

Stephen H White

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/1696513/stephen-h-white-publications-by-year.pdf>

Version: 2024-04-29

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

149
papers

18,742
citations

63
h-index

136
g-index

181
ext. papers

19,931
ext. citations

7
avg. IF

6.8
L-index

#	Paper	IF	Citations
149	A Hydrophilic Microenvironment in the Substrate-Translocating Groove of the YidC Membrane Insertase is Essential for Enzyme Function.. <i>Journal of Biological Chemistry</i> , 2022 , 101690	5.4	0
148	TOPOLOGY OF THE SecA ATPase BOUND TO LARGE UNILAMELLAR VESICLES.. <i>Journal of Molecular Biology</i> , 2022 , 167607	6.5	0
147	The SecA ATPase motor protein binds to Escherichia coli liposomes only as monomers. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020 , 1862, 183358	3.8	3
146	Binding of SecA ATPase monomers and dimers to lipid vesicles. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020 , 1862, 183112	3.8	3
145	Dropping Out and Other Fates of Transmembrane Segments Inserted by the SecA ATPase. <i>Journal of Molecular Biology</i> , 2019 , 431, 2006-2019	6.5	
144	Stabilization of SecA ATPase by the primary cytoplasmic salt of Escherichia coli. <i>Protein Science</i> , 2019 , 28, 984-989	6.3	4
143	Structural Relaxation Processes and Collective Dynamics of Water in Biomolecular Environments. <i>Journal of Physical Chemistry B</i> , 2019 , 123, 480-486	3.4	12
142	Computed Free Energies of Peptide Insertion into Bilayers are Independent of Computational Method. <i>Journal of Membrane Biology</i> , 2018 , 251, 345-356	2.3	15
141	The importance of the membrane interface as the reference state for membrane protein stability. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018 , 1860, 2539-2548	3.8	6
140	Transmembrane helices containing a charged arginine are thermodynamically stable. <i>European Biophysics Journal</i> , 2017 , 46, 627-637	1.9	15
139	YidC Insertase of Escherichia coli: Water Accessibility and Membrane Shaping. <i>Structure</i> , 2017 , 25, 1403-1414.e30	14.3	0
138	Determination of the Structure of Fluid Lipid Bilayer Membranes 2017 , 1-19		3
137	Interleaflet mixing and coupling in liquid-disordered phospholipid bilayers. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016 , 1858, 354-62	3.8	23
136	Anomalous behavior of water inside the SecY translocon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 9016-21	11.5	34
135	SecA drives transmembrane insertion of RodZ, an unusual single-span membrane protein. <i>Journal of Molecular Biology</i> , 2015 , 427, 1023-37	6.5	21
134	Mechanisms of integral membrane protein insertion and folding. <i>Journal of Molecular Biology</i> , 2015 , 427, 999-1022	6.5	221
133	The messy process of guiding proteins into membranes. <i>ELife</i> , 2015 , 4,	8.9	1

