

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 | The Tat protein export pathway. <i>Molecular Microbiology</i> , 2000, 35, 260-274. | 2.5 | 525 |
| 2 | Overlapping functions of components of a bacterial Sec-independent protein export pathway. <i>EMBO Journal</i> , 1998, 17, 3640-3650. | 7.8 | 489 |
| 3 | Prediction of twin-arginine signal peptides. <i>BMC Bioinformatics</i> , 2005, 6, 167. | 2.6 | 465 |
| 4 | The twin-arginine translocation (Tat) protein export pathway. <i>Nature Reviews Microbiology</i> , 2012, 10, 483-496. | 28.6 | 447 |
| 5 | The complex extracellular biology of <i>Streptomyces</i> . <i>FEMS Microbiology Reviews</i> , 2010, 34, 171-198. | 8.6 | 415 |
| 6 | 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 |
| 7 | 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 |
| 8 | Sec-independent Protein Translocation in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 36073-36082. | 3.4 | 266 |
| 9 | 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 |
| 10 | TatD Is a Cytoplasmic Protein with DNase Activity. <i>Journal of Biological Chemistry</i> , 2000, 275, 16717-16722. | 3.4 | 244 |
| 11 | The Tat protein translocation pathway and its role in microbial physiology. <i>Advances in Microbial Physiology</i> , 2003, 47, 187-254. | 2.4 | 227 |
| 12 | Bacterial formate hydrogenlyase complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3948-56. | 7.1 | 209 |
| 13 | Role of the <i>Escherichia coli</i> Tat pathway in outer membrane integrity. <i>Molecular Microbiology</i> , 2003, 48, 1183-1193. | 2.5 | 207 |
| 14 | 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 |
| 15 | 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 |
| 16 | Protein targeting by the bacterial twin-arginine translocation (Tat) pathway. <i>Current Opinion in Microbiology</i> , 2005, 8, 174-181. | 5.1 | 199 |
| 17 | Export of complex cofactor-containing proteins by the bacterial Tat pathway. <i>Trends in Microbiology</i> , 2005, 13, 175-180. | 7.7 | 188 |
| 18 | Coordinating assembly and export of complex bacterial proteins. <i>EMBO Journal</i> , 2004, 23, 3962-3972. | 7.8 | 186 |

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|----|---|------|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | <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 |
| 22 | Structure of the TatC core of the twin-arginine protein transport system. <i>Nature</i> , 2012, 492, 210-214. | 27.8 | 164 |
| 23 | Involvement of the narJ and mob gene products in distinct steps in the biosynthesis of the molybdoenzyme nitrate reductase in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1996, 20, 875-884. | 2.5 | 158 |
| 24 | 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 |
| 25 | 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 |
| 26 | 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 |
| 27 | 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 |
| 28 | Genetic Analysis of the Twin Arginine Translocator Secretion Pathway in Bacteria. <i>Journal of Biological Chemistry</i> , 2002, 277, 29825-29831. | 3.4 | 133 |
| 29 | 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 |
| 30 | Secretion by numbers: protein traffic in prokaryotes. <i>Molecular Microbiology</i> , 2006, 62, 308-319. | 2.5 | 129 |
| 31 | 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 |
| 32 | A subset of bacterial inner membrane proteins integrated by the twin-arginine translocase. <i>Molecular Microbiology</i> , 2003, 49, 1377-1390. | 2.5 | 117 |
| 33 | The Enigmatic Esx Proteins: Looking Beyond Mycobacteria. <i>Trends in Microbiology</i> , 2017, 25, 192-204. | 7.7 | 109 |
| 34 | 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 |
| 35 | A naturally occurring bacterial Tat signal peptide lacking one of the \hat{e} -invariant arginine residues of the consensus targeting motif. <i>FEBS Letters</i> , 2001, 497, 45-49. | 2.8 | 104 |
