

# Tracy Palmer

## List of Publications by Year in descending order

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150  
papers

12,078  
citations

23567

58  
h-index

29157

104  
g-index

268  
all docs

268  
docs citations

268  
times ranked

6726  
citing authors

#	ARTICLE	IF	CITATIONS
1	A holin/peptidoglycan hydrolase-dependent protein secretion system. <i>Molecular Microbiology</i> , 2021, 115, 345-355.	2.5	58
2	Activation of a bacterial killing machine. <i>PLoS Genetics</i> , 2021, 17, e1009261.	3.5	5
3	Extreme genetic diversity in the type VII secretion system of <i>Listeria monocytogenes</i> suggests a role in bacterial antagonism. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	1.8	25
4	Multiple evolutionary origins reflect the importance of sialic acid transporters in the colonization potential of bacterial pathogens and commensals. <i>Microbial Genomics</i> , 2021, 7, .	2.0	12
5	The Carbapenemase BKC-1 from <i>Klebsiella pneumoniae</i> Is Adapted for Translocation by Both the Tat and Sec Translocons. <i>MBio</i> , 2021, 12, e0130221.	4.1	5
6	The Type VII Secretion System of <i>Staphylococcus</i> . <i>Annual Review of Microbiology</i> , 2021, 75, 471-494.	7.3	38
7	A membrane-depolarizing toxin substrate of the <i>Staphylococcus aureus</i> type VII secretion system mediates intraspecies competition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20836-20847.	7.1	57
8	Targeting of proteins to the twin-arginine translocation pathway. <i>Molecular Microbiology</i> , 2020, 113, 861-871.	2.5	47
9	Ferric Citrate Regulator FecR Is Translocated across the Bacterial Inner Membrane via a Unique Twin-Arginine Transport-Dependent Mechanism. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	4
10	Activation of a [NiFe]-hydrogenase-4 isoenzyme by maturation proteases. <i>Microbiology (United Kingdom)</i> , 2020, 166, 1233-1244.	1.8	3
11	Controlling and co-ordinating chitinase secretion in a <i>Serratia marcescens</i> population. <i>Microbiology (United Kingdom)</i> , 2019, 165, 1233-1244.	1.8	8
12	Evolution of mitochondrial TAT translocases illustrates the loss of bacterial protein transport machines in mitochondria. <i>BMC Biology</i> , 2018, 16, 141.	3.8	21
13	EssC is a specificity determinant for <i>Staphylococcus aureus</i> type VII secretion. <i>Microbiology (United Kingdom)</i> , 2017, 161, 1707-1714.	1.8	26
14	A signal sequence suppressor mutant that stabilizes an assembled state of the twin arginine translocase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1958-E1967.	7.1	27
15	Structural biology: Mycobacterial ESX secrets revealed. <i>Nature Microbiology</i> , 2017, 2, 17074.	13.3	1
16	Substrate-triggered position switching of TatA and TatB during Tat transport in <i>Escherichia coli</i> . <i>Open Biology</i> , 2017, 7, 170091.	3.6	24
17	Signal Peptide Hydrophobicity Modulates Interaction with the Twin-Arginine Translocase. <i>MBio</i> , 2017, 8, .	4.1	31
18	The type VII secretion system of <i>Staphylococcus aureus</i> secretes a nuclease toxin that targets competitor bacteria. <i>Nature Microbiology</i> , 2017, 2, 16183.	13.3	206

