

CITATION REPORT

List of articles citing

Membrane protein folding and stability: physical principles

DOI: 10.1146/annurev.biophys.28.1.319

Annual Review of Biophysics and Biomolecular
Structure, 1999, 28, 319-65.

Source: <https://exaly.com/paper-pdf/30839976/citation-report.pdf>

Version: 2024-04-28

This report has been generated based on the citations recorded by exaly.com for the above article. 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.

#	Paper	IF	Citations
1530	Thermally activated transitions in a bistable three-dimensional optical trap. 1999 , 402, 785-787		132
1529	Injection and detection of a spin-polarized current in a light-emitting diode. 1999 , 402, 787-790		1595
1528	Peptide structural analysis by solid-state NMR spectroscopy. 1999 , 51, 174-90		67
1527	Factors important for fusogenic activity of peptides: molecular modeling study of analogs of fusion peptide of influenza virus hemagglutinin. 1999 , 462, 205-10		37
1526	Membrane protein folding and stability: physical principles. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1999 , 28, 319-65		1468
1525	Hydrophobic forces drive spontaneous membrane insertion of the bacteriophage Pf3 coat protein without topological control. 1999 , 18, 6299-306		84
1524	Structure of bacteriorhodopsin at 1.55 Å resolution. 1999 , 291, 899-911		1309
1523	Probing Membrane Protein Structure and Dynamics by Fluorescence Spectroscopy. 2000 , 1-21		
1522	Turning a reference inside-out: Commentary on an article by Stevens and Arkin entitled: Are membrane proteins 'inside-out' proteins? (Proteins 1999;36:135-143). 2000 , 38, 121-122		16
1521	Turning an opinion inside-out: Rees and Eisenberg's commentary (Proteins 2000;38:121-122) on "Are membrane proteins 'inside-out' proteins?" (Proteins 1999;36:135-143). 2000 , 40, 463-4		13
1520	Dipole lattice membrane model for protein calculations. 2000 , 41, 211-23		24
1519	How to measure and analyze tryptophan fluorescence in membranes properly, and why bother?. 2000 , 285, 235-45		368
1518	Riding the wave: structural and energetic principles of helical membrane proteins. 2000 , 11, 67-71		31
1517	Relating helix tilt in a bilayer to lipid disorder: a mean-field theory. 2000 , 86, 79-83		4
1516	Are we destined to repeat history?. 2000 , 10, 435-7		23
1515	Misfolding of membrane proteins in health and disease: the lady or the tiger?. 2000 , 10, 438-42		85
1514	How proteins adapt to a membrane-water interface. 2000 , 25, 429-34		580

1513	Age-related structural and functional changes of brain mitochondria. 2000 , 28, 329-38	62
1512	An improved tripod amphiphile for membrane protein solubilization. 2000 , 9, 2518-27	46
1511	Influence of the C-terminus of the glycoporphin A transmembrane fragment on the dimerization process. 2000 , 9, 1246-53	28
1510	Unfolding pathways of individual bacteriorhodopsins. 2000 , 288, 143-6	626
1509	A host-guest system to study structure-function relationships of membrane fusion peptides. 2000 , 97, 13097-102	128
1508	Deciphering the folding kinetics of transmembrane helical proteins. 2000 , 97, 14229-34	10
1507	Lattice model of transmembrane polypeptide folding. <i>Physical Review E</i> , 2000 , 63,	2.4 13
1506	Membrane interface-interacting sequences within the ectodomain of the human immunodeficiency virus type 1 envelope glycoprotein: putative role during viral fusion. 2000 , 74, 8038-47	158
1505	Reversible loss of crystallinity on photobleaching purple membrane in the presence of hydroxylamine. 2000 , 301, 869-79	36
1504	Modulation of glycoporphin A transmembrane helix interactions by lipid bilayers: molecular dynamics calculations. 2000 , 302, 727-46	105
1503	Calculations suggest a pathway for the transverse diffusion of a hydrophobic peptide across a lipid bilayer. 2000 , 79, 2322-30	21
1502	The topology of lysine-containing amphipathic peptides in bilayers by circular dichroism, solid-state NMR, and molecular modeling. 2000 , 79, 2644-56	64
1501	Area per lipid and acyl length distributions in fluid phosphatidylcholines determined by (2)H NMR spectroscopy. 2000 , 79, 3172-92	522
1500	Interactions of peptides with liposomes: pore formation and fusion. 2000 , 39, 181-206	71
1499	Structural determinants of purple membrane assembly. 2000 , 1460, 15-26	56
1498	Atomic force microscopy of native purple membrane. 2000 , 1460, 27-38	104
1497	Atomic resolution structures of bacteriorhodopsin photocycle intermediates: the role of discrete water molecules in the function of this light-driven ion pump. 2000 , 1460, 133-56	121
1496	The pre-transmembrane region of the Human immunodeficiency virus type-1 glycoprotein: a novel fusogenic sequence. 2000 , 477, 145-9	81