| 36 | 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 |

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|----|--|-----|-----------|
| 37 | Behaviour of topological marker proteins targeted to the Tat protein transport pathway. <i>Molecular Microbiology</i> , 2002, 43, 1005-1021. | 2.5 | 98 |
| 38 | The Ess/Type VII secretion system of <i>Staphylococcus aureus</i> shows unexpected genetic diversity. <i>BMC Genomics</i> , 2016, 17, 222. | 2.8 | 95 |
| 39 | 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 |
| 40 | Moving folded proteins across the bacterial cell membrane. <i>Microbiology (United Kingdom)</i> , 2003, 149, 547-556. | 1.8 | 92 |
| 41 | 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 |
| 42 | 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 |
| 43 | 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 |
| 44 | Heterogeneity in <i>Ess</i> transcriptional organization and variable contribution of the <i>Ess</i> / <i>Type VII</i> protein secretion system to virulence across closely related <i>S</i> / <i>taphylococcus aureus</i> strains. <i>Molecular Microbiology</i> , 2014, 93, 928-943. | 2.5 | 84 |
| 45 | Pathfinders and trailblazers: a prokaryotic targeting system for transport of folded proteins. <i>FEMS Microbiology Letters</i> , 2006, 254, 198-207. | 1.8 | 82 |
| 46 | Characterisation of the Molybdenum-Responsive ModE Regulatory Protein and its Binding to the Promoter Region of the modABCD (Molybdenum Transport) Operon of <i>Escherichia Coli</i> . <i>FEBS Journal</i> , 1997, 246, 119-126. | 0.2 | 80 |
| 47 | Assembly of membrane-bound respiratory complexes by the Tat protein-transport system. <i>Archives of Microbiology</i> , 2002, 178, 77-84. | 2.2 | 80 |
| 48 | 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 |
| 49 | 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 |
| 50 | 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 |
| 51 | 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 |
| 52 | Conserved Network of Proteins Essential for Bacterial Viability. <i>Journal of Bacteriology</i> , 2009, 191, 4732-4749. | 2.2 | 71 |
| 53 | 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 |
| 54 | The Entire N-Terminal Half of TatC is Involved in Twin-Arginine Precursor Binding. <i>Biochemistry</i> , 2007, 46, 2892-2898. | 2.5 | 69 |

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|----|---|-----|-----------|
| 55 | 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 |
| 56 | Reassignment of the gene encoding the <i>Escherichia coli</i> hydrogenase 2 small subunit. FEBS Journal, 1998, 255, 746-754. | 0.2 | 67 |
| 57 | The <i>Escherichia coli</i> twin-arginine translocase: conserved residues of TatA and TatB family components involved in protein transport. FEBS Letters, 2003, 539, 61-67. | 2.8 | 65 |
| 58 | Novel Phenotypes of <i>Escherichia coli</i> tat Mutants Revealed by Global Gene Expression and Phenotypic Analysis. Journal of Biological Chemistry, 2004, 279, 47543-47554. | 3.4 | 62 |
| 59 | Assembling the Tat protein translocase. ELife, 2016, 5, . | 6.0 | 62 |
| 60 | Cysteine-scanning Mutagenesis and Disulfide Mapping Studies of the Conserved Domain of the Twin-arginine Translocase TatB Component. Journal of Biological Chemistry, 2006, 281, 34072-34085. | 3.4 | 60 |
| 61 | Proteolytic processing of <i>Escherichia coli</i> twin-arginine signal peptides by LepB. Archives of Microbiology, 2009, 191, 919-925. | 2.2 | 60 |
| 62 | Targeting signals for a bacterial Sec-independent export system direct plant thylakoid import by the pH pathway. FEBS Letters, 1998, 431, 339-342. | 2.8 | 59 |
| 63 | A holin/peptidoglycan hydrolase-dependent protein secretion system. Molecular Microbiology, 2021, 115, 345-355. | 2.5 | 58 |