132	Spontaneous transmembrane helix insertion thermodynamically mimics translocon-guided insertion. <i>Nature Communications</i> , 2014 , 5, 4863	17.4	79
131	Galactoside-binding site in LacY. <i>Biochemistry</i> , 2014 , 53, 1536-43	3.2	11
130	Topology, dimerization, and stability of the single-span membrane protein CadC. <i>Journal of Molecular Biology</i> , 2014 , 426, 2942-57	6.5	17
129	Copper-transporting P-type ATPases use a unique ion-release pathway. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 43-8	17.6	77
128	Structural interactions of a voltage sensor toxin with lipid membranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E5463-70	11.5	43
127	Conformational states of melittin at a bilayer interface. <i>Biophysical Journal</i> , 2013 , 104, L12-4	2.9	45
126	Charge composition features of model single-span membrane proteins that determine selection of YidC and SecYEG translocase pathways in Escherichia coli. <i>Journal of Biological Chemistry</i> , 2013 , 288, 7704-7716	5.4	30
125	Ser/Thr motifs in transmembrane proteins: conservation patterns and effects on local protein structure and dynamics. <i>Journal of Membrane Biology</i> , 2012 , 245, 717-30	2.3	30
124	Hydrogen-bond energetics drive helix formation in membrane interfaces. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 178-82	3.8	40
123	Water wires in atomistic models of the Hv1 proton channel. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 286-93	3.8	58
122	Hydrogen bond dynamics in membrane protein function. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 942-50	3.8	54
121	Coupling between the voltage-sensing and pore domains in a voltage-gated potassium channel. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 1726-36	3.8	17
120	Assembly and Stability of Helical Membrane Proteins. <i>Soft Matter</i> , 2012 , 8, 7742-7752	3.6	24
119	Microscopic origin of gating current fluctuations in a potassium channel voltage sensor. <i>Biophysical Journal</i> , 2012 , 102, L44-6	2.9	21
118	Proton-coupled dynamics in lactose permease. <i>Structure</i> , 2012 , 20, 1893-904	5.2	46
117	Acyl-chain methyl distributions of liquid-ordered and -disordered membranes. <i>Biophysical Journal</i> , 2011 , 100, 1455-62	2.9	60
116	In silico partitioning and transmembrane insertion of hydrophobic peptides under equilibrium conditions. <i>Journal of the American Chemical Society</i> , 2011 , 133, 15487-95	16.4	79
115	Membrane partitioning: "classical" and "nonclassical" hydrophobic effects. <i>Journal of Membrane Biology</i> , 2011 , 239, 5-14	2.3	52

114	Structure and dynamics of cholesterol-containing polyunsaturated lipid membranes studied by neutron diffraction and NMR. <i>Journal of Membrane Biology</i> , 2011 , 239, 63-71	2.3	31
113	Arginine in membranes: the connection between molecular dynamics simulations and translocon-mediated insertion experiments. <i>Journal of Membrane Biology</i> , 2011 , 239, 35-48	2.3	94
112	Structural dynamics of the S4 voltage-sensor helix in lipid bilayers lacking phosphate groups. <i>Journal of Physical Chemistry B</i> , 2011 , 115, 8732-8	3.4	15
111	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, E359-64	11.5	45
110	Down-state model of the voltage-sensing domain of a potassium channel. <i>Biophysical Journal</i> , 2010 , 98, 2857-66	2.9	29
109	CD spectroscopy of peptides and proteins bound to large unilamellar vesicles. <i>Journal of Membrane Biology</i> , 2010 , 236, 247-53	2.3	63
108	Dynamics of SecY translocons with translocation-defective mutations. <i>Structure</i> , 2010 , 18, 847-57	5.2	41
107	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, 11588-93	11.5	72
106	Rhomboid protease dynamics and lipid interactions. <i>Structure</i> , 2009 , 17, 395-405	5.2	91
105	MPEX: a tool for exploring membrane proteins. <i>Protein Science</i> , 2009 , 18, 2624-8	6.3	196
104	Biophysical dissection of membrane proteins. <i>Nature</i> , 2009 , 459, 344-6	50.4	223
103	Structure and hydration of membranes embedded with voltage-sensing domains. <i>Nature</i> , 2009 , 462, 473-9	50.4	166
102	pH dependence of sphingosine aggregation. <i>Biophysical Journal</i> , 2009 , 96, 2727-33	2.9	38
101	A novel fluorescent probe that senses the physical state of lipid bilayers. <i>Biophysical Journal</i> , 2009 , 96, 4631-41	2.9	15
100	Aggregation behavior of an ultra-pure lipopolysaccharide that stimulates TLR-4 receptors. <i>Biophysical Journal</i> , 2008 , 95, 986-93	2.9	49
99	How translocons select transmembrane helices. <i>Annual Review of Biophysics</i> , 2008 , 37, 23-42	21.1	164
98	Selective approach to use of upper gastroesophageal imaging study after laparoscopic Roux-en-Y gastric bypass. <i>Surgery for Obesity and Related Diseases</i> , 2008 , 4, 122-5	3	32
97	Molecular code for protein insertion in the endoplasmic reticulum membrane is similar for N(in)-C(out) and N(out)-C(in) transmembrane helices. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 15702-7	11.5	63

