

# Gunnar Von Heijne

## List of Publications by Year in descending order

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Version: 2024-02-01

351  
papers

99,523  
citations

1877

105  
h-index

285

303  
g-index

385  
all docs

385  
docs citations

385  
times ranked

96008  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | SignalP 6.0 predicts all five types of signal peptides using protein language models. <i>Nature Biotechnology</i> , 2022, 40, 1023-1025.   | 9.4 | 883       |
| 2  | Upstream charged and hydrophobic residues impact the timing of membrane insertion of transmembrane helices. <i>FEBS Letters</i> , 2022, 596, 1004-1012.  | 1.3 | 1         |
| 3  | Probing Interplays between Human XBP1u Translational Arrest Peptide and 80S Ribosome. <i>Journal of Chemical Theory and Computation</i> , 2022, 18, 1905-1914.   | 2.3 | 5         |
| 4  | Residue-by-residue analysis of cotranslational membrane protein integration in vivo. <i>ELife</i> , 2021, 10, .  | 2.8 | 26        |
| 5  | The ribosome modulates folding inside the ribosomal exit tunnel. <i>Communications Biology</i> , 2021, 4, 523.   | 2.0 | 27        |
| 6  | Introduction to the Theme on Membrane Channels. <i>Annual Review of Biochemistry</i> , 2021, 90, 503-505.  | 5.0 | 0         |
| 7  | Cotranslational Translocation and Folding of a Periplasmic Protein Domain in <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2021, 433, 167047.  | 2.0 | 9         |
| 8  | Molten globules lure transmembrane helices away from the membrane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2112899118.                      | 3.3 | 0         |
| 9  | Structural basis of <i>l</i> -tryptophan-dependent inhibition of release factor 2 by the TnaC arrest peptide. <i>Nucleic Acids Research</i> , 2021, 49, 9539-9547.                                       | 6.5 | 12        |
| 10 | Membrane integration and topology of RIFIN and STEVOR proteins of the <i>Plasmodium falciparum</i> parasite. <i>FEBS Journal</i> , 2020, 287, 2744-2762.   | 2.2 | 7         |
| 11 | The Mgr2 subunit of the TIM23 complex regulates membrane insertion of marginal stopâ€transfer signals in the mitochondrial inner membrane. <i>FEBS Letters</i> , 2020, 594, 1081-1087.                   | 1.3 | 11        |
| 12 | Cotranslational folding of alkaline phosphatase in the periplasm of <i>Escherichia coli</i> . <i>Protein Science</i> , 2020, 29, 2028-2037.  | 3.1 | 9         |
| 13 | Cotranslational folding cooperativity of contiguous domains of $\hat{\pm}$ -spectrin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14119-14126.   | 3.3 | 24        |
| 14 | Dynamic membrane topology in an unassembled membrane protein. <i>Nature Chemical Biology</i> , 2019, 15, 945-948.  | 3.9 | 21        |
| 15 | A Brief History of Protein Sorting Prediction. <i>Protein Journal</i> , 2019, 38, 200-216.   | 0.7 | 154       |
| 16 | Silencing of Aberrant Secretory Protein Expression by Disease-Associated Mutations. <i>Journal of Molecular Biology</i> , 2019, 431, 2567-2580.  | 2.0 | 13        |
| 17 | Murine astrotactins 1 and 2 have a similar membrane topology and mature via endoproteolytic cleavage catalyzed by a signal peptidase. <i>Journal of Biological Chemistry</i> , 2019, 294, 4538-4545.     | 1.6 | 5         |
| 18 | Force-Profile Analysis of the Cotranslational Folding of HemK and Filamin Domains: Comparison of Biochemical and Biophysical Folding Assays. <i>Journal of Molecular Biology</i> , 2019, 431, 1308-1314. | 2.0 | 30        |