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19	The Enigmatic Esx Proteins: Looking Beyond Mycobacteria. Trends in Microbiology, 2017, 25, 192-204.	7.7	109
20	Expanding the substrates for a bacterial hydrogenlyase reaction. Microbiology (United Kingdom), 2017, 163, 649-653.	1.8	12
21	Haem-iron plays a key role in the regulation of the Ess/type VII secretion system of Staphylococcus aureus RN6390. Microbiology (United Kingdom), 2017, 163, 1839-1850.	1.8	25
22	Functional analysis of the EsaB component of the Staphylococcus aureus Type VII secretion system. Microbiology (United Kingdom), 2017, 163, 1851-1863.	1.8	19
23	A unifying mechanism for the biogenesis of membrane proteins co-operatively integrated by the Sec and Tat pathways. ELife, 2017, 6, .	6.0	11
24	Assembling the Tat protein translocase. ELife, 2016, 5, .	6.0	62
25	Spotlight on Tracy Palmer. FEMS Microbiology Letters, 2016, 363, fnw271.	1.8	3
26	The Ess/Type VII secretion system of Staphylococcus aureus shows unexpected genetic diversity. BMC Genomics, 2016, 17, 222.	2.8	95
27	Organophosphate Hydrolase Is a Lipoprotein and Interacts with Pi-specific Transport System to Facilitate Growth of Brevundimonas diminuta Using OP Insecticide as Source of Phosphate. Journal of Biological Chemistry, 2016, 291, 7774-7785.	3.4	14
28	Cosmid based mutagenesis causes genetic instability in Streptomyces coelicolor, as shown by targeting of the lipoprotein signal peptidase gene. Scientific Reports, 2016, 6, 29495.	3.3	4
29	EssC: domain structures inform on the elusive translocation channel in the Type VII secretion system. Biochemical Journal, 2016, 473, 1941-1952.	3.7	48
30	Membrane interactions and self-association of components of the Ess/Type VII secretion system of Staphylococcus aureus. FEBS Letters, 2016, 590, 349-357.	2.8	27
31	Integration of an [FeFe]-hydrogenase into the anaerobic metabolism of Escherichia coli. Biotechnology Reports (Amsterdam, Netherlands), 2015, 8, 94-104.	4.4	8
32	Cross-species chimeras reveal BamA POTRA and $\beta$ -barrel domains must be fine-tuned for efficient OMP insertion. Molecular Microbiology, 2015, 97, 646-659.	2.5	17
33	The TatC component of the twin-arginine protein translocase functions as an obligate oligomer. Molecular Microbiology, 2015, 98, 111-129.	2.5	27
34	Dissection and engineering of the Escherichia coli formate hydrogenlyase complex. FEBS Letters, 2015, 589, 3141-3147.	2.8	24
35	A holin and an endopeptidase are essential for chitinolytic protein secretion in Serratia marcescens. Journal of Cell Biology, 2014, 207, 615-626.	5.2	47
36	Heterogeneity in Ess/Type VII transcriptional organization and variable contribution of the Ess/Type VII protein secretion system to virulence across closely related Staphylococcus aureus strains. Molecular Microbiology, 2014, 93, 928-943.	2.5	84