96	Self-induced docking site of a deeply embedded peripheral membrane protein. <i>Biophysical Journal</i> , 2007 , 92, 517-24	2.9	49
95	Molecular code for transmembrane-helix recognition by the Sec61 translocon. <i>Nature</i> , 2007 , 450, 1026-30	30.4	545
94	Hydration of POPC bilayers studied by 1H-PFG-MAS-NOESY and neutron diffraction. <i>European Biophysics Journal</i> , 2007 , 36, 281-91	1.9	71
93	Membrane protein insertion: the biology-physics nexus. <i>Journal of General Physiology</i> , 2007 , 129, 363-9	3.4	57
92	Biochemistry. Crowds of syntaxins. <i>Science</i> , 2007 , 317, 1045-6	33.3	3
91	Folding amphipathic helices into membranes: amphiphilicity trumps hydrophobicity. <i>Journal of Molecular Biology</i> , 2007 , 370, 459-70	6.5	129
90	Translocon-Assisted Folding of Membrane Proteins: New Insights into Lipid-Protein Interactions. <i>FASEB Journal</i> , 2007 , 21, A208	0.9	
89	Membrane Protein Insertion: The Biology/Physics Nexus. <i>Journal of Cell Biology</i> , 2007 , 177, i11-i11	7.3	
88	Membrane proteins pumping along [Current Opinion in Structural Biology 2005, 15:375-377]. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 137	8.1	
87	AND/R: Advanced neutron diffractometer/reflectometer for investigation of thin films and multilayers for the life sciences. <i>Review of Scientific Instruments</i> , 2006 , 77, 74301-7430111	1.7	114
86	Diffraction-based density restraints for membrane and membrane-peptide molecular dynamics simulations. <i>Biophysical Journal</i> , 2006 , 91, 3617-29	2.9	16
85	A voltage-sensor water pore. <i>Biophysical Journal</i> , 2006 , 91, L90-2	2.9	78
84	Investigation of finite system-size effects in molecular dynamics simulations of lipid bilayers. <i>Journal of Physical Chemistry B</i> , 2006 , 110, 24157-64	3.4	47
83	Lipid Bilayers, Translocons and the Shaping of Polypeptide Structure 2006 , 1-25		1
82	Asn- and Asp-mediated interactions between transmembrane helices during translocon-mediated membrane protein assembly. <i>EMBO Reports</i> , 2006 , 7, 1111-6	6.5	60
81	Experimental validation of molecular dynamics simulations of lipid bilayers: a new approach. <i>Biophysical Journal</i> , 2005 , 88, 805-17	2.9	144
80	An experiment-based algorithm for predicting the partitioning of unfolded peptides into phosphatidylcholine bilayer interfaces. <i>Biochemistry</i> , 2005 , 44, 12614-9	3.2	42
79	Membrane insertion of a potassium-channel voltage sensor. <i>Science</i> , 2005 , 307, 1427	33.3	158