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|----|---|-----|-----------|
| 19 | SignalP 5.0 improves signal peptide predictions using deep neural networks. <i>Nature Biotechnology</i> , 2019, 37, 420-423.  | 9.4 | 3,317     |
| 20 | Detecting sequence signals in targeting peptides using deep learning. <i>Life Science Alliance</i> , 2019, 2, e201900429.   | 1.3 | 561       |
| 21 | Structural and mutational analysis of the ribosome-arresting human XBP1u. <i>ELife</i> , 2019, 8, .   | 2.8 | 51        |
| 22 | Membrane protein serendipity. <i>Journal of Biological Chemistry</i> , 2018, 293, 3470-3476.  | 1.6 | 2         |
| 23 | Folding pathway of an Ig domain is conserved on and off the ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11284-E11293.                                      | 3.3 | 86        |
| 24 | Cotranslational Folding of a Pentarepeat $\hat{I}^2$ -Helix Protein. <i>Journal of Molecular Biology</i> , 2018, 430, 5196-5206.  | 2.0 | 25        |
| 25 | Transmembrane but not soluble helices fold inside the ribosome tunnel. <i>Nature Communications</i> , 2018, 9, 5246.  | 5.8 | 36        |
| 26 | Forces on Nascent Polypeptides during Membrane Insertion and Translocation via the Sec Translocon. <i>Biophysical Journal</i> , 2018, 115, 1885-1894.   | 0.2 | 30        |
| 27 | Effects of protein size, thermodynamic stability, and net charge on cotranslational folding on the ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9280-E9287. | 3.3 | 59        |
| 28 | Direct Detection of Membrane-Inserting Fragments Defines the Translocation Pores of a Family of Pathogenic Toxins. <i>Journal of Molecular Biology</i> , 2018, 430, 3190-3199.  | 2.0 | 4         |
| 29 | Protein Evolution and Design. <i>Annual Review of Biochemistry</i> , 2018, 87, 101-103.   | 5.0 | 7         |
| 30 | The shape of the bacterial ribosome exit tunnel affects cotranslational protein folding. <i>ELife</i> , 2018, 7, .  | 2.8 | 65        |
| 31 | Cotranslational folding of spectrin domains via partially structured states. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 221-225.  | 3.6 | 97        |
| 32 | Transmembrane helices containing a charged arginine are thermodynamically stable. <i>European Biophysics Journal</i> , 2017, 46, 627-637.   | 1.2 | 21        |
| 33 | Gene Duplication Leads to Altered Membrane Topology of a Cytochrome P450 Enzyme in Seed Plants. <i>Molecular Biology and Evolution</i> , 2017, 34, 2041-2056.   | 3.5 | 20        |
| 34 | Mutational analysis of protein folding inside the ribosome exit tunnel. <i>FEBS Letters</i> , 2017, 591, 155-163.   | 1.3 | 28        |
| 35 | Stable membrane orientations of small dual-topology membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7987-7992.   | 3.3 | 33        |
| 36 | The force-sensing peptide VemP employs extreme compaction and secondary structure formation to induce ribosomal stalling. <i>ELife</i> , 2017, 6, .   | 2.8 | 81        |