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37	Bacterial formate hydrogenlyase complex. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3948-56.	7.1	209
38	Characterization of a periplasmic nitrate reductase in complex with its biosynthetic chaperone. FEBS Journal, 2014, 281, 246-260.	4.7	11
39	Role of the Twin Arginine Protein Transport Pathway in the Assembly of the Streptomyces coelicolor Cytochrome bc1 Complex. Journal of Bacteriology, 2014, 196, 50-59.	2.2	13
40	Signal peptide etiquette during assembly of a complex respiratory enzyme. Molecular Microbiology, 2013, 90, 400-414.	2.5	27
41	Characterization of Staphylococcus aureus EssB, an integral membrane component of the Type VII secretion system: atomic resolution crystal structure of the cytoplasmic segment. Biochemical Journal, 2013, 449, 469-477.	3.7	25
42	The ESX type VII secretion system modulates development, but not virulence, of the plant pathogen Streptomyces scabies. Molecular Plant Pathology, 2013, 14, 119-130.	4.2	31
43	A regulatory domain controls the transport activity of a twin-arginine signal peptide. FEBS Letters, 2013, 587, 3365-3370.	2.8	4
44	The Architecture of EssB, an Integral Membrane Component of the Type VII Secretion System. Structure, 2013, 21, 595-603.	3.3	19
45	A synthetic system for expression of components of a bacterial microcompartment. Microbiology (United Kingdom), 2013, 159, 2427-2436.	1.8	26
46	Characterization of a pre-export enzyme-chaperone complex on the twin-arginine transport pathway. Biochemical Journal, 2013, 452, 57-66.	3.7	16
47	Live cell imaging shows reversible assembly of the TatA component of the twin-arginine protein transport system. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3650-9.	7.1	69
48	Escherichia coli TatA and TatB Proteins Have N-out, C-in Topology in Intact Cells. Journal of Biological Chemistry, 2012, 287, 14420-14431.	3.4	46
49	Dynamic Localization of Tat Protein Transport Machinery Components in Streptomyces coelicolor. Journal of Bacteriology, 2012, 194, 6272-6281.	2.2	19
50	Co-operation between different targeting pathways during integration of a membrane protein. Journal of Cell Biology, 2012, 199, 303-315.	5.2	46
51	Structure of the TatC core of the twin-arginine protein transport system. Nature, 2012, 492, 210-214.	27.8	164
52	The twin-arginine translocation (Tat) protein export pathway. Nature Reviews Microbiology, 2012, 10, 483-496.	28.6	447
53	How Salmonella oxidises H <sub>2</sub> under aerobic conditions. FEBS Letters, 2012, 586, 536-544.	2.8	34
54	Processing by rhomboid protease is required for Providencia stuartii TatA to interact with TatC and to form functional homooligomeric complexes. Molecular Microbiology, 2012, 84, 1108-1123.	2.5	17

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55	Molecular dissection of TatC defines critical regions essential for protein transport and a TatB-TatC contact site. <i>Molecular Microbiology</i> , 2012, 85, 945-961.	2.5	49
56	Topology and Accessibility of the Transmembrane Helices and the Sensory Site in the Bifunctional Transporter DcuB of <i>Escherichia coli</i> . <i>Biochemistry</i> , 2011, 50, 5925-5938.	2.5	9
57	Dissecting the complete lipoprotein biogenesis pathway in <i>Streptomyces scabies</i> . <i>Molecular Microbiology</i> , 2011, 80, 1395-1412.	2.5	42
58	Characterisation of the membrane-extrinsic domain of the TatB component of the twin arginine protein translocase. <i>FEBS Letters</i> , 2011, 585, 478-484.	2.8	19
59	Genetic Evidence for a TatC Dimer at the Core of the <i>Escherichia coli</i> Twin Arginine (Tat) Protein Translocase. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2011, 20, 168-175.	1.0	22
60	The Tat Protein Export Pathway. <i>EcoSal Plus</i> , 2010, 4, .	5.4	26
61	The complex extracellular biology of <i>Streptomyces</i> . <i>FEMS Microbiology Reviews</i> , 2010, 34, 171-198.	8.6	415
62	The twin arginine protein transport pathway exports multiple virulence proteins in the plant pathogen <i>Streptomyces scabies</i> . <i>Molecular Microbiology</i> , 2010, 77, 252-271.	2.5	71
63	Investigating lipoprotein biogenesis and function in the model Gram-positive bacterium <i>Streptomyces coelicolor</i> . <i>Molecular Microbiology</i> , 2010, 77, 943-957.	2.5	56
64	C-terminal amino acid residues of the trimeric autotransporter adhesin YadA of <i>Yersinia enterocolitica</i> are decisive for its recognition and assembly by BamA. <i>Molecular Microbiology</i> , 2010, 78, 932-946.	2.5	75
65	How <i>Escherichia coli</i> Is Equipped to Oxidize Hydrogen under Different Redox Conditions. <i>Journal of Biological Chemistry</i> , 2010, 285, 3928-3938.	3.4	204
66	Analysis of Tat Targeting Function and Twin-Arginine Signal Peptide Activity in <i>Escherichia coli</i> . <i>Methods in Molecular Biology</i> , 2010, 619, 191-216.	0.9	19
67	Remnant signal peptides on non-exported enzymes: implications for the evolution of prokaryotic respiratory chains. <i>Microbiology (United Kingdom)</i> , 2009, 155, 3992-4004.	1.8	36
68	Structural analysis of substrate binding by the TatBC component of the twin-arginine protein transport system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13284-13289.	7.1	84
69	Conserved Network of Proteins Essential for Bacterial Viability. <i>Journal of Bacteriology</i> , 2009, 191, 4732-4749.	2.2	71
70	The Orientation of a Tandem POTRA Domain Pair, of the Beta-Barrel Assembly Protein BamA, Determined by PELDOR Spectroscopy. <i>Structure</i> , 2009, 17, 1187-1194.	3.3	54
71	Proteolytic processing of <i>Escherichia coli</i> twin-arginine signal peptides by LepB. <i>Archives of Microbiology</i> , 2009, 191, 919-925.	2.2	60
72	Lipoprotein biogenesis in Gram-positive bacteria: knowing when to hold $\hat{e}m$ , knowing when to fold $\hat{e}m$ . <i>Trends in Microbiology</i> , 2009, 17, 13-21.	7.7	181