1495	Structural biology. Unraveling a membrane protein. 2000 , 288, 63-4	9
1494	Helical membrane protein folding, stability, and evolution. 2000 , 69, 881-922	546
1493	Fluorescence Spectroscopy in Peptide and Protein Analysis. 2000 ,	35
1492	Alignment of lysine-anchored membrane peptides under conditions of hydrophobic mismatch: a CD, 15N and 31P solid-state NMR spectroscopy investigation. 2000 , 39, 13106-14	119
1491	Effects of aromatic residues at the ends of transmembrane alpha-helices on helix interactions with lipid bilayers. 2000 , 39, 2071-8	57
1490	Designing transmembrane alpha-helices that insert spontaneously. 2000 , 39, 4432-42	126
1489	Determining the membrane topology of peptides by fluorescence quenching. 2000 , 39, 161-70	73
1488	Prediction of the transmembrane regions of beta-barrel membrane proteins with a neural network-based predictor. 2001 , 10, 779-87	103
1487	Kinetic study of folding and misfolding of diacylglycerol kinase in model membranes. 2001 , 40, 8971-80	57
1486	Hydration of Aromatic Hydrocarbons. 2001 , 105, 10367-10372	60
1485	Ratcheting in post-translational protein translocation: a mathematical model. 2001 , 305, 643-56	48
1484	Protein chemistry at membrane interfaces: non-additivity of electrostatic and hydrophobic interactions. 2001 , 309, 543-52	105
1483	The protein capsid of filamentous bacteriophage PH75 from <i>Thermus thermophilus</i> . 2001 , 309, 401-21	38
1482	Folding of beta-sheets in membranes: specificity and promiscuity in peptide model systems. 2001 , 309, 975-88	44
1481	Energetics, stability, and prediction of transmembrane helices. 2001 , 312, 927-34	211
1480	Interactions of cholesterol with lipid bilayers: the preferred configuration and fluctuations. 2001 , 81, 643-58	107
1479	Structural models of the MscL gating mechanism. 2001 , 81, 917-36	181
1478	Membrane insertion and lipid-protein interactions of bovine seminal plasma protein PDC-109 investigated by spin-label electron spin resonance spectroscopy. 2001 , 81, 2215-25	60

1477	Membrane insertion and orientation of polyalanine peptides: a (15)N solid-state NMR spectroscopy investigation. 2001 , 81, 2251-6	44
1476	Calculation of rigid-body conformational changes using restraint-driven Cartesian transformations. 2001 , 81, 2530-46	20
1475	Structural implications of a Val-->Glu mutation in transmembrane peptides from the EGF receptor. 2001 , 81, 3231-9	7
1474	Voltage-dependent insertion of alamethicin at phospholipid/water and octane/water interfaces. 2001 , 80, 331-46	110
1473	Implicit solvent model studies of the interactions of the influenza hemagglutinin fusion peptide with lipid bilayers. 2001 , 80, 643-55	35
1472	Dynamics of membrane penetration of the fluorescent 7-nitrobenz-2-oxa-1,3-diazol-4-yl (NBD) group attached to an acyl chain of phosphatidylcholine. 2001 , 80, 822-31	101
1471	A simple approach to membrane protein secondary structure and topology based on NMR spectroscopy. 2001 , 80, 994-1003	75
1470	Differential interaction of equinatoxin II with model membranes in response to lipid composition. 2001 , 80, 1343-53	68
1469	Continuum solvent model studies of the interactions of an anticonvulsant drug with a lipid bilayer. 2001 , 80, 2536-45	34
1468	Role of medium--and long-range interactions in discriminating globular and membrane proteins. 2001 , 29, 25-34	17
1467	Dimer interface of transmembrane domains for neu/erbB-2 receptor dimerization and transforming activation: a model revealed by molecular dynamics simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2001 , 19, 15-31	3.6 11
1466	Detergents as tools in membrane biochemistry. 2001 , 276, 32403-6	426
1465	Solid-state NMR investigations of interaction contributions that determine the alignment of helical polypeptides in biological membranes. 2001 , 504, 161-5	24
1464	Investigating the conformational coupling between the transmembrane and cytoplasmic domains of a single-spanning membrane protein. A 1H-NMR study. 2001 , 505, 431-5	4
1463	Concerted influence of key amino acids on the lipid binding properties of a single-spanning membrane protein: NMR and mutational analysis. 2001 , 40, 9993-10000	8
1462	Peptide backbone chemistry and membrane channel function: effects of a single amide-to-ester replacement on gramicidin channel structure and function. 2001 , 40, 1460-72	9
1461	Self-association and membrane-binding behavior of melittins containing trifluoroisoleucine. 2001 , 123, 7407-13	79
1460	Conversion of phospholamban into a soluble pentameric helical bundle. 2001 , 40, 6636-45	33