| 64 | A membrane-depolarizing toxin substrate of the <i>Staphylococcus aureus</i> type VII secretion system mediates intraspecies competition. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20836-20847. | 7.1 | 57 |
| 65 | Investigating lipoprotein biogenesis and function in the model Gram-positive bacterium <i>Streptomyces coelicolor</i> . Molecular Microbiology, 2010, 77, 943-957. | 2.5 | 56 |
| 66 | Isolation of protein FA, a product of the mob locus required for molybdenum cofactor biosynthesis in <i>Escherichia coli</i> . FEBS Journal, 1994, 222, 687-692. | 0.2 | 55 |
| 67 | The Orientation of a Tandem POTRA Domain Pair, of the Beta-Barrel Assembly Protein BamA, Determined by PELDOR Spectroscopy. Structure, 2009, 17, 1187-1194. | 3.3 | 54 |
| 68 | Cysteine Scanning Mutagenesis and Disulfide Mapping Studies of the TatA Component of the Bacterial Twin Arginine Translocase. Journal of Biological Chemistry, 2007, 282, 23937-23945. | 3.4 | 51 |
| 69 | 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. Archives of Microbiology, 2001, 177, 107-112. | 2.2 | 50 |
| 70 | TatBC, TatB, and TatC form structurally autonomous units within the twin arginine protein transport system of <i>Escherichia coli</i> . FEBS Letters, 2007, 581, 4091-4097. | 2.8 | 50 |
| 71 | Molecular dissection of TatC defines critical regions essential for protein transport and a TatB-TatC contact site. Molecular Microbiology, 2012, 85, 945-961. | 2.5 | 49 |
| 72 | Purification and properties of the H ⁺ -nicotinamide nucleotide transhydrogenase from <i>Rhodobacter capsulatus</i> . FEBS Journal, 1991, 197, 247-255. | 0.2 | 48 |

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|----|---|-----|-----------|
| 73 | 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 |
| 74 | 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 |
| 75 | EssC: domain structures inform on the elusive translocation channel in the Type VII secretion system. <i>Biochemical Journal</i> , 2016, 473, 1941-1952. | 3.7 | 48 |
| 76 | A holin and an endopeptidase are essential for chitinolytic protein secretion in <i>Serratia marcescens</i> . <i>Journal of Cell Biology</i> , 2014, 207, 615-626. | 5.2 | 47 |
| 77 | Targeting of proteins to the twin-arginine translocation pathway. <i>Molecular Microbiology</i> , 2020, 113, 861-871. | 2.5 | 47 |
| 78 | 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 |
| 79 | <i>Escherichia coli</i> TatA and TatB Proteins Have N-out, C-in Topology in Intact Cells. <i>Journal of Biological Chemistry</i> , 2012, 287, 14420-14431. | 3.4 | 46 |
| 80 | Co-operation between different targeting pathways during integration of a membrane protein. <i>Journal of Cell Biology</i> , 2012, 199, 303-315. | 5.2 | 46 |
| 81 | 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 |
| 82 | Dissecting the complete lipoprotein biogenesis pathway in <i>Streptomyces scabies</i> . <i>Molecular Microbiology</i> , 2011, 80, 1395-1412. | 2.5 | 42 |
| 83 | 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 |
| 84 | 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 |
| 85 | 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 |
| 86 | 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 |
| 87 | The Type VII Secretion System of <i>Staphylococcus</i> . <i>Annual Review of Microbiology</i> , 2021, 75, 471-494. | 7.3 | 38 |
| 88 | 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 |
| 89 | 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 |
| 90 | 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 |

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| 91 | How <i>Salmonella</i> oxidises H ₂ under aerobic conditions. <i>FEBS Letters</i> , 2012, 586, 536-544. | 2.8 | 34 |
| 92 | Characterisation of Tat protein transport complexes carrying inactivating mutations. <i>Biochemical and Biophysical Research Communications</i> , 2005, 329, 693-698. | 2.1 | 33 |
| 93 | 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 |
