ELife, 2022, 11, .	2.8	17
4	Tall tails: cryo-electron microscopy of phage tail DNA ejection conduits. Biochemical Society Transactions, 2022, 50, 459-22W.	1.6	11
5	A Structurally Characterized <i>Staphylococcus aureus</i> Evolutionary Escape Route from Treatment with the Antibiotic Linezolid. Microbiology Spectrum, 2022, 10, .	1.2	4
6	Bacteriophages evolve enhanced persistence to a mucosal surface. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	17
7	DeepVF: a deep learning-based hybrid framework for identifying virulence factors using the stacking strategy. Briefings in Bioinformatics, 2021, 22, .	3.2	40
8	BastionHub: a universal platform for integrating and analyzing substrates secreted by Gram-negative bacteria. Nucleic Acids Research, 2021, 49, D651-D659.	6.5	34
9	AcrDB: a database of anti-CRISPR operons in prokaryotes and viruses. Nucleic Acids Research, 2021, 49, D622-D629.	6.5	31
10	AcrHub: an integrative hub for investigating, predicting and mapping anti-CRISPR proteins. Nucleic Acids Research, 2021, 49, D630-D638.	6.5	24
11	Bacteriophage-resistant <i>Acinetobacter baumannii</i> are resensitized to antimicrobials. Nature Microbiology, 2021, 6, 157-161.	5.9	159
12	Isolation and Characterization of <i>Klebsiella</i> Phages for Phage Therapy. Phage, 2021, 2, 26-42.	0.8	36
13	Three-Dimensional Micropatterning Deters Early Bacterial Adherence and Can Eliminate Colonization. ACS Applied Materials & Interfaces, 2021, 13, 23339-23351.	4.0	5
14	Component Parts of Bacteriophage Virions Accurately Defined by a Machine-Learning Approach Built on Evolutionary Features. MSystems, 2021, 6, e0024221.	1.7	6
15	The Carbapenemase BKC-1 from <i>Klebsiella pneumoniae</i> Is Adapted for Translocation by Both the Tat and Sec Translocons. MBio, 2021, 12, e0130221.	1.8	5
16	Why predicting secreted effectors and what they do is important. Physics of Life Reviews, 2021, 39, 85-87.	1.5	0
17	BonA from <i>Acinetobacter baumannii</i> Forms a Divisome-Localized Decamer That Supports Outer Envelope Function. MBio, 2021, 12, e0148021.	1.8	5
18	Mechanistic Insights into the Capsule-Targeting Depolymerase from a <i>Klebsiella pneumoniae</i> Bacteriophage. Microbiology Spectrum, 2021, 9, e0102321.	1.2	28

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19	Substrate-dependent arrangements of the subunits of the BAM complex determined by neutron reflectometry. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2021, 1863, 183587.	1.4	9
20	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
21	First description of antimicrobial resistance in carbapenem-susceptible <i>Klebsiella pneumoniae</i> after imipenem treatment, driven by outer membrane remodeling. <i>BMC Microbiology</i> , 2020, 20, 218.	1.3	14
22	Formation and function of bacterial organelles. <i>Nature Reviews Microbiology</i> , 2020, 18, 677-689.	13.6	112
23	The architecture and stabilisation of flagellotropic tailed bacteriophages. <i>Nature Communications</i> , 2020, 11, 3748.	5.8	28
24	PaCRISPR: a server for predicting and visualizing anti-CRISPR proteins. <i>Nucleic Acids Research</i> , 2020, 48, W348-W357.	6.5	37
25	Characterization of the Core Ribosomal Binding Region for the Oxazolidone Family of Antibiotics Using Cryo-EM. <i>ACS Pharmacology and Translational Science</i> , 2020, 3, 425-432.	2.5	21
26	Mapping bacterial effector arsenals: in vivo and in silico approaches to defining the protein features dictating effector secretion by bacteria. <i>Current Opinion in Microbiology</i> , 2020, 57, 13-21.	2.3	11
27	Hyperosmotic Infusion and Oxidized Surfaces Are Essential for Biofilm Formation of <i>Staphylococcus capitis</i> From the Neonatal Intensive Care Unit. <i>Frontiers in Microbiology</i> , 2020, 11, 920.	1.5	11
28	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
29	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
30	&lt;p&gt;Dynamic Epidemiology and Virulence Characteristics of Carbapenem-Resistant &lt;em&gt; <i>Klebsiella pneumoniae</i> &lt;/em&gt; in Wenzhou, China from 2003 to 2016&lt;/p&gt;. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 931-940.	1.1	10
31	Characterization of BamA reconstituted into a solid-supported lipid bilayer as a platform for measuring dynamics during substrate protein assembly into the membrane. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183317.	1.4	8