1459	Topology of membrane proteins. 2001 , 41, 364-8		32
1458	Thermal destabilization of rhodopsin and opsin by proteolytic cleavage in bovine rod outer segment disk membranes. 2001 , 40, 11176-83		40
1457	Beta-barrel pore-forming toxins: intriguing dimorphic proteins. 2001 , 40, 9065-73		127
1456	A polyaniline-based peptide cannot form a stable transmembrane alpha-helix in fully hydrated phospholipid bilayers. 2001 , 40, 12103-11		34
1455	Membrane-anchoring interactions of M13 major coat protein. 2001 , 40, 8815-20		28
1454	Distinct molecular surfaces and hydrophobicity of amino acid residues in proteins. 2001 , 41, 1427-35		26
1453	Conformationally specific misfolding of an integral membrane protein. 2001 , 40, 5111-8		23
1452	The effect of cyclization of magainin 2 and melittin analogues on structure, function, and model membrane interactions: implication to their mode of action. 2001 , 40, 6388-97		71
1451	What the structure of a calcium pump tells us about its mechanism. 2001 , 356, 665-83		64
1450	What the structure of a calcium pump tells us about its mechanism. 2001 , 356, 665-683		106
1449	Molecular recognition within the membrane milieu: implications for the structure and function of membrane Pproteins. <i>Journal of Membrane Biology</i> , 2001 , 182, 91-104	2.3	23
1448	Interactions of cyclic AMP and its dibutyryl analogue with model membrane: X-ray diffraction and Raman spectroscopic study using cubic liquid-crystalline phases of monoolein. 2001 , 90, 75-87		9
1447	Approaches to determining membrane protein structures to high resolution: do selections of subpopulations occur?. 2001 , 32, 75-90		23
1446	Molecular dynamics simulations of antimicrobial peptides: From membrane binding to trans-membrane channels. 2001 , 83, 166-179		36
1445	Computation and mutagenesis suggest a right-handed structure for the synaptobrevin transmembrane dimer. 2001 , 45, 313-7		50
1444	Model of the 3-D structure of the GLUT3 glucose transporter and molecular dynamics simulation of glucose transport. 2001 , 42, 531-541		39
1443	A high-throughput screen for identifying transmembrane pore-forming peptides. 2001 , 293, 258-63		40
1442	Desaturases fused to their electron donor. 2001 , 103, 158-180		56

1441	Inactivation mechanism of the membrane protein diacylglycerol kinase in detergent solution. 2001 , 10, 378-83	39
1440	MPtopo: A database of membrane protein topology. 2001 , 10, 455-8	150
1439	Anionic lipids stimulate Sec-independent insertion of a membrane protein lacking charged amino acid side chains. 2001 , 2, 403-8	38
1438	Interhelical hydrogen bonds in the CFTR membrane domain. 2001 , 8, 597-601	87
1437	Helical membrane proteins: diversity of functions in the context of simple architecture. 2001 , 11, 370-6	81
1436	Cholesterol-dependent formation of GM1 ganglioside-bound amyloid beta-protein, an endogenous seed for Alzheimer amyloid. 2001 , 276, 24985-90	305
1435	Calorimetric investigations of the structural stability and interactions of colicin B domains in aqueous solution and in the presence of phospholipid bilayers. 2001 , 276, 13563-72	6
1434	Structural Mimicry in G Protein-Coupled Receptors: Implications of the High-Resolution Structure of Rhodopsin for Structure-Function Analysis of Rhodopsin-Like Receptors. 2001 , 60, 1-19	407
1433	The transmembrane domain of syntaxin 1A is critical for cytoplasmic domain protein-protein interactions. 2001 , 276, 15458-65	31
1432	Specificity in transmembrane helix-helix interactions can define a hierarchy of stability for sequence variants. 2001 , 98, 14340-4	158
1431	Insertion of PsaK into the thylakoid membrane in a "Horseshoe" conformation occurs in the absence of signal recognition particle, nucleoside triphosphates, or functional albino3. 2001 , 276, 36200-6	44
1430	How membranes shape protein structure. 2001 , 276, 32395-8	255
1429	Polar side chains drive the association of model transmembrane peptides. 2001 , 98, 880-5	310
1428	A central role for the T1 domain in voltage-gated potassium channel formation and function. 2001 , 276, 28493-502	38
1427	Conformation of a purified "spontaneously" inserting thylakoid membrane protein precursor in aqueous solvent and detergent micelles. 2001 , 276, 14607-13	8
1426	Agonist-induced conformational changes at the cytoplasmic side of transmembrane segment 6 in the beta 2 adrenergic receptor mapped by site-selective fluorescent labeling. 2001 , 276, 9279-90	123
1425	Self-Assembling Peptide Systems in Biology, Medicine and Engineering. 2002 ,	2
1424	Sequence determinants of the energetics of folding of a transmembrane four-helix-bundle protein. 2002 , 99, 8568-72	63