78	A comprehensive classification system for lipids. <i>Journal of Lipid Research</i> , 2005 , 46, 839-61	6.3	1060
77	Recognition of transmembrane helices by the endoplasmic reticulum translocon. <i>Nature</i> , 2005 , 433, 377-81	8.1	801
76	Transmembrane helices before, during, and after insertion. <i>Current Opinion in Structural Biology</i> , 2005 , 15, 378-86	8.1	113
75	A comprehensive classification system for lipids. <i>European Journal of Lipid Science and Technology</i> , 2005 , 107, 337-364	3	71
74	How hydrogen bonds shape membrane protein structure. <i>Advances in Protein Chemistry</i> , 2005 , 72, 157-72		36
73	Interface connections of a transmembrane voltage sensor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 15059-64	11.5	192
72	The machinery of membrane protein assembly. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 397-404	8.1	103
71	The progress of membrane protein structure determination. <i>Protein Science</i> , 2004 , 13, 1948-9	6.3	248
70	Interfacial folding and membrane insertion of a designed helical peptide. <i>Biochemistry</i> , 2004 , 43, 5782-91	3.2	84
69	Reversible refolding of the diphtheria toxin T-domain on lipid membranes. <i>Biochemistry</i> , 2004 , 43, 7451-8	3.2	53
68	Reversible unfolding of beta-sheets in membranes: a calorimetric study. <i>Journal of Molecular Biology</i> , 2004 , 342, 703-11	6.5	32
67	Translocons, thermodynamics, and the folding of membrane proteins. <i>FEBS Letters</i> , 2003 , 555, 116-21	3.8	48
66	Determining the membrane topology of proteins: insertion pathway of a transmembrane helix of annexin 12. <i>Biochemistry</i> , 2002 , 41, 13617-26	3.2	42
65	MPtopo: A database of membrane protein topology. <i>Protein Science</i> , 2001 , 10, 455-8	6.3	150
64	How membranes shape protein structure. <i>Journal of Biological Chemistry</i> , 2001 , 276, 32395-8	5.4	255
63	Protein chemistry at membrane interfaces: non-additivity of electrostatic and hydrophobic interactions. <i>Journal of Molecular Biology</i> , 2001 , 309, 543-52	6.5	105
62	Energetics, stability, and prediction of transmembrane helices. <i>Journal of Molecular Biology</i> , 2001 , 312, 927-34	6.5	211
61	Alphas and taus of tryptophan fluorescence in membranes. <i>Biophysical Journal</i> , 2001 , 81, 1825-7	2.9	19

60	Structure, location, and lipid perturbations of melittin at the membrane interface. <i>Biophysical Journal</i> , 2001 , 80, 801-11	2.9	245
59	Detergent-like permeabilization of anionic lipid vesicles by melittin. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2001 , 1514, 253-60	3.8	191
58	Peptides in Lipid Bilayers: Determination of Location by Absolute-Scale X-ray Refinement 2001 , 189-206		1
57	How to measure and analyze tryptophan fluorescence in membranes properly, and why bother?. <i>Analytical Biochemistry</i> , 2000 , 285, 235-45	3.1	368
56	Formation and characterization of a single Trp-Trp cross-link in indolicidin that confers protease stability without altering antimicrobial activity. <i>Journal of Biological Chemistry</i> , 2000 , 275, 12017-22	5.4	30
55	Designing transmembrane alpha-helices that insert spontaneously. <i>Biochemistry</i> , 2000 , 39, 4432-42	3.2	126
54	Determining the membrane topology of peptides by fluorescence quenching. <i>Biochemistry</i> , 2000 , 39, 161-70	3.2	73
53	Membrane protein folding and stability: physical principles. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1999 , 28, 319-65		1468
52	CD spectra of indolicidin antimicrobial peptides suggest turns, not polyproline helix. <i>Biochemistry</i> , 1999 , 38, 12313-9	3.2	122
51	Folding of amphipathic alpha-helices on membranes: energetics of helix formation by melittin. <i>Journal of Molecular Biology</i> , 1999 , 285, 1363-9	6.5	291
50	An amphipathic alpha-helix at a membrane interface: a structural study using a novel X-ray diffraction method. <i>Journal of Molecular Biology</i> , 1999 , 290, 99-117	6.5	178
49	Hydrophobic interactions of peptides with membrane interfaces. <i>BBA - Biomembranes</i> , 1998 , 1376, 339-52		428
48	Protein folding in membranes: determining energetics of peptide-bilayer interactions. <i>Methods in Enzymology</i> , 1998 , 295, 62-87	1.7	208
47	Folding of beta-sheet membrane proteins: a hydrophobic hexapeptide model. <i>Journal of Molecular Biology</i> , 1998 , 277, 1091-110	6.5	188
46	Determination of the hydrocarbon core structure of fluid dioleoylphosphocholine (DOPC) bilayers by x-ray diffraction using specific bromination of the double-bonds: effect of hydration. <i>Biophysical Journal</i> , 1998 , 74, 2419-33	2.9	146
45	The preference of tryptophan for membrane interfaces. <i>Biochemistry</i> , 1998 , 37, 14713-8	3.2	829
44	Critical role of lipid composition in membrane permeabilization by rabbit neutrophil defensins. <i>Journal of Biological Chemistry</i> , 1997 , 272, 24224-33	5.4	118
43	Bilayer interactions of indolicidin, a small antimicrobial peptide rich in tryptophan, proline, and basic amino acids. <i>Biophysical Journal</i> , 1997 , 72, 794-805	2.9	148