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|----|--|------|-----------|
| 37 | Structure and topology around the cleavage site regulate post-translational cleavage of the HIV-1 gp160 signal peptide. <i>ELife</i> , 2017, 6, .  | 2.8  | 41        |
| 38 | The topogenic function of S4 promotes membrane insertion of the voltage-sensor domain in the KvAP channel. <i>Biochemical Journal</i> , 2016, 473, 4361-4372.  | 1.7  | 4         |
| 39 | Biological insertion of computationally designed short transmembrane segments. <i>Scientific Reports</i> , 2016, 6, 23397.   | 1.6  | 18        |
| 40 | Global profiling of SRP interaction with nascent polypeptides. <i>Nature</i> , 2016, 536, 219-223.   | 13.7 | 125       |
| 41 | Hydrophobic Clusters Raise the Threshold Hydrophilicity for Insertion of Transmembrane Sequences in Vivo. <i>Biochemistry</i> , 2016, 55, 5772-5779.   | 1.2  | 4         |
| 42 | Energetics of side-chain snorkeling in transmembrane helices probed by nonproteinogenic amino acids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10559-10564.  | 3.3  | 26        |
| 43 | Coordinated disassembly of the divisome complex in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2016, 101, 425-438.   | 1.2  | 42        |
| 44 | Small protein domains fold inside the ribosome exit tunnel. <i>FEBS Letters</i> , 2016, 590, 655-660.  | 1.3  | 69        |
| 45 | Trigger Factor Reduces the Force Exerted on the Nascent Chain by a Cotranslationally Folding Protein. <i>Journal of Molecular Biology</i> , 2016, 428, 1356-1364.  | 2.0  | 74        |
| 46 | Cotranslational Protein Folding. <i>Biophysical Journal</i> , 2016, 110, 4a.   | 0.2  | 0         |
| 47 | RIFINs are adhesins implicated in severe <i>Plasmodium falciparum</i> malaria. <i>Nature Medicine</i> , 2015, 21, 314-317.   | 15.2 | 166       |
| 48 | Thermodynamics of Membrane Insertion and Refolding of the Diphtheria Toxin T-Domain. <i>Journal of Membrane Biology</i> , 2015, 248, 383-394.  | 1.0  | 14        |
| 49 | Hydrophobic Blocks Facilitate Lipid Compatibility and Translocon Recognition of Transmembrane Protein Sequences. <i>Biochemistry</i> , 2015, 54, 1465-1473.  | 1.2  | 5         |
| 50 | Tissue-based map of the human proteome. <i>Science</i> , 2015, 347, 1260419.   | 6.0  | 10,802    |
| 51 | Charge-driven dynamics of nascent-chain movement through the SecYEG translocon. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 145-149.  | 3.6  | 70        |
| 52 | Exploration of the Arrest Peptide Sequence Space Reveals Arrest-enhanced Variants. <i>Journal of Biological Chemistry</i> , 2015, 290, 10208-10215.  | 1.6  | 54        |
| 53 | Cotranslational Protein Folding inside the Ribosome Exit Tunnel. <i>Cell Reports</i> , 2015, 12, 1533-1540.  | 2.9  | 234       |
| 54 | Differential repositioning of the second transmembrane helices from <i>E. coli</i> Tar and EnvZ upon moving the flanking aromatic residues. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 615-621. | 1.4  | 7         |