1423	Lipid-protein interactions in DHPC micelles containing the integral membrane protein OmpX investigated by NMR spectroscopy. 2002 , 99, 13533-7	118
1422	The streptococcal hyaluronan synthases are inhibited by sulfhydryl-modifying reagents, but conserved cysteine residues are not essential for enzyme function. 2002 , 277, 13943-51	20
1421	Refolding of Thermally Denatured Bacteriorhodopsin in Purple Membrane□ 2002 , 106, 723-729	15
1420	Introducing an Implicit Membrane in Generalized Born/Solvent Accessibility Continuum Solvent Models. 2002 , 106, 8726-8738	143
1419	The alpha-helix and the organization and gating of channels. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2002 , 31, 207-33	57
1418	Lateral sequestration of phosphatidylinositol 4,5-bisphosphate by the basic effector domain of myristoylated alanine-rich C kinase substrate is due to nonspecific electrostatic interactions. 2002 , 277, 34401-12	177
1417	Multiple membrane-associated tryptophan residues contribute to the transport activity and substrate specificity of the human multidrug resistance protein, MRP1. 2002 , 277, 49495-503	42
1416	Sphingomyelin and cholesterol promote HIV-1 gp41 pretransmembrane sequence surface aggregation and membrane restructuring. 2002 , 277, 21776-85	109
1415	Surface-sensitive X-ray and neutron scattering characterization of planar lipid model membranes and lipid/peptide interactions. 2002 , 52, 117-161	16
1414	The energetics of peptide-lipid interactions: Modulation by interfacial dipoles and cholesterol. 2002 , 309-338	6
1413	Guanidine hydrochloride induced equilibrium unfolding studies of colicin B and its channel-forming fragment. 2002 , 41, 5340-7	9
1412	A critical residue in the folding pathway of an integral membrane protein. 2002 , 41, 9021-5	16
1411	Membrane Perturbations Induced by Integral Proteins: Role of Conformational Restrictions of the Lipid Chains. 2002 , 18, 6356-6364	30
1410	Effect of variations in the structure of a polyleucine-based alpha-helical transmembrane peptide on its interaction with phosphatidylcholine bilayers. 2002 , 41, 9197-207	34
1409	Deciphering the role of individual acyl chains in the interaction network between phosphatidylserines and a single-spanning membrane protein. 2002 , 41, 13611-6	12
1408	Conformation and stability of alpha-helical membrane proteins. 2. Influence of pH and salts on stability and unfolding of rhodopsin. 2002 , 41, 3536-45	33
1407	Evidence of a tendency to self-association of the transmembrane domain of ErbB-2 in fluid phospholipid bilayers. 2002 , 41, 2341-52	29
1406	Positioning and Stabilization of Dynorphin Peptides in Membrane Bilayers: the Mechanistic Role of Aromatic and Basic Residues Revealed from Comparative MD Simulations. 2002 , 106, 209-218	19

1405	Lipid dependence of membrane anchoring properties and snorkeling behavior of aromatic and charged residues in transmembrane peptides. 2002 , 41, 7190-8		99
1404	Polar residues in membrane domains of proteins: molecular basis for helix-helix association in a mutant CFTR transmembrane segment. 2002 , 41, 3647-53		53
1403	Membrane insertion and dissociation processes of a model transmembrane helix. 2002 , 41, 12407-13		25
1402	Stability of an ion channel in lipid bilayers: implicit solvent model calculations with gramicidin. 2002 , 41, 6946-54		20
1401	Mechanism and kinetics of delta-lysine interaction with phospholipid vesicles. 2002 , 41, 11044-56		106
1400	Computer simulation studies of model biological membranes. 2002 , 35, 482-9		170
1399	Topological stability and self-association of a completely hydrophobic model transmembrane helix in lipid bilayers. 2002 , 41, 3073-80		49
1398	Structures of neat and hydrated 1-octanol from computer simulations. 2002 , 124, 15085-93		101
1397	Conformations, flexibility, and interactions observed on individual membrane proteins by atomic force microscopy. 2002 , 68, 257-99		13
1396	Free energy determinants of peptide association with lipid bilayers. 2002 , 52, 205-253		36
1395	Amino Acid Side-chain Hydrophobicity. 2002 ,		6
1394	Mechanism of fast protein folding. 2002 , 71, 783-815		106
1393	Membrane Protein Insertion into Bacterial Membranes and the Endoplasmic Reticulum. 2002 , 107-130		1
1392	The role of electrostatic and nonpolar interactions in the association of peripheral proteins with membranes. 2002 , 277-307		51
1391	Stability of the lactose permease in detergent solutions. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2002 , 1564, 47-56	3.8	35
1390	Crystal structure of rhodopsin: a template for cone visual pigments and other G protein-coupled receptors. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2002 , 1565, 168-82	3.8	89
1389	Structural studies on rhodopsin. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2002 , 1565, 183-95	3.8	18
1388	High free energy of lipid/protein interaction in biological membranes. 2002 , 514, 340-2		6

1387	Interaction between ErbB-1 and ErbB-2 transmembrane domains in bilayer membranes. 2002 , 519, 103-7		12
1386	The activation energy for insertion of transmembrane alpha-helices is dependent on membrane composition. 2002 , 319, 839-53		57
1385	The membrane-bound conformation of alpha-lactalbumin studied by NMR-monitored 1H exchange. 2002 , 321, 99-110		68
1384	A novel scoring function for predicting the conformations of tightly packed pairs of transmembrane alpha-helices. 2002 , 321, 363-78		68
1383	Standardizing the free energy change of transmembrane helix-helix interactions. 2002 , 323, 563-71		110
1382	Secondary and tertiary structure formation of the beta-barrel membrane protein OmpA is synchronized and depends on membrane thickness. 2002 , 324, 319-30		145
1381	Ca ²⁺ -ATPase structure in the E1 and E2 conformations: mechanism, helix-helix and helix-lipid interactions. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2002 , 1565, 246-66	3.8	49
1380	Geometry and intrinsic tilt of a tryptophan-anchored transmembrane alpha-helix determined by (2)H NMR. 2002 , 83, 1479-88		156
1379	Interactions of phospholipids with the potassium channel KcsA. 2002 , 83, 2026-38		90
1378	Interaction of cardiotoxins with membranes: a molecular modeling study. 2002 , 83, 144-53		43
1377	Organization of model helical peptides in lipid bilayers: insight into the behavior of single-span protein transmembrane domains. 2002 , 83, 345-58		40
1376	Analysis and evaluation of channel models: simulations of alamethicin. 2002 , 83, 2393-407		117
1375	Stability of bacteriorhodopsin alpha-helices and loops analyzed by single-molecule force spectroscopy. 2002 , 83, 3578-88		150
1374	Segregation of photosystems in thylakoid membranes as a critical phenomenon. 2002 , 82, 1719-30		15
1373	Deuterium/hydrogen exchange factors measured by solution nuclear magnetic resonance spectroscopy as indicators of the structure and topology of membrane proteins. 2002 , 82, 2176-83		45
1372	Constant normal pressure, constant surface tension, and constant temperature molecular dynamics simulation of hydrated 1,2-dilignoceroylphosphatidylcholine monolayer. 2002 , 82, 2511-9		20
1371	Influence of the environment in the conformation of alpha-helices studied by protein database search and molecular dynamics simulations. 2002 , 82, 3207-13		29
1370	Hydrophobic Matching Mechanism Investigated by Molecular Dynamics Simulations. 2002 , 18, 1340-1351		79