42	Mechanism of leakage of contents of membrane vesicles determined by fluorescence reequencing. <i>Methods in Enzymology</i> , 1997 , 278, 474-86	1.7	51
41	Solvation energies of amino acid side chains and backbone in a family of host-guest pentapeptides. <i>Biochemistry</i> , 1996 , 35, 5109-24	3.2	475
40	Interactions of monomeric rabbit neutrophil defensins with bilayers: comparison with dimeric human defensin HNP-2. <i>Biochemistry</i> , 1996 , 35, 11888-94	3.2	79
39	Experimentally determined hydrophobicity scale for proteins at membrane interfaces. <i>Nature Structural and Molecular Biology</i> , 1996 , 3, 842-8	17.6	1366
38	The Liquid-Crystallographic Structure of Fluid Lipid Bilayer Membranes 1996 , 127-144		15
37	Structure, function, and membrane integration of defensins. <i>Current Opinion in Structural Biology</i> , 1995 , 5, 521-7	8.1	357
36	The evolution of proteins from random amino acid sequences: II. Evidence from the statistical distributions of the lengths of modern protein sequences. <i>Journal of Molecular Evolution</i> , 1994 , 38, 383-94 ¹	3.1	14
35	Interactions between human defensins and lipid bilayers: evidence for formation of multimeric pores. <i>Protein Science</i> , 1994 , 3, 1362-73	6.3	321
34	Peptides in lipid bilayers: structural and thermodynamic basis for partitioning and folding. <i>Current Opinion in Structural Biology</i> , 1994 , 4, 79-86	8.1	173
33	Hydropathy Plots and the Prediction of Membrane Protein Topology 1994 , 97-124		15
32	Partitioning of tryptophan side-chain analogs between water and cyclohexane. [Erratum to document cited in CA118(1):7358m]. <i>Biochemistry</i> , 1993 , 32, 9262-9262	3.2	4
31	Membrane partitioning: distinguishing bilayer effects from the hydrophobic effect. <i>Biochemistry</i> , 1993 , 32, 6307-12	3.2	201
30	The evolution of proteins from random amino acid sequences. I. Evidence from the lengthwise distribution of amino acids in modern protein sequences. <i>Journal of Molecular Evolution</i> , 1993 , 36, 79-95 ^{3.1}	3.1	38
29	Appreciation. Jane s. Richardson: biophysical society national lecturer 1992. <i>Biophysical Journal</i> , 1992 , 63, 1185	2.9	73
28	Structure of a fluid dioleoylphosphatidylcholine bilayer determined by joint refinement of x-ray and neutron diffraction data. III. Complete structure. <i>Biophysical Journal</i> , 1992 , 61, 434-47	2.9	585
27	Partitioning of tryptophan side-chain analogs between water and cyclohexane. <i>Biochemistry</i> , 1992 , 31, 12813-8	3.2	48
26	Amino acid preferences of small proteins. Implications for protein stability and evolution. <i>Journal of Molecular Biology</i> , 1992 , 227, 991-5	6.5	45
25	Membrane structures in normal and essential fatty acid-deficient stratum corneum: characterization by ruthenium tetroxide staining and x-ray diffraction. <i>Journal of Investigative Dermatology</i> , 1991 , 96, 215-23	4.3	252