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73	Crystal Structure of the Acid-Induced Arginine Decarboxylase from <i>Escherichia coli</i> : Reversible Decamer Assembly Controls Enzyme Activity. <i>Biochemistry</i> , 2009, 48, 3915-3927.	2.5	48
74	<i>Escherichia coli</i> tat mutant strains are able to transport maltose in the absence of an active malE gene. <i>Archives of Microbiology</i> , 2008, 189, 597-604.	2.2	9
75	Biosynthesis of the respiratory formate dehydrogenases from <i>Escherichia coli</i> : characterization of the FdhE protein. <i>Archives of Microbiology</i> , 2008, 190, 685-696.	2.2	30
76	Fold and function of polypeptide transport-associated domains responsible for delivering unfolded proteins to membranes. <i>Molecular Microbiology</i> , 2008, 68, 1216-1227.	2.5	142
77	A new way out: protein localization on the bacterial cell surface via Tat and a novel Type II secretion system. <i>Molecular Microbiology</i> , 2008, 69, 1331-1335.	2.5	6
78	Features of a twin-arginine signal peptide required for recognition by a Tat proofreading chaperone. <i>FEBS Letters</i> , 2008, 582, 3979-3984.	2.8	31
79	A Facile Reporter System for the Experimental Identification of Twin-Arginine Translocation (Tat) Signal Peptides from All Kingdoms of Life. <i>Journal of Molecular Biology</i> , 2008, 375, 595-603.	4.2	34
80	Variable stoichiometry of the TatA component of the twin-arginine protein transport system observed by <i>in vivo</i> single-molecule imaging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 15376-15381.	7.1	172
81	The <i>c</i> -Type Cytochrome OmcA Localizes to the Outer Membrane upon Heterologous Expression in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2008, 190, 5127-5131.	2.2	23
82	Export Pathway Selectivity of <i>Escherichia coli</i> Twin Arginine Translocation Signal Peptides. <i>Journal of Biological Chemistry</i> , 2007, 282, 8309-8316.	3.4	120
83	Structural diversity in twin-arginine signal peptide-binding proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15641-15646.	7.1	71
84	Cysteine Scanning Mutagenesis and Topological Mapping of the <i>Escherichia coli</i> Twin-Arginine Translocase TatC Component. <i>Journal of Bacteriology</i> , 2007, 189, 5482-5494.	2.2	40
85	Cysteine Scanning Mutagenesis and Disulfide Mapping Studies of the TatA Component of the Bacterial Twin Arginine Translocase. <i>Journal of Biological Chemistry</i> , 2007, 282, 23937-23945.	3.4	51
86	An Essential Role for the DnaK Molecular Chaperone in Stabilizing Over-expressed Substrate Proteins of the Bacterial Twin-arginine Translocation Pathway. <i>Journal of Molecular Biology</i> , 2007, 367, 715-730.	4.2	46
87	TatBC, TatB, and TatC form structurally autonomous units within the twin arginine protein transport system of <i>Escherichia coli</i> . <i>FEBS Letters</i> , 2007, 581, 4091-4097.	2.8	50
88	The Entire N-Terminal Half of TatC is Involved in Twin-Arginine Precursor Binding. <i>Biochemistry</i> , 2007, 46, 2892-2898.	2.5	69
89	The Tat Pathway of the Plant Pathogen <i>Pseudomonas syringae</i> is Required for Optimal Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 200-212.	2.6	40
90	Pathfinders and trailblazers: a prokaryotic targeting system for transport of folded proteins. <i>FEMS Microbiology Letters</i> , 2006, 254, 198-207.	1.8	82