1369	On the regulatory role of dipeptidyl peptidase IV (=CD=adenosine deaminase complexing protein) on adenosine deaminase activity. 2002 , 1587, 21-30	8
1368	The evolution of structural databases. 2002 , 20, 498-501	13
1367	Crystal structure of rhodopsin: a G-protein-coupled receptor. 2002 , 3, 963-7	36
1366	Polar mutations in membrane proteins as a biophysical basis for disease. 2002 , 66, 350-8	46
1365	Imaging and manipulation of biological structures with the AFM. 2002 , 33, 385-97	324
1364	Experimental and computational studies of determinants of membrane-protein folding. 2002 , 6, 878-84	31
1363	Interhelical hydrogen bonds and spatial motifs in membrane proteins: polar clamps and serine zippers. 2002 , 47, 209-18	141
1362	Optimal potentials for predicting inter-helical packing in transmembrane proteins. 2002 , 49, 342-9	21
1361	Stability scale and atomic solvation parameters extracted from 1023 mutation experiments. 2002 , 49, 483-92	68
1360	A protein sequence that can encode native structure by disfavoring alternate conformations. 2002 , 9, 381-8	38
1359	Position of residues in transmembrane peptides with respect to the lipid bilayer: a combined lipid Noes and water chemical exchange approach in phospholipid bicelles. 2002 , 22, 57-64	27
1358	Towards high-resolution solid-state NMR on large uniformly ¹⁵ N- and [¹³ C, ¹⁵ N]-labeled membrane proteins in oriented lipid bilayers. 2002 , 22, 225-47	47
1357	Attraction within the membrane. Forces behind transmembrane protein folding and supramolecular complex assembly. 2002 , 3, 1133-8	43
1356	Pore-forming protein structure analysis in membranes using multiple independent fluorescence techniques. 2002 , 36, 89-101	35
1355	Effects of membrane lipids on ion channel structure and function. 2003 , 38, 161-90	194
1354	[Interaction of cardiotoxin A5 with a membrane: role of conformational heterogeneity and hydrophilic properties]. 2003 , 29, 577-88	4
1353	Domain organization of the MscS mechanosensitive channel of Escherichia coli. 2003 , 22, 36-46	107
1352	Unfolding pathways of native bacteriorhodopsin depend on temperature. 2003 , 22, 5220-9	100

1351	The potassium channel KcsA and its interaction with the lipid bilayer. 2003 , 60, 1581-90	37
1350	Functional significance of the lipid-protein interface in photosynthetic membranes. 2003 , 60, 1591-606	60
1349	The versatile beta-barrel membrane protein. 2003 , 13, 404-11	349
1348	Oligomer formation by Na ⁺ -Cl ⁻ -coupled neurotransmitter transporters. 2003 , 479, 229-36	41
1347	Methodological development of solid-state NMR for characterization of membrane proteins. 2003 , 18A, 111-129	12
1346	Quantitative analysis of membrane protein-amphiphile interactions using resonance energy transfer. 2003 , 317, 171-9	6
1345	Interaction of peptides with binary phospholipid membranes: application of fluorescence methodologies. 2003 , 122, 77-96	29
1344	Influence of cation-pi interactions in different folding types of membrane proteins. 2003 , 103, 251-8	60
1343	An Escherichia coli twin-arginine signal peptide switches between helical and unstructured conformations depending on the hydrophobicity of the environment. 2003 , 270, 3345-52	37
1342	Effective energy function for proteins in lipid membranes. 2003 , 52, 176-92	218
1341	Single molecule mechanochemistry of macromolecules. 2003 , 28, 1271-1295	220
1340	Immobilization and aggregation of the antimicrobial peptide protegrin-1 in lipid bilayers investigated by solid-state NMR. 2003 , 42, 13725-34	78
1339	Hydrophobicity of transmembrane proteins: spatially profiling the distribution. 2003 , 12, 586-99	14
1338	How do helix-helix interactions help determine the folds of membrane proteins? Perspectives from the study of homo-oligomeric helical bundles. 2003 , 12, 647-65	145
1337	Determination of membrane protein stability via thermodynamic coupling of folding to thiol-disulfide interchange. 2003 , 12, 1732-40	41
1336	Alpha-synuclein association with phosphatidylglycerol probed by lipid spin labels. 2003 , 42, 12919-26	94
1335	Aromatic stacking in the sugar binding site of the lactose permease. 2003 , 42, 1377-82	68
1334	Thermal Properties of Bacteriorhodopsin. 2003 , 107, 12045-12053	23