| 94 | The ESX/VII secretion system modulates development, but not virulence, of the plant pathogen <i>Sclerotinia sclerotiorum</i> . <i>Molecular Plant Pathology</i> , 2013, 14, 119-130. | 4.2 | 31 |
| 95 | Signal Peptide Hydrophobicity Modulates Interaction with the Twin-Arginine Translocase. <i>MBio</i> , 2017, 8, . | 4.1 | 31 |
| 96 | 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 |
| 97 | The Product of the Molybdenum Cofactor Gene <i>mobB</i> of <i>Escherichia coli</i> is a GTP-Binding Protein. <i>FEBS Journal</i> , 1997, 246, 690-697. | 0.2 | 28 |
| 98 | Signal peptide etiquette during assembly of a complex respiratory enzyme. <i>Molecular Microbiology</i> , 2013, 90, 400-414. | 2.5 | 27 |
| 99 | The TatC component of the twin-arginine protein translocase functions as an obligate oligomer. <i>Molecular Microbiology</i> , 2015, 98, 111-129. | 2.5 | 27 |
| 100 | Membrane interactions and self-association of components of the Ess/Type VII secretion system of <i>Staphylococcus aureus</i> . <i>FEBS Letters</i> , 2016, 590, 349-357. | 2.8 | 27 |
| 101 | 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 |
| 102 | The Tat Protein Export Pathway. <i>EcoSal Plus</i> , 2010, 4, . | 5.4 | 26 |
| 103 | A synthetic system for expression of components of a bacterial microcompartment. <i>Microbiology (United Kingdom)</i> , 2013, 159, 2427-2436. | 1.8 | 26 |
| 104 | EssC is a specificity determinant for <i>Staphylococcus aureus</i> type VII secretion. <i>Microbiology (United Kingdom)</i> , 2017, 161, 1839-1850. | 1.8 | 26 |
| 105 | Characterization of <i>Staphylococcus aureus</i> EssB, an integral membrane component of the Type VII secretion system: atomic resolution crystal structure of the cytoplasmic segment. <i>Biochemical Journal</i> , 2013, 449, 469-477. | 3.7 | 25 |
| 106 | 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 |
| 107 | Haem-iron plays a key role in the regulation of the Ess/type VII secretion system of <i>Staphylococcus aureus</i> RN6390. <i>Microbiology (United Kingdom)</i> , 2017, 163, 1839-1850. | 1.8 | 25 |
| 108 | Biochemical and Structural Analysis of the Molybdenum Cofactor Biosynthesis Protein MobA. <i>Journal of Biological Chemistry</i> , 2003, 278, 25302-25307. | 3.4 | 24 |

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|-----|--|------|-----------|
| 109 | Dissection and engineering of the <i>Escherichia coli</i> formate hydrogenlyase complex. FEBS Letters, 2015, 589, 3141-3147. | 2.8 | 24 |
| 110 | Substrate-triggered position switching of TatA and TatB during Tat transport in <i>Escherichia coli</i> . Open Biology, 2017, 7, 170091. | 3.6 | 24 |
| 111 | The <i>C</i> -Type Cytochrome OmcA Localizes to the Outer Membrane upon Heterologous Expression in <i>Escherichia coli</i> . Journal of Bacteriology, 2008, 190, 5127-5131. | 2.2 | 23 |
| 112 | Genetic Evidence for a TatC Dimer at the Core of the <i>Escherichia coli</i> Twin Arginine (Tat) Protein Translocase. Journal of Molecular Microbiology and Biotechnology, 2011, 20, 168-175. | 1.0 | 22 |
| 113 | Evolution of mitochondrial TAT translocases illustrates the loss of bacterial protein transport machines in mitochondria. BMC Biology, 2018, 16, 141. | 3.8 | 21 |
| 114 | Characterization of a molybdenum cofactor biosynthetic gene cluster in <i>Rhodobacter capsulatus</i> which is specific for the biogenesis of dimethylsulfoxide reductase. Microbiology (United Kingdom), 1999, 145, 1421-1429. | 1.8 | 20 |
| 115 | mRNA Secondary Structure Modulates Translation of Tat-Dependent Formate Dehydrogenase N. Journal of Bacteriology, 2004, 186, 6311-6315. | 2.2 | 19 |
| 116 | Characterisation of the membrane-extrinsic domain of the TatB component of the twin arginine protein translocase. FEBS Letters, 2011, 585, 478-484. | 2.8 | 19 |
| 117 | Dynamic Localization of Tat Protein Transport Machinery Components in <i>Streptomyces coelicolor</i> . Journal of Bacteriology, 2012, 194, 6272-6281. | 2.2 | 19 |