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|----|---|------|-----------|
| 55 | Forcing the Issue: Aromatic Tuning Facilitates Stimulus-Independent Modulation of a Two-Component Signaling Circuit. <i>ACS Synthetic Biology</i> , 2015, 4, 474-481.   | 1.9  | 9         |
| 56 | Mechanisms of Integral Membrane Protein Insertion and Folding. <i>Journal of Molecular Biology</i> , 2015, 427, 999-1022.   | 2.0  | 292       |
| 57 | The Code for Directing Proteins for Translocation across ER Membrane: SRP Cotranslationally Recognizes Specific Features of a Signal Sequence. <i>Journal of Molecular Biology</i> , 2015, 427, 1191-1201.          | 2.0  | 60        |
| 58 | Identification of novel sphingolipid-binding motifs in mammalian membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 2066-2070.  | 1.4  | 49        |
| 59 | Do Acidic Residues in TH8-TH9 Play a Role in Transmembrane Insertion of the Diphtheria Toxin T-Domain?. <i>Biophysical Journal</i> , 2014, 106, 716a-717a.  | 0.2  | 0         |
| 60 | Weak pulling forces exerted on N<sub>in</sub>-orientated transmembrane segments during coâ€œtranslational insertion into the inner membrane of <i>Escherichia coli</i>. <i>FEBS Letters</i> , 2014, 588, 1930-1934. | 1.3  | 21        |
| 61 | Why Have Small Multidrug Resistance Proteins Not Evolved into Fused, Internally Duplicated Structures?. <i>Journal of Molecular Biology</i> , 2014, 426, 2246-2254.   | 2.0  | 10        |
| 62 | Inefficient SRP Interaction with a Nascent Chain Triggers a mRNA Quality Control Pathway. <i>Cell</i> , 2014, 156, 146-157.   | 13.5 | 77        |
| 63 | Spontaneous transmembrane helix insertion thermodynamically mimics translocon-guided insertion. <i>Nature Communications</i> , 2014, 5, 4863.   | 5.8  | 91        |
| 64 | Disassembly of the divisome in <sc><i>E</i></sc><i>scherichia coli</i>: evidence that <sc>FtsZ</sc> dissociates before compartmentalization. <i>Molecular Microbiology</i> , 2014, 92, 1-9.                         | 1.2  | 70        |
| 65 | Partitioning Charged Side Chains into Lipid Bilayer Membranes. <i>Biophysical Journal</i> , 2014, 106, 297a.  | 0.2  | 0         |
| 66 | Large Tilts in Transmembrane Helices Can Be Induced during Tertiary Structure Formation. <i>Journal of Molecular Biology</i> , 2014, 426, 2529-2538.  | 2.0  | 5         |
| 67 | GPCRs AND TRANSPORTERS: LIGANDS, COFACTORS, DRUG DEVELOPMENT. , 2014, , .   |      | 0         |
| 68 | Positional editing of transmembrane domains during ion channel assembly. <i>Journal of Cell Science</i> , 2013, 126, 464-472.   | 1.2  | 9         |
| 69 | In Vivo Trp Scanning of the Small Multidrug Resistance Protein EmrE Confirms 3D Structure Models'. <i>Journal of Molecular Biology</i> , 2013, 425, 4642-4651.  | 2.0  | 15        |
| 70 | Quantitative Analysis of SecYEG-Mediated Insertion of Transmembrane Î±-Helices into the Bacterial Inner Membrane. <i>Journal of Molecular Biology</i> , 2013, 425, 2813-2822.                                       | 2.0  | 27        |
| 71 | A short Câ€œterminal tail prevents misâ€œtargeting of hydrophobic mitochondrial membrane proteins to the ER. <i>FEBS Letters</i> , 2013, 587, 3480-3486.  | 1.3  | 3         |
| 72 | Improved production of membrane proteins in <i>Escherichia coli</i> by selective codon substitutions. <i>FEBS Letters</i> , 2013, 587, 2352-2358.   | 1.3  | 34        |