1333	Structural and dynamical changes of the bindin B18 peptide upon binding to lipid membranes. A solid-state NMR study. 2003 , 42, 8377-86		51
1332	Molecular dynamics simulation of dark-adapted rhodopsin in an explicit membrane bilayer: coupling between local retinal and larger scale conformational change. 2003 , 333, 493-514		88
1331	Proteomics of membrane proteins. 2003 , 65, 271-307		24
1330	Characterization of the ABCA transporter subfamily: identification of prokaryotic and eukaryotic members, phylogeny and topology. 2003 , 325, 259-74		103
1329	Utilising structural knowledge in drug design strategies: applications using Relibase. 2003 , 326, 621-36		114
1328	Higher-order interhelical spatial interactions in membrane proteins. 2003 , 327, 251-72		46
1327	A simple method for modeling transmembrane helix oligomers. 2003 , 329, 831-40		69
1326	Pre-transmembrane sequence of Ebola glycoprotein. Interfacial hydrophobicity distribution and interaction with membranes. 2003 , 533, 47-53		36
1325	Translocons, thermodynamics, and the folding of membrane proteins. 2003 , 555, 116-21		48
1324	Synthetic peptides as models for intrinsic membrane proteins. 2003 , 555, 134-8		127
1323	Widespread production of novel soluble protein isoforms by alternative splicing removal of transmembrane anchoring domains. 2003 , 555, 572-8		52
1322	The trials and tribulations of membrane protein folding in vitro. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2003 , 1610, 51-6	3.8	46
1321	Lipid-protein interactions in biological membranes: a structural perspective. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2003 , 1612, 1-40	3.8	664
1320	Hypothesis: spring-loaded boomerang mechanism of influenza hemagglutinin-mediated membrane fusion. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2003 , 1614, 14-23	3.8	71
1319	Solid-state NMR investigation of the depth of insertion of protegrin-1 in lipid bilayers using paramagnetic Mn ²⁺ . 2003 , 85, 2363-73		119
1318	Interactions of hydrophobic peptides with lipid bilayers: Monte Carlo simulations with M2delta. 2003 , 85, 3431-44		45
1317	Interactions of the M2delta segment of the acetylcholine receptor with lipid bilayers: a continuum-solvent model study. 2003 , 85, 3687-95		15
1316	Structural and functional roles of HIV-1 gp41 pretransmembrane sequence segmentation. 2003 , 85, 3769-80		71

1315	Computer simulations of membrane protein folding: structure and dynamics. 2003 , 84, 1902-8		24
1314	Energetics and self-assembly of amphipathic peptide pores in lipid membranes. 2003 , 84, 2242-55		55
1313	Liposome encapsulated nisin Z: optimization, stability and release during milk fermentation. 2003 , 13, 325-336		162
1312	Cotranslational protein integration into the ER membrane is mediated by the binding of nascent chains to translocon proteins. 2003 , 12, 329-41		94
1311	Use of thiol-disulfide equilibria to measure the energetics of assembly of transmembrane helices in phospholipid bilayers. 2003 , 100, 14772-7		126
1310	Molecular dynamics simulations of pentapeptides at interfaces: salt bridge and cation-pi interactions. 2003 , 42, 8976-87		97
1309	Binding of the C-terminal sterile alpha motif (SAM) domain of human p73 to lipid membranes. 2003 , 278, 46878-85		66
1308	Binding of peptides with basic and aromatic residues to bilayer membranes: phenylalanine in the myristoylated alanine-rich C kinase substrate effector domain penetrates into the hydrophobic core of the bilayer. 2003 , 278, 21459-66		94
1307	An ENSEMBLE machine learning approach for the prediction of all-alpha membrane proteins. 2003 , 19 Suppl 1, i205-11		71
1306	Membrane recognition and targeting by lipid-binding domains. <i>Science Signaling</i> , 2003 , 2003, re16	8.8	108
1305	The interaction of peripheral proteins and membranes studied with alpha-lactalbumin and phospholipid bilayers of various compositions. 2003 , 278, 21790-7		54
1304	In silico prediction of the structure of membrane proteins: is it feasible?. 2003 , 4, 341-8		20
1303	Interfacial domains in Sindbis virus 6K protein. Detection and functional characterization. 2003 , 278, 2051-7		47
1302	Hydrophobic coupling of lipid bilayer energetics to channel function. 2003 , 121, 477-93		77
1301	MaxSubSeq: an algorithm for segment-length optimization. The case study of the transmembrane spanning segments. 2003 , 19, 500-5		22
1300	Molecular dynamics simulations of the transmembrane domain of the oncogenic ErbB2 receptor dimer in a DMPC bilayer. <i>Journal of Biomolecular Structure and Dynamics</i> , 2003 , 21, 179-200	3.6	12
1299	Molecular dynamics simulations of ionic concentration gradients across model bilayers. 2003 , 118, 1957-1969		9
1298	Exploiting luminescence spectroscopy to elucidate the interaction between sugar and a tryptophan residue in the lactose permease of Escherichia coli. 2003 , 100, 12706-11		55