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91	Subunit composition and <i>in vivo</i> substrate-binding characteristics of <i>Escherichia coli</i> Tat protein complexes expressed at native levels. <i>FEBS Journal</i> , 2006, 273, 5656-5668.	4.7	48
92	Secretion by numbers: protein traffic in prokaryotes. <i>Molecular Microbiology</i> , 2006, 62, 308-319.	2.5	129
93	Formation of functional Tat translocases from heterologous components. <i>BMC Microbiology</i> , 2006, 6, 64.	3.3	11
94	MICROBIOLOGY: Mycobacteria's Export Strategy. <i>Science</i> , 2006, 313, 1583-1584.	12.6	17
95	Cysteine-scanning Mutagenesis and Disulfide Mapping Studies of the Conserved Domain of the Twin-arginine Translocase TatB Component. <i>Journal of Biological Chemistry</i> , 2006, 281, 34072-34085.	3.4	60
96	The twin-arginine translocation pathway is a major route of protein export in <i>Streptomyces coelicolor</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17927-17932.	7.1	134
97	Prediction of twin-arginine signal peptides. <i>BMC Bioinformatics</i> , 2005, 6, 167.	2.6	465
98	The TatA component of the twin-arginine protein transport system forms channel complexes of variable diameter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10482-10486.	7.1	245
99	Positive Selection for Loss-of-Function <i>tat</i> Mutations Identifies Critical Residues Required for TatA Activity. <i>Journal of Bacteriology</i> , 2005, 187, 2920-2925.	2.2	36
100	Protein targeting by the bacterial twin-arginine translocation (Tat) pathway. <i>Current Opinion in Microbiology</i> , 2005, 8, 174-181.	5.1	199
101	Characterisation of Tat protein transport complexes carrying inactivating mutations. <i>Biochemical and Biophysical Research Communications</i> , 2005, 329, 693-698.	2.1	33
102	Export of complex cofactor-containing proteins by the bacterial Tat pathway. <i>Trends in Microbiology</i> , 2005, 13, 175-180.	7.7	188
103	Novel Phenotypes of <i>Escherichia coli</i> <i>tat</i> Mutants Revealed by Global Gene Expression and Phenotypic Analysis. <i>Journal of Biological Chemistry</i> , 2004, 279, 47543-47554.	3.4	62
104	mRNA Secondary Structure Modulates Translation of Tat-Dependent Formate Dehydrogenase N. <i>Journal of Bacteriology</i> , 2004, 186, 6311-6315.	2.2	19
105	Phage Shock Protein PspA of <i>Escherichia coli</i> Relieves Saturation of Protein Export via the Tat Pathway. <i>Journal of Bacteriology</i> , 2004, 186, 366-373.	2.2	144
106	Coordinating assembly and export of complex bacterial proteins. <i>EMBO Journal</i> , 2004, 23, 3962-3972.	7.8	186
107	Light traffic: photo-crosslinking a novel transport system. <i>Trends in Biochemical Sciences</i> , 2004, 29, 55-57.	7.5	7
108	A subset of bacterial inner membrane proteins integrated by the twin-arginine translocase. <i>Molecular Microbiology</i> , 2003, 49, 1377-1390.	2.5	117