| 118 | The Architecture of EssB, an Integral Membrane Component of the Type VII Secretion System. Structure, 2013, 21, 595-603. | 3.3 | 19 |
| 119 | Analysis of Tat Targeting Function and Twin-Arginine Signal Peptide Activity in <i>Escherichia coli</i> . Methods in Molecular Biology, 2010, 619, 191-216. | 0.9 | 19 |
| 120 | Functional analysis of the EsaB component of the <i>Staphylococcus aureus</i> Type VII secretion system. Microbiology (United Kingdom), 2017, 163, 1851-1863. | 1.8 | 19 |
| 121 | MICROBIOLOGY: Mycobacteria's Export Strategy. Science, 2006, 313, 1583-1584. | 12.6 | 17 |
| 122 | Processing by rhomboid protease is required for <i>Providencia stuartii</i> TatA to interact with TatC and to form functional homo-oligomeric complexes. Molecular Microbiology, 2012, 84, 1108-1123. | 2.5 | 17 |
| 123 | Cross-species chimeras reveal <i>BamA</i> POTRA and β -barrel domains must be fine-tuned for efficient OMP insertion. Molecular Microbiology, 2015, 97, 646-659. | 2.5 | 17 |
| 124 | Characterization of a pre-export enzyme-chaperone complex on the twin-arginine transport pathway. Biochemical Journal, 2013, 452, 57-66. | 3.7 | 16 |
| 125 | Characterisation of the mob locus from <i>Rhodobacter sphaeroides</i> required for molybdenum cofactor biosynthesis. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1998, 1395, 135-140. | 2.4 | 14 |
| 126 | Organophosphate Hydrolase Is a Lipoprotein and Interacts with Pi-specific Transport System to Facilitate Growth of <i>Brevundimonas diminuta</i> Using OP Insecticide as Source of Phosphate. Journal of Biological Chemistry, 2016, 291, 7774-7785. | 3.4 | 14 |

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| 127 | Role of the Twin Arginine Protein Transport Pathway in the Assembly of the Streptomyces coelicolor Cytochrome bc ₁ Complex. <i>Journal of Bacteriology</i> , 2014, 196, 50-59. | 2.2 | 13 |
| 128 | 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 |
| 129 | Expanding the substrates for a bacterial hydrogenlyase reaction. <i>Microbiology (United Kingdom)</i> , 2017, 163, 649-653. | 1.8 | 12 |
| 130 | Formation of functional Tat translocases from heterologous components. <i>BMC Microbiology</i> , 2006, 6, 64. | 3.3 | 11 |
| 131 | Characterization of a periplasmic nitrate reductase in complex with its biosynthetic chaperone. <i>FEBS Journal</i> , 2014, 281, 246-260. | 4.7 | 11 |
| 132 | A unifying mechanism for the biogenesis of membrane proteins co-operatively integrated by the Sec and Tat pathways. <i>ELife</i> , 2017, 6, . | 6.0 | 11 |
| 133 | Escherichia coli 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 |
| 134 | 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 |
| 135 | Characterisation of the mob locus of Rhodobacter sphaeroides WS8: mobA is the only gene required for molybdopterin guanine dinucleotide synthesis. <i>Archives of Microbiology</i> , 2001, 176, 62-68. | 2.2 | 8 |
| 136 | Integration of an [FeFe]-hydrogenase into the anaerobic metabolism of Escherichia coli. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2015, 8, 94-104. | 4.4 | 8 |
| 137 | Controlling and co-ordinating chitinase secretion in a Serratia marcescens population. <i>Microbiology (United Kingdom)</i> , 2019, 165, 1233-1244. | 1.8 | 8 |
| 138 | Light traffic: photo-crosslinking a novel transport system. <i>Trends in Biochemical Sciences</i> , 2004, 29, 55-57. | 7.5 | 7 |
| 139 | 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 |
| 140 | Activation of a bacterial killing machine. <i>PLoS Genetics</i> , 2021, 17, e1009261. | 3.5 | 5 |
| 141 | The Carbapenemase BKC-1 from Klebsiella pneumoniae Is Adapted for Translocation by Both the Tat and Sec Translocons. <i>MBio</i> , 2021, 12, e0130221. | 4.1 | 5 |
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