1297	How hydrophobic is alanine?. 2003 , 278, 29389-93	26
1296	Folding and insertion of the outer membrane protein OmpA is assisted by the chaperone Skp and by lipopolysaccharide. 2003 , 278, 9092-9	132
1295	X-ray crystallographic analysis of lipid-protein interactions in the bacteriorhodopsin purple membrane. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2003 , 32, 285-310	47
1294	Position-dependence of stabilizing polar interactions of asparagine in transmembrane helical bundles. 2003 , 42, 6400-7	65
1293	Construction of helix-bundle membrane proteins. 2003 , 63, 19-46	36
1292	Membrane-Macromolecule Interactions and their Structural Consequences. 2003 , 7, 315-346	
1291	Intermolecular interactions with/within cell membranes and the trinity of membrane potentials: kinetics and imaging. 2003 , 31, 990-6	76
1290	Crystallization of Membrane Proteins. 2003 , 27-54	
1289	The interface between self-assembling erythropoietin receptor transmembrane segments corresponds to a membrane-spanning leucine zipper. 2004 , 279, 3273-9	61
1288	Predicting transmembrane beta-barrels in proteomes. 2004 , 32, 2566-77	123
1287	Genetic analysis of yeast Yip1p function reveals a requirement for Golgi-localized rab proteins and rab-Guanine nucleotide dissociation inhibitor. 2004 , 168, 1827-41	22
1286	Disease-related misassembly of membrane proteins. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2004 , 33, 25-51	209
1285	Identification of core amino acids stabilizing rhodopsin. 2004 , 101, 7246-51	130
1284	Role of the transmembrane domain in the stability of TrwB, an integral protein involved in bacterial conjugation. 2004 , 279, 10955-61	24
1283	Extending molecular modeling methodology to study insertion of membrane nanopores. 2004 , 101, 4337-8	20
1282	Cotranslational integration and initial sorting at the endoplasmic reticulum translocon of proteins destined for the inner nuclear membrane. 2004 , 101, 12537-42	54
1281	The role of the length and sequence of the linker domain of cytochrome b5 in stimulating cytochrome P450 2B4 catalysis. 2004 , 279, 36809-18	29
1280	Effect of the Pore Region of a Transmembrane Ion Channel on the Physical Properties of a Simple Membrane. 2004 , 108, 2608-2613	20

1279	Transmembrane proteins in the Protein Data Bank: identification and classification. 2004 , 20, 2964-72	188
1278	Membrane interaction and cellular internalization of penetratin peptides. 2004 , 271, 1187-97	94
1277	Reversible site-selective labeling of membrane proteins in live cells. 2004 , 22, 440-4	260
1276	Probing the energy landscape of the membrane protein bacteriorhodopsin. 2004 , 12, 871-9	74
1275	Membrane-protein integration and the role of the translocation channel. 2004 , 14, 568-75	142
1274	Quality control of integral membrane proteins. 2004 , 29, 648-55	32
1273	The machinery of membrane protein assembly. 2004 , 14, 397-404	103
1272	Folding of helical membrane proteins: the role of polar, GxxxG-like and proline motifs. 2004 , 14, 465-79	368
1271	Membrane integration of E. coli model membrane proteins. 2004 , 1694, 55-66	28
1270	The interface of a membrane-spanning leucine zipper mapped by asparagine-scanning mutagenesis. 2004 , 13, 555-9	34
1269	Binding and insertion of alpha-helical anti-microbial peptides in POPC bilayers studied by molecular dynamics simulations. 2004 , 132, 113-32	58
1268	Implicit solvent model estimates of the stability of model structures of the alamethicin channel. 2004 , 33, 16-28	24
1267	Membrane destabilization by ricin. 2004 , 33, 572-9	17
1266	Backbone-backbone geometry of tertiary contacts between alpha-helices. 2004 , 56, 693-703	6
1265	Novel scoring function for modeling structures of oligomers of transmembrane alpha-helices. 2004 , 57, 577-85	22
1264	Implicit solvent simulations of peptide interactions with anionic lipid membranes. 2005 , 58, 518-27	79
1263	Membrane-mediated capillary electrophoresis: interaction of cationic peptides with bicelles. 2004 , 25, 1237-42	25
1262	Determination of helical membrane protein topology using residual dipolar couplings and exhaustive search algorithm: application to phospholamban. 2004 , 132, 133-44	20