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109	Role of the <i>Escherichia coli</i> Tat pathway in outer membrane integrity. <i>Molecular Microbiology</i> , 2003, 48, 1183-1193.	2.5	207
110	The Tat protein translocation pathway and its role in microbial physiology. <i>Advances in Microbial Physiology</i> , 2003, 47, 187-254.	2.4	227
111	The <i>Escherichia coli</i> twin-arginine translocase: conserved residues of TatA and TatB family components involved in protein transport. <i>FEBS Letters</i> , 2003, 539, 61-67.	2.8	65
112	The Tat Protein Export Pathway. , 2003, , 51-64.		0
113	Moving folded proteins across the bacterial cell membrane. <i>Microbiology (United Kingdom)</i> , 2003, 149, 547-556.	1.8	92
114	Biochemical and Structural Analysis of the Molybdenum Cofactor Biosynthesis Protein MobA. <i>Journal of Biological Chemistry</i> , 2003, 278, 25302-25307.	3.4	24
115	Genetic Analysis of the Twin Arginine Translocator Secretion Pathway in Bacteria. <i>Journal of Biological Chemistry</i> , 2002, 277, 29825-29831.	3.4	133
116	Truncation Analysis of TatA and TatB Defines the Minimal Functional Units Required for Protein Translocation. <i>Journal of Bacteriology</i> , 2002, 184, 5871-5879.	2.2	77
117	Characterization and Membrane Assembly of the TatA Component of the <i>Escherichia coli</i> Twin-Arginine Protein Transport System. <i>Biochemistry</i> , 2002, 41, 13690-13697.	2.5	108
118	In vivo dissection of the Tat translocation pathway in <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2002, 317, 327-335.	4.2	89
119	Oligomeric Properties and Signal Peptide Binding by <i>Escherichia coli</i> Tat Protein Transport Complexes. <i>Journal of Molecular Biology</i> , 2002, 322, 1135-1146.	4.2	101
120	Assembly of membrane-bound respiratory complexes by the Tat protein-transport system. <i>Archives of Microbiology</i> , 2002, 178, 77-84.	2.2	80
121	Behaviour of topological marker proteins targeted to the Tat protein transport pathway. <i>Molecular Microbiology</i> , 2002, 43, 1005-1021.	2.5	98
122	Functional complexity of the twin-arginine translocase TatC component revealed by site-directed mutagenesis. <i>Molecular Microbiology</i> , 2002, 43, 1457-1470.	2.5	92
123	How bacteria get energy from hydrogen: a genetic analysis of periplasmic hydrogen oxidation in <i>Escherichia coli</i> . <i>International Journal of Hydrogen Energy</i> , 2002, 27, 1413-1420.	7.1	88
124	A naturally occurring bacterial Tat signal peptide lacking one of the "invariant" arginine residues of the consensus targeting motif. <i>FEBS Letters</i> , 2001, 497, 45-49.	2.8	104
125	Membrane interactions and self-association of the TatA and TatB components of the twin-arginine translocation pathway. <i>FEBS Letters</i> , 2001, 506, 143-148.	2.8	74
126	<i>Escherichia coli</i> Strains Blocked in Tat-Dependent Protein Export Exhibit Pleiotropic Defects in the Cell Envelope. <i>Journal of Bacteriology</i> , 2001, 183, 139-144.	2.2	165