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|----|---|------|-----------|
| 73 | Dislocation by the m-AAA Protease Increases the Threshold Hydrophobicity for Retention of Transmembrane Helices in the Inner Membrane of Yeast Mitochondria. <i>Journal of Biological Chemistry</i> , 2013, 288, 4792-4798. | 1.6  | 13        |
| 74 | Cotranslational folding of membrane proteins probed by arrest-peptide-mediated force measurements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14640-14645.         | 3.3  | 79        |
| 75 | Sequential Closure of the Cytoplasm and Then the Periplasm during Cell Division in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2012, 194, 584-586.   | 1.0  | 10        |
| 76 | A biphasic pulling force acts on transmembrane helices during translocon-mediated membrane integration. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1018-1022.   | 3.6  | 161       |
| 77 | Efficient Glycosylphosphatidylinositol (GPI) Modification of Membrane Proteins Requires a C-terminal Anchoring Signal of Marginal Hydrophobicity. <i>Journal of Biological Chemistry</i> , 2012, 287, 16399-16409.          | 1.6  | 35        |
| 78 | Antiparallel Dimers of the Small Multidrug Resistance Protein EmrE Are More Stable Than Parallel Dimers. <i>Journal of Biological Chemistry</i> , 2012, 287, 26052-26059.   | 1.6  | 39        |
| 79 | Production of human tetraspanin proteins in <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 2012, 82, 373-379.   | 0.6  | 7         |
| 80 | Orientational Preferences of Neighboring Helices Can Drive ER Insertion of a Marginally Hydrophobic Transmembrane Helix. <i>Molecular Cell</i> , 2012, 45, 529-540.   | 4.5  | 52        |
| 81 | Manipulating the genetic code for membrane protein production: What have we learnt so far?. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 1091-1096.  | 1.4  | 24        |
| 82 | Application of split-green fluorescent protein for topology mapping membrane proteins in <i>Escherichia coli</i> . <i>Protein Science</i> , 2012, 21, 1571-1576.  | 3.1  | 9         |
| 83 | Glycosylatable GFP as a compartment-specific membrane topology reporter. <i>Biochemical and Biophysical Research Communications</i> , 2012, 427, 780-784.   | 1.0  | 13        |
| 84 | Molecular recognition of a single sphingolipid species by a protein's transmembrane domain. <i>Nature</i> , 2012, 481, 525-529.   | 13.7 | 330       |
| 85 | Mapping out forces that act on transmembrane helices during membrane insertion. <i>FASEB Journal</i> , 2012, 26, 229.1.   | 0.2  | 0         |
| 86 | Pre-Insertion Topology of Transmembrane Proteins is Highly Plastic and Can Be Controlled by a Single C-Terminal Residue. <i>Biophysical Journal</i> , 2011, 100, 345a-346a.   | 0.2  | 0         |
| 87 | Introduction to Theme "Membrane Protein Folding and Insertion". <i>Annual Review of Biochemistry</i> , 2011, 80, 157-160.   | 5.0  | 18        |
| 88 | SignalP 4.0: discriminating signal peptides from transmembrane regions. <i>Nature Methods</i> , 2011, 8, 785-786.   | 9.0  | 8,521     |
| 89 | Converting a Marginally Hydrophobic Soluble Protein into a Membrane Protein. <i>Journal of Molecular Biology</i> , 2011, 407, 171-179.  | 2.0  | 5         |
| 90 | TIM23-mediated insertion of transmembrane $\alpha$ -helices into the mitochondrial inner membrane. <i>EMBO Journal</i> , 2011, 30, 1003-1011.   | 3.5  | 42        |

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|-----|--|-----|-----------|
| 91  | Charged flanking residues control the efficiency of membrane insertion of the first transmembrane segment in yeast mitochondrial Mgm1p. <i>FEBS Letters</i> , 2011, 585, 1238-1242.  | 1.3 | 7         |
| 92  | Arginine in Membranes: The Connection Between Molecular Dynamics Simulations and Translocon-Mediated Insertion Experiments. <i>Journal of Membrane Biology</i> , 2011, 239, 35-48.   | 1.0 | 104       |
| 93  | Membrane proteins: from bench to bits. <i>Biochemical Society Transactions</i> , 2011, 39, 747-750.  | 1.6 | 13        |
| 94  | Flanking Residues Help Determine Whether a Hydrophobic Segment Adopts a Monotopic or Bitopic Topology in the Endoplasmic Reticulum Membrane. <i>Journal of Biological Chemistry</i> , 2011, 286, 25284-25290.                                    | 1.6 | 17        |
| 95  | Apolar surface area determines the efficiency of translocon-mediated membrane-protein integration into the endoplasmic reticulum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E359-E364. | 3.3 | 52        |
| 96  | Prediction of the human membrane proteome. <i>Proteomics</i> , 2010, 10, 1141-1149.  | 1.3 | 347       |
| 97  | Estimating Zâ€ring radius and contraction in dividing <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2010, 76, 151-158.   | 1.2 | 6         |
| 98  | Disulfide Bond Formation and Cysteine Exclusion in Gram-positive Bacteria. <i>Journal of Biological Chemistry</i> , 2010, 285, 3300-3309.  | 1.6 | 80        |
| 99  | Functionality of the voltage-gated proton channel truncated in S4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2313-2318.  | 3.3 | 48        |
| 100 | Membrane Topology of S4 of the Mouse Voltage-Gated Proton Channel. <i>Biophysical Journal</i> , 2010, 98, 539a.  | 0.2 | 0         |
| 101 | Membrane Insertion of Marginally Hydrophobic Transmembrane Helices Depends on Sequence Context. <i>Journal of Molecular Biology</i> , 2010, 396, 221-229.  | 2.0 | 82        |
| 102 | Repositioning of Transmembrane Î±-Helices during Membrane Protein Folding. <i>Journal of Molecular Biology</i> , 2010, 397, 190-201.   | 2.0 | 59        |
| 103 | Control of Membrane Protein Topology by a Single C-Terminal Residue. <i>Science</i> , 2010, 328, 1698-1700.  | 6.0 | 128       |
| 104 | Insertion of short transmembrane helices by the Sec61 translocon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11588-11593.   | 3.3 | 76        |
| 105 | Prediction of partial membrane protein topologies using a consensus approach. <i>Protein Science</i> , 2009, 11, 2974-2980.  | 3.1 | 35        |
| 106 | LumenP-A neural network predictor for protein localization in the thylakoid lumen. <i>Protein Science</i> , 2009, 12, 2360-2366.   | 3.1 | 31        |
| 107 | Improved detection of homologous membrane proteins by inclusion of information from topology predictions. <i>Protein Science</i> , 2009, 11, 652-658.  | 3.1 | 23        |
| 108 | Bioinformatics of Myelin Membrane Proteins. , 2009, , 35-53.   |     | 1         |