32	Investigation of LuxS-mediated quorum sensing in <i>Klebsiella pneumoniae</i> . <i>Journal of Medical Microbiology</i> , 2020, 69, 402-413.	0.7	29
33	Forensic genomics of a novel <i>Klebsiella quasipneumoniae</i> type from a neonatal intensive care unit in China reveals patterns of colonization, evolution and epidemiology. <i>Microbial Genomics</i> , 2020, 6, .	1.0	12
34	Structure of dual BON-domain protein DolP identifies phospholipid binding as a new mechanism for protein localisation. <i>ELife</i> , 2020, 9, .	2.8	25
35	The crystal structure of the TonB-dependent transporter YncD reveals a positively charged substrate-binding site. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 484-495.	1.1	8
36	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

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37	Protease-associated import systems are widespread in Gram-negative bacteria. PLoS Genetics, 2019, 15, e1008435.	1.5	15
38	The structure of the bacterial iron catecholate transporter Fiu suggests that it imports substrates via a two-step mechanism. Journal of Biological Chemistry, 2019, 294, 19523-19534.	1.6	22
39	The flagellotropic bacteriophage YSD1 targets <i>Salmonella</i> Typhi with a Chi-like protein tail fibre. Molecular Microbiology, 2019, 112, 1831-1846.	1.2	24
40	Atlas of group A streptococcal vaccine candidates compiled using large-scale comparative genomics. Nature Genetics, 2019, 51, 1035-1043.	9.4	120
41	Positive-unlabelled learning of glycosylation sites in the human proteome. BMC Bioinformatics, 2019, 20, 112.	1.2	60
42	The TAM: A Translocation and Assembly Module of the $\beta$ -Barrel Assembly Machinery in Bacterial Outer Membranes. EcoSal Plus, 2019, 8, .	2.1	23
43	Filamentous phages: masters of a microbial sharing economy. EMBO Reports, 2019, 20, .	2.0	128
44	Porin Associates with Tom22 to Regulate the Mitochondrial Protein Gate Assembly. Molecular Cell, 2019, 73, 1044-1055.e8.	4.5	47
45	cryoEM-Guided Development of Antibiotics for Drug-Resistant Bacteria. ChemMedChem, 2019, 14, 527-531.	1.6	20
46	Structure of the mitochondrial import gate reveals distinct preprotein paths. Nature, 2019, 575, 395-401.	13.7	146
47	Twenty years of bioinformatics research for protease-specific substrate and cleavage site prediction: a comprehensive revisit and benchmarking of existing methods. Briefings in Bioinformatics, 2019, 20, 2150-2166.	3.2	70
48	Bastion3: a two-layer ensemble predictor of type III secreted effectors. Bioinformatics, 2019, 35, 2017-2028.	1.8	69
49	Systematic analysis and prediction of type IV secreted effector proteins by machine learning approaches. Briefings in Bioinformatics, 2019, 20, 931-951.	3.2	65
50	The multifunctional enzyme S-adenosylhomocysteine/methylthioadenosine nucleosidase is a key metabolic enzyme in the virulence of <i>Salmonella enterica</i> var Typhimurium. Biochemical Journal, 2019, 476, 3435-3453.	1.7	2
51	Determination of the molecular basis for coprogen import by Gram-negative bacteria. IUCr, 2019, 6, 401-411.	1.0	19
52	Protease-associated import systems are widespread in Gram-negative bacteria. , 2019, 15, e1008435.		0
53	Protease-associated import systems are widespread in Gram-negative bacteria. , 2019, 15, e1008435.		0
54	Protease-associated import systems are widespread in Gram-negative bacteria. , 2019, 15, e1008435.		0

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55	Protease-associated import systems are widespread in Gram-negative bacteria. , 2019, 15, e1008435.		0
56	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
57	Methionine biosynthesis and transport are functionally redundant for the growth and virulence of Salmonella Typhimurium. Journal of Biological Chemistry, 2018, 293, 9506-9519.	1.6	26
58	Bastion6: a bioinformatics approach for accurate prediction of type VI secreted effectors. Bioinformatics, 2018, 34, 2546-2555.	1.8	108
59	Genome-scale metabolic modeling of responses to polymyxins in <i>Pseudomonas aeruginosa</i> . GigaScience, 2018, 7, .	3.3	44
60	Structure and Membrane Topography of the Vibrio-Type Secretin Complex from the Type 2 Secretion System of Enteropathogenic Escherichia coli. Journal of Bacteriology, 2018, 200, .	1.0	33