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127	A genetic screen for suppressors of <i>Escherichia coli</i> Tat signal peptide mutations establishes a critical role for the second arginine within the twin-arginine motif. <i>Archives of Microbiology</i> , 2001, 177, 107-112.	2.2	50
128	Characterisation of the mob locus of <i>Rhodobacter sphaeroides</i> WS8: mobA is the only gene required for molybdopterin guanine dinucleotide synthesis. <i>Archives of Microbiology</i> , 2001, 176, 62-68.	2.2	8
129	Purified components of the <i>Escherichia coli</i> Tat protein transport system form a double-layered ring structure. <i>FEBS Journal</i> , 2001, 268, 3361-3367.	0.2	143
130	Constitutive Expression of <i>Escherichia coli</i> tat Genes Indicates an Important Role for the Twin-Arginine Translocase during Aerobic and Anaerobic Growth. <i>Journal of Bacteriology</i> , 2001, 183, 1801-1804.	2.2	130
131	The Tat protein export pathway. <i>Molecular Microbiology</i> , 2000, 35, 260-274.	2.5	525
132	Crystal Structure of the Molybdenum Cofactor Biosynthesis Protein MobA from <i>Escherichia coli</i> at Near-Atomic Resolution. <i>Structure</i> , 2000, 8, 1115-1125.	3.3	40
133	TatD Is a Cytoplasmic Protein with DNase Activity. <i>Journal of Biological Chemistry</i> , 2000, 275, 16717-16722.	3.4	244
134	The Twin Arginine Consensus Motif of Tat Signal Peptides Is Involved in Sec-independent Protein Targeting in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 11591-11596.	3.4	273
135	A novel protein transport system involved in the biogenesis of bacterial electron transfer chains. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2000, 1459, 325-330.	1.0	41
136	Mutations in the molybdenum cofactor biosynthetic protein Cnx1G from <i>Arabidopsis thaliana</i> define functions for molybdopterin binding, molybdenum insertion, and molybdenum cofactor stabilization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 6475-6480.	7.1	42
137	Sec-independent Protein Translocation in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 36073-36082.	3.4	266
138	Characterization of a molybdenum cofactor biosynthetic gene cluster in <i>Rhodobacter capsulatus</i> which is specific for the biogenesis of dimethylsulfoxide reductase. <i>Microbiology (United Kingdom)</i> , 1999, 145, 1421-1429.	1.8	20
139	An Essential Component of a Novel Bacterial Protein Export System with Homologues in Plastids and Mitochondria. <i>Journal of Biological Chemistry</i> , 1998, 273, 18003-18006.	3.4	346
140	Overlapping functions of components of a bacterial Sec-independent protein export pathway. <i>EMBO Journal</i> , 1998, 17, 3640-3650.	7.8	489
141	Characterisation of the mob locus from <i>Rhodobacter sphaeroides</i> required for molybdenum cofactor biosynthesis. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1998, 1395, 135-140.	2.4	14
142	Reassignment of the gene encoding the <i>Escherichia coli</i> hydrogenase 2 small subunit. <i>FEBS Journal</i> , 1998, 255, 746-754.	0.2	67
143	Targeting signals for a bacterial Sec-independent export system direct plant thylakoid import by the $\Delta$ pH pathway. <i>FEBS Letters</i> , 1998, 431, 339-342.	2.8	59
144	Sec-independent protein translocation in chloroplasts and bacteria. , 1998, , 3111-3114.		0

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145	Characterisation of the Molybdenum-Responsive ModE Regulatory Protein and its Binding to the Promoter Region of the modABCD (Molybdenum Transport) Operon of Escherichia Coli. FEBS Journal, 1997, 246, 119-126.	0.2	80
146	The Product of the Molybdenum Cofactor Gene mobB of Escherichia Coli is a GTP-Binding Protein. FEBS Journal, 1997, 246, 690-697.	0.2	28
147	Involvement of the narJ and mob gene products in distinct steps in the biosynthesis of the molybdoenzyme nitrate reductase in Escherichia coli. Molecular Microbiology, 1996, 20, 875-884.	2.5	158
148	Isolation of protein FA, a product of the mob locus required for molybdenum cofactor biosynthesis in Escherichia coli. FEBS Journal, 1994, 222, 687-692.	0.2	55
149	Purification and properties of the H <sup>+</sup> -nicotinamide nucleotide transhydrogenase from Rhodobacter capsulatus. FEBS Journal, 1991, 197, 247-255.	0.2	48
150	The Tat Protein Export Pathway. , 0, , 16-29.		2