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|-----|--|------|-----------|
| 109 | Analysis of Transmembrane Helix Integration in the Endoplasmic Reticulum in <i>S. cerevisiae</i> . <i>Journal of Molecular Biology</i> , 2009, 386, 1222-1228.   | 2.0  | 29        |
| 110 | Membrane-integration Characteristics of Two ABC Transporters, CFTR and P-glycoprotein. <i>Journal of Molecular Biology</i> , 2009, 387, 1153-1164.   | 2.0  | 49        |
| 111 | Sequence-based feature prediction and annotation of proteins. <i>Genome Biology</i> , 2009, 10, 206.   | 13.9 | 53        |
| 112 | GFP-based optimization scheme for the overexpression and purification of eukaryotic membrane proteins in <i>Saccharomyces cerevisiae</i> . <i>Nature Protocols</i> , 2008, 3, 784-798.   | 5.5  | 289       |
| 113 | Membranes: reading between the lines. <i>Current Opinion in Structural Biology</i> , 2008, 18, 403-405.  | 2.6  | 11        |
| 114 | Confronting Fusion Protein-Based Membrane Protein Topology Mapping with Reality: The <i>Escherichia coli</i> ClcA H <sup>+</sup> /Cl <sup>-</sup> Exchange Transporter. <i>Journal of Molecular Biology</i> , 2008, 381, 860-866.                                      | 2.0  | 17        |
| 115 | How Translocons Select Transmembrane Helices. <i>Annual Review of Biophysics</i> , 2008, 37, 23-42.  | 4.5  | 176       |
| 116 | Prediction of membrane-protein topology from first principles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7177-7181.  | 3.3  | 288       |
| 117 | Molecular code for protein insertion in the endoplasmic reticulum membrane is similar for N <sub>in</sub> and N <sub>out</sub> transmembrane helices. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 15702-15707. | 3.3  | 69        |
| 118 | Contribution of positively charged flanking residues to the insertion of transmembrane helices into the endoplasmic reticulum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4127-4132.                          | 3.3  | 60        |
| 119 | Contribution of hydrophobic and electrostatic interactions to the membrane integration of the Shaker K <sup>+</sup> channel voltage sensor domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8263-8268.      | 3.3  | 64        |
| 120 | Formation of Transmembrane Helices In Vivo—Is Hydrophobicity All that Matters?. <i>Journal of General Physiology</i> , 2007, 129, 353-356.   | 0.9  | 33        |
| 121 | Emulating Membrane Protein Evolution by Rational Design. <i>Science</i> , 2007, 315, 1282-1284.  | 6.0  | 116       |
| 122 | Membrane protein structural biology—How far can the bugs take us? (Review). <i>Molecular Membrane Biology</i> , 2007, 24, 329-332.   | 2.0  | 37        |
| 123 | Features of Transmembrane Segments That Promote the Lateral Release from the Translocase into the Lipid Phase. <i>Biochemistry</i> , 2007, 46, 15153-15161.  | 1.2  | 46        |
| 124 | Membrane Protein Structure: Prediction versus Reality. <i>Annual Review of Biochemistry</i> , 2007, 76, 125-140.   | 5.0  | 220       |
| 125 | Assembly of the Cytochrome bo <sub>3</sub> Complex. <i>Journal of Molecular Biology</i> , 2007, 371, 765-773.  | 2.0  | 47        |
| 126 | Stable insertion of Alzheimer A $\beta$ peptide into the ER membrane strongly correlates with its length. <i>FEBS Letters</i> , 2007, 581, 3809-3813.  | 1.3  | 5         |