61	An investigation into the Omp85 protein BamK in hypervirulent <i>Klebsiella pneumoniae</i> , and its role in outer membrane biogenesis. Molecular Microbiology, 2018, 109, 584-599.	1.2	5
62	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
63	<i>Quokka</i> : a comprehensive tool for rapid and accurate prediction of kinase family-specific phosphorylation sites in the human proteome. Bioinformatics, 2018, 34, 4223-4231.	1.8	151
64	FusC, a member of the M16 protease family acquired by bacteria for iron piracy against plants. PLoS Biology, 2018, 16, e2006026.	2.6	17
65	Outer membrane vesicles from Neisseria gonorrhoeae target PorB to mitochondria and induce apoptosis. PLoS Pathogens, 2018, 14, e1006945.	2.1	105
66	SecretEPDB: a comprehensive web-based resource for secreted effector proteins of the bacterial types III, IV and VI secretion systems. Scientific Reports, 2017, 7, 41031.	1.6	38
67	Structural Basis for Linezolid Binding Site Rearrangement in the <i>Staphylococcus aureus</i> Ribosome. MBio, 2017, 8, .	1.8	37
68	POSSUM: a bioinformatics toolkit for generating numerical sequence feature descriptors based on PSSM profiles. Bioinformatics, 2017, 33, 2756-2758.	1.8	145
69	The Assembly of Beta-Barrel Proteins into Bacterial Outer Membranes. Biophysical Journal, 2017, 112, 329a.	0.2	0
70	The TPR domain of BepA is required for productive interaction with substrate proteins and the $\beta$ -barrel assembly machinery complex. Molecular Microbiology, 2017, 106, 760-776.	1.2	26
71	Structural Basis of Type 2 Secretion System Engagement between the Inner and Outer Bacterial Membranes. MBio, 2017, 8, .	1.8	58
72	Structural basis for substrate selection by the translocation and assembly module of the $\beta$ -barrel assembly machinery. Molecular Microbiology, 2017, 106, 142-156.	1.2	29

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73	Knowledge-transfer learning for prediction of matrix metalloprotease substrate-cleavage sites. <i>Scientific Reports</i> , 2017, 7, 5755.	1.6	17
74	The Structure of a Conserved Domain of TamB Reveals a Hydrophobic $\beta^2$ Taco Fold. <i>Structure</i> , 2017, 25, 1898-1906.e5.	1.6	33
75	Constraints on lateral gene transfer in promoting fimbrial usher protein diversity and function. <i>Open Biology</i> , 2017, 7, 170144.	1.5	10
76	Reductive evolution in outer membrane protein biogenesis has not compromised cell surface complexity in <i>Helicobacter pylori</i> . <i>MicrobiologyOpen</i> , 2017, 6, e00513.	1.2	10
77	Bacteriophage Transcytosis Provides a Mechanism To Cross Epithelial Cell Layers. <i>MBio</i> , 2017, 8, .	1.8	273
78	Defining Membrane Protein Localization by Isopycnic Density Gradients. <i>Methods in Molecular Biology</i> , 2017, 1615, 81-86.	0.4	11
79	Super-Resolution Imaging of Protein Secretion Systems and the Cell Surface of Gram-Negative Bacteria. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 220.	1.8	19
80	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
81	Phylogenetic Analysis of <i>Klebsiella pneumoniae</i> from Hospitalized Children, Pakistan. <i>Emerging Infectious Diseases</i> , 2017, 23, 1872-1875.	2.0	32
82	Antibacterial poly(ethylene glycol) hydrogels from combined epoxy $\alpha$ -amine and thiol $\alpha$ -ene click reaction. <i>Journal of Polymer Science Part A</i> , 2016, 54, 656-667.	2.5	31
83	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
84	The modular nature of the $\beta$ -barrel assembly machinery, illustrated in <i>Borrelia burgdorferi</i> . <i>Molecular Microbiology</i> , 2016, 102, 753-756.	1.2	15
85	Effective assembly of fimbriae in <i>Escherichia coli</i> depends on the translocation assembly module nanomachine. <i>Nature Microbiology</i> , 2016, 1, 16064.	5.9	52
86	Eliminating <i>Legionella</i> by inhibiting BCL-XL to induce macrophage apoptosis. <i>Nature Microbiology</i> , 2016, 1, 15034.	5.9	75
87	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
88	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
89	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
90	Assembly of the secretion pores $\langle scp \rangle GspD \langle /scp \rangle$ , $\langle scp \rangle W \langle /scp \rangle_{za}$ and $\langle scp \rangle CsgG \langle /scp \rangle$ into bacterial outer membranes does not require the $\langle scp \rangle O \langle /scp \rangle_{mp85}$ proteins $\langle scp \rangle BamA \langle /scp \rangle$ or $\langle scp \rangle TamA \langle /scp \rangle$ . <i>Molecular Microbiology</i> , 2015, 97, 616-629.	1.2	47