24	Transbilayer distribution of bromine in fluid bilayers containing a specifically brominated analogue of dioleoylphosphatidylcholine. <i>Biochemistry</i> , 1991 , 30, 6997-7008	3.2	65
23	Observations concerning topology and locations of helix ends of membrane proteins of known structure. <i>Journal of Membrane Biology</i> , 1990 , 115, 145-58	2.3	31
22	The nature of the hydrophobic binding of small peptides at the bilayer interface: implications for the insertion of transbilayer helices. <i>Biochemistry</i> , 1989 , 28, 3421-37	3.2	437
21	Linear optimization of predictors for secondary structure. Application to transbilayer segments of membrane proteins. <i>Journal of Molecular Biology</i> , 1989 , 210, 195-209	6.5	15
20	Structure of lamellar lipid domains and corneocyte envelopes of murine stratum corneum. An X-ray diffraction study. <i>Biochemistry</i> , 1988 , 27, 3725-32	3.2	319
19	Lipid bilayer perturbations induced by simple hydrophobic peptides. <i>Biochemistry</i> , 1987 , 26, 6127-34	3.2	31
18	Mixtures of a series of homologous hydrophobic peptides with lipid bilayers: a simple model system for examining the protein-lipid interface. <i>Biochemistry</i> , 1986 , 25, 2605-12	3.2	53
17	Solubility of Volatile Hydrocarbons in Lipid Bilayers 1986 , 279-295		1
16	The Physical Nature of Planar Bilayer Membranes 1986 , 3-35		28
15	Hexane dissolved in dioleoyllecithin bilayers has a partial molar volume of approximately zero. <i>Biochemistry</i> , 1985 , 24, 4637-45	3.2	53
14	Preparation of multilamellar vesicles of defined size-distribution by solvent-spherule evaporation. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1985 , 812, 793-801	3.8	23
13	Behavior of hexane dissolved in dioleoylphosphatidylcholine bilayers: an NMR and calorimetric study. <i>Journal of the American Chemical Society</i> , 1984 , 106, 6909-6912	16.4	16
12	Behavior of hexane dissolved in dimyristoylphosphatidylcholine bilayers: an NMR and calorimetric study. <i>Journal of the American Chemical Society</i> , 1984 , 106, 915-920	16.4	24
11	Oriental Waves in Cell Membranes. <i>Molecular Crystals and Liquid Crystals</i> , 1982 , 88, 127-135		4
10	Location of hexane in lipid bilayers determined by neutron diffraction. <i>Nature</i> , 1981 , 290, 161-163	50.4	128
9	The lipid bilayer as a "solvent" for small hydrophobic molecules. <i>Nature</i> , 1976 , 262, 421-2	50.4	50
8	High precision capacitance bridge for studying lipid bilayer membranes. <i>Review of Scientific Instruments</i> , 1975 , 46, 1462-6	1.7	12
7	Temperature-dependent structural changes in planar bilayer membranes: solvent "freeze-out". <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1974 , 356, 8-16	3.8	47

6	The surface charge and double layers of thin lipid films formed from neutral lipids. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1973 , 323, 343-50	3.8	36
5	Capacitance, area, and thickness variations in thin lipid films. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1973 , 323, 7-22	3.8	117
4	The buffer value and transmembrane potential of Escherichia coli. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1972 , 255, 780-5	3.8	5
3	Analysis of the torus surrounding planar lipid bilayer membranes. <i>Biophysical Journal</i> , 1972 , 12, 432-45	2.9	90
2	A study of lipid bilayer membrane stability using precise measurements of specific capacitance. <i>Biophysical Journal</i> , 1970 , 10, 1127-48	2.9	129
1	Lipid Bilayers, Translocons and the Shaping of Polypeptide Structure ³		