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|-----|---|------|-----------|
| 127 | Membrane topology of the <i>Drosophila</i> OR83b odorant receptor. FEBS Letters, 2007, 581, 5601-5604.  | 1.3  | 194       |
| 128 | High-throughput fluorescent-based optimization of eukaryotic membrane protein overexpression and purification in <i>Saccharomyces cerevisiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 13936-13941. | 3.3  | 214       |
| 129 | Membrane proteins up for grabs. Nature Biotechnology, 2007, 25, 646-647.  | 9.4  | 3         |
| 130 | Locating proteins in the cell using TargetP, SignalP and related tools. Nature Protocols, 2007, 2, 953-971.   | 5.5  | 2,940     |
| 131 | Molecular code for transmembrane-helix recognition by the Sec61 translocon. Nature, 2007, 450, 1026-1030.   | 13.7 | 644       |
| 132 | The membrane protein universe: what's out there and why bother?. Journal of Internal Medicine, 2007, 261, 543-557.  | 2.7  | 177       |
| 133 | Formation of Transmembrane Helices In Vivo—Is Hydrophobicity All that Matters?. Journal of Cell Biology, 2007, 177, i9-i9.  | 2.3  | 0         |
| 134 | New Escherichia coli outer membrane proteins identified through prediction and experimental verification. Protein Science, 2006, 15, 884-889.   | 3.1  | 43        |
| 135 | Membrane topology of the human seipin protein. FEBS Letters, 2006, 580, 2281-2284.  | 1.3  | 105       |
| 136 | Lipid Bilayers, Translocons and the Shaping of Polypeptide Structure. , 2006, , 1-25.   |      | 1         |
| 137 | Membrane-protein topology. Nature Reviews Molecular Cell Biology, 2006, 7, 909-918.   | 16.1 | 450       |
| 138 | Identification and evolution of dual-topology membrane proteins. Nature Structural and Molecular Biology, 2006, 13, 112-116.  | 3.6  | 189       |
| 139 | Asn- and Asp-mediated interactions between transmembrane helices during translocon-mediated membrane protein assembly. EMBO Reports, 2006, 7, 1111-1116.  | 2.0  | 65        |
| 140 | Membranes. Current Opinion in Structural Biology, 2006, 16, 431.  | 2.6  | 2         |
| 141 | PONGO: a web server for multiple predictions of all-alpha transmembrane proteins. Nucleic Acids Research, 2006, 34, W169-W172.  | 6.5  | 37        |
| 142 | Phenotypic effects of membrane protein overexpression in <i>Saccharomyces cerevisiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11148-11153.   | 3.3  | 36        |
| 143 | The Use of Phylogenetic Profiles for Gene Predictions Revisited. Current Genomics, 2006, 7, 79-86.  | 0.7  | 1         |
| 144 | A global topology map of the <i>Saccharomyces cerevisiae</i> membrane proteome. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11142-11147.  | 3.3  | 124       |

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