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91	Evolution of the Translocation and Assembly Module (TAM). <i>Genome Biology and Evolution</i> , 2015, 7, 1628-1643.	1.1	62
92	Prebiotic-chemistry inspired polymer coatings for biomedical and material science applications. <i>NPG Asia Materials</i> , 2015, 7, e225-e225.	3.8	41
93	Mitochondrial Biogenesis: Cell-Cycle-Dependent Investment in Making Mitochondria. <i>Current Biology</i> , 2015, 25, R78-R80.	1.8	24
94	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
95	Positive Autoregulation of <i>mrkH</i> by the Cyclic Di-GMP-Dependent MrkH Protein in the Biofilm Regulatory Circuit of <i>Klebsiella pneumoniae</i> . <i>Journal of Bacteriology</i> , 2015, 197, 1659-1667.	1.0	24
96	Molecular architecture of the active mitochondrial protein gate. <i>Science</i> , 2015, 349, 1544-1548.	6.0	169
97	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
98	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
99	The $\beta$ -Barrel Assembly Machinery Complex. <i>Methods in Molecular Biology</i> , 2015, 1329, 1-16.	0.4	11
100	Identification of BamC on the Surface of <i>E. coli</i> . <i>Methods in Molecular Biology</i> , 2015, 1329, 215-225.	0.4	4
101	A comprehensive analysis of the Omp85/TpsB protein superfamily structural diversity, taxonomic occurrence, and evolution. <i>Frontiers in Microbiology</i> , 2014, 5, 370.	1.5	78
102	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
103	Assembly of $\beta$ -barrel proteins into bacterial outer membranes. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 1542-1550.	1.9	65
104	Emerging rules for effective antimicrobial coatings. <i>Trends in Biotechnology</i> , 2014, 32, 82-90.	4.9	257
105	Reconstitution of a nanomachine driving the assembly of proteins into bacterial outer membranes. <i>Nature Communications</i> , 2014, 5, 5078.	5.8	71
106	Efficient construction of unmarked recombinant mycobacteria using an improved system. <i>Journal of Microbiological Methods</i> , 2014, 103, 29-36.	0.7	13
107	Modifications and Innovations in the Evolution of Mitochondrial Protein Import Pathways. , 2014, , 19-35.		5
108	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

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109	Structural insight into the biogenesis of $\beta$ -barrel membrane proteins. <i>Nature</i> , 2013, 501, 385-390.	13.7	368
110	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
111	Self-assembly of ciprofloxacin and a tripeptide into an antimicrobial nanostructured hydrogel. <i>Biomaterials</i> , 2013, 34, 3678-3687.	5.7	162
112	Back to basics: A revealing secondary reduction of the mitochondrial protein import pathway in diverse intracellular parasites. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2013, 1833, 295-303.	1.9	24
113	Assembly of the Type II Secretion System such as Found in <i>Vibrio cholerae</i> Depends on the Novel Pilotin AspS. <i>PLoS Pathogens</i> , 2013, 9, e1003117.	2.1	59
114	Transcriptional Activation of the mrkA Promoter of the <i>Klebsiella pneumoniae</i> Type 3 Fimbrial Operon by the c-di-GMP-Dependent MrkH Protein. <i>PLoS ONE</i> , 2013, 8, e79038.	1.1	23
115	Preparation of Mitochondria from <i>Candida albicans</i> . <i>Bio-protocol</i> , 2013, 3, .	0.2	1
116	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
117	Mitochondrial Sorting and Assembly Machinery Subunit Sam37 in <i>Candida albicans</i> : Insight into the Roles of Mitochondria in Fitness, Cell Wall Integrity, and Virulence. <i>Eukaryotic Cell</i> , 2012, 11, 532-544.	3.4	57
118	A Small Tim Homohexamer in the Relict Mitochondrion of <i>Cryptosporidium</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 113-122.	3.5	22
119	<i>Legionella pneumophila</i> Secretes a Mitochondrial Carrier Protein during Infection. <i>PLoS Pathogens</i> , 2012, 8, e1002459.	2.1	64
120	The Type II Secretion System and Its Ubiquitous Lipoprotein Substrate, SslE, Are Required for Biofilm Formation and Virulence of Enteropathogenic <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2012, 80, 2042-2052.	1.0	78
121	Dynamic Association of BAM Complex Modules Includes Surface Exposure of the Lipoprotein BamC. <i>Journal of Molecular Biology</i> , 2012, 422, 545-555.	2.0	79
122	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
123	Evolution of the $\beta$ -barrel assembly machinery. <i>Trends in Microbiology</i> , 2012, 20, 612-620.	3.5	139
124	A Bioinformatic Strategy for the Detection, Classification and Analysis of Bacterial Autotransporters. <i>PLoS ONE</i> , 2012, 7, e43245.	1.1	65
125	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
126	Response to Zarsky et al.. <i>Current Biology</i> , 2012, 22, R481-R482.	1.8	7



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127	The evolution of new lipoprotein subunits of the bacterial outer membrane BAM complex. <i>Molecular Microbiology</i> , 2012, 84, 832-844.	1.2	65
128	Minor modifications and major adaptations: The evolution of molecular machines driving mitochondrial protein import. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 947-954.	1.4	54
129	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
130	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
131	Cell wall integrity is linked to mitochondria and phospholipid homeostasis in <i>Candida albicans</i> through the activity of the post-transcriptional regulator Ccr4 $\Delta$ Pop2. <i>Molecular Microbiology</i> , 2011, 79, 968-989.	1.2	115
132	Targeting of Neisserial PorB to the mitochondrial outer membrane: an insight on the evolution of $\beta$ -barrel protein assembly machines. <i>Molecular Microbiology</i> , 2011, 82, 976-987.	1.2	24
133	PUF proteins: repression, activation and mRNA localization. <i>Trends in Cell Biology</i> , 2011, 21, 104-112.	3.6	263
134	Mitochondrial Preprotein Translocase of Trypanosomatids Has a Bacterial Origin. <i>Current Biology</i> , 2011, 21, 1738-1743.	1.8	104
135	A Functional Tom70 in the Human Parasite <i>Blastocystis sp.</i> : Implications for the Evolution of the Mitochondrial Import Apparatus. <i>Molecular Biology and Evolution</i> , 2011, 28, 781-791.	3.5	25
136	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
137	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
138	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
139	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
140	Mitochondrial Biogenesis: Sorting Mechanisms Cooperate in ABC Transporter Assembly. <i>Current Biology</i> , 2010, 20, R564-R567.	1.8	7
141	Systems Biology: The Next Frontier for Bioinformatics. <i>Advances in Bioinformatics</i> , 2010, 2010, 1-10.	5.7	51
142	A Modular BAM Complex in the Outer Membrane of the $\alpha$ -Proteobacterium <i>Caulobacter crescentus</i> . <i>PLoS ONE</i> , 2010, 5, e8619.	1.1	62
143	Tinkering Inside the Organelle. <i>Science</i> , 2010, 327, 649-650.	6.0	40
144	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

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145	The Essentials of Protein Import in the Degenerate Mitochondrion of <i>Entamoeba histolytica</i> . <i>PLoS Pathogens</i> , 2010, 6, e1000812.	2.1	64
146	Using Hidden Markov Models to Discover New Protein Transport Machines. <i>Methods in Molecular Biology</i> , 2010, 619, 271-284.	0.4	27
147	Both the p33 and p55 Subunits of the <i>Helicobacter pylori</i> VacA Toxin Are Targeted to Mammalian Mitochondria. <i>Journal of Molecular Biology</i> , 2010, 401, 792-798.	2.0	53
148	The Yeast PUF Protein Puf5 Has Pop2-Independent Roles in Response to DNA Replication Stress. <i>PLoS ONE</i> , 2010, 5, e10651.	1.1	11
149	Evidence of a Reduced and Modified Mitochondrial Protein Import Apparatus in Microsporidian Mitosomes. <i>Eukaryotic Cell</i> , 2009, 8, 19-26.	3.4	47
150	The Protein Import Channel in the Outer Mitosomal Membrane of <i>Giardia intestinalis</i> . <i>Molecular Biology and Evolution</i> , 2009, 26, 1941-1947.	3.5	59
151	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
152	Jid1 is a $\beta$ -protein functioning in the mitochondrial matrix, unable to directly participate in endoplasmic reticulum associated protein degradation. <i>FEBS Letters</i> , 2009, 583, 2954-2958.	1.3	7
153	Importing Mitochondrial Proteins: Machineries and Mechanisms. <i>Cell</i> , 2009, 138, 628-644.	13.5	1,199
154	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
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