1261	Structure prediction of small transmembrane helix bundles. 2004 , 23, 99-110	7
1260	Self-assembly of transmembrane helices of bacteriorhodopsin by a replica-exchange Monte Carlo simulation. 2004 , 392, 168-175	24
1259	Thermodynamics of glycophorin A transmembrane helix dimerization in C14 betaine micelles. 2004 , 108, 43-9	43
1258	Generalized mean-field theory relating helix tilt in a bilayer to lipid disorder. 2004 , 111, 191-5	9
1257	Fungal rhodopsins and opsin-related proteins: eukaryotic homologues of bacteriorhodopsin with unknown functions. 2004 , 3, 555-65	75
1256	Techniques and applications of NMR to membrane proteins. 2004 , 21, 129-41	34
1255	Functional characterization and NMR spectroscopy on full-length Vpu from HIV-1 prepared by total chemical synthesis. 2004 , 126, 2439-46	57
1254	Imaging forster resonance energy transfer measurements of transmembrane helix interactions in lipid bilayers on a solid support. 2004 , 20, 9053-60	24
1253	Primary amphipathic cell-penetrating peptides: structural requirements and interactions with model membranes. 2004 , 43, 7698-706	94
1252	A knowledge-based scale for the analysis and prediction of buried and exposed faces of transmembrane domain proteins. 2004 , 20, 1822-35	66
1251	Non-native interhelical hydrogen bonds in the cystic fibrosis transmembrane conductance regulator domain modulated by polar mutations. 2004 , 43, 8077-83	29
1250	Destabilizing mutations promote membrane protein misfolding. 2004 , 43, 19-25	43
1249	Calcium activation of the Ca-ATPase enhances conformational heterogeneity between nucleotide binding and phosphorylation domains. 2004 , 43, 4366-74	9
1248	Thermodynamics of glycophorin A transmembrane helix dimerization in C14 betaine micelles. 2004 ,	0
1247	Membrane potentials: measurement, occurrence and roles in cellular functions. 2004 , 23-59	7
1246	Interfacial folding and membrane insertion of a designed helical peptide. 2004 , 43, 5782-91	84
1245	Structure determination of membrane proteins by NMR spectroscopy. 2004 , 104, 3587-606	368
1244	Reversible refolding of the diphtheria toxin T-domain on lipid membranes. 2004 , 43, 7451-8	53

1243	Association of a model transmembrane peptide containing gly in a heptad sequence motif. 2004 , 87, 3421-9		36
1242	Infrared reflection absorption spectroscopy of amphipathic model peptides at the air/water interface. 2004 , 86, 3750-8		59
1241	Effect of nanomolar concentrations of sodium dodecyl sulfate, a catalytic inductor of alpha-helices, on human calcitonin incorporation and channel formation in planar lipid membranes. 2004 , 87, 1065-75		16
1240	How environment supports a state: molecular dynamics simulations of two states in bacteriorhodopsin suggest lipid and water compensation. 2004 , 87, 129-45		21
1239	Analysis of side-chain rotamers in transmembrane proteins. 2004 , 87, 3460-9		48
1238	Direct simulation of transmembrane helix association: role of asparagines. 2004 , 87, 1650-6		36
1237	Tertiary structure predictions on a comprehensive benchmark of medium to large size proteins. 2004 , 87, 2647-55		68
1236	An automatic method for predicting transmembrane protein structures using cryo-EM and evolutionary data. 2004 , 87, 3448-59		48
1235	HIV fusion inhibitor peptide T-1249 is able to insert or adsorb to lipidic bilayers. Putative correlation with improved efficiency. 2004 , 126, 14758-63		65
1234	Enthalpy-driven apolipoprotein A-I and lipid bilayer interaction indicating protein penetration upon lipid binding. 2004 , 43, 12258-64		40
1233	Characterization of peptides corresponding to the seven transmembrane domains of human adenosine A2a receptor. 2004 , 43, 12945-54		42
1232	Computer modeling of poly-leucine-based coiled coil dimers in a realistic membrane environment: insight into helix-helix interactions in membrane proteins. 2004 , 43, 9050-60		20
1231	Structural commonalities among integral membrane enzymes. 2004 , 567, 159-65		43
1230	Computer simulations of membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2004 , 1666, 158-89	3.8	205
1229	How lipids affect the activities of integral membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2004 , 1666, 62-87	3.8	907
1228	Folding and assembly of beta-barrel membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2004 , 1666, 250-63	3.8	228
1227	The protein-lipid interface: perspectives from magnetic resonance and crystal structures. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2004 , 1666, 118-41	3.8	70
1226	Stirring up controversy with a voltage sensor paddle. 2004 , 27, 303-7		71

1225	Side-chain contributions to membrane protein structure and stability. 2004 , 335, 297-305	179
1224	Influence of proline residues in transmembrane helix packing. 2004 , 335, 631-40	54
1223	De novo folding of membrane proteins: an exploration of the structure and NMR properties of the fd coat protein. 2004 , 337, 513-9	58
1222	Snorkeling preferences foster an amino acid composition bias in transmembrane helices. 2004 , 339, 471-9	72
1221	Controlled unfolding and refolding of a single sodium-proton antiporter using atomic force microscopy. 2004 , 340, 1143-52	90
1220	Proline substitutions are not easily accommodated in a membrane protein. 2004 , 341, 1-6	69
1219	Reversible unfolding of beta-sheets in membranes: a calorimetric study. 2004 , 342, 703-11	32
1218	Hetero-assembly between all-L- and all-D-amino acid transmembrane domains: forces involved and implication for inactivation of membrane proteins. 2004 , 344, 855-64	28
1217	Insertion kinetics of a denatured alpha helical membrane protein into phospholipid bilayer vesicles. 2004 , 344, 1109-21	42
1216	Secondary structure, phospholipid membrane interactions, and fusion activity of two glutamate-rich analogs of influenza hemagglutinin fusion peptide. 2004 , 425, 173-83	10
1215	The evolution of transmembrane helix kinks and the structural diversity of G protein-coupled receptors. 2004 , 101, 959-63	191
1214	Structural features of transmembrane helices. 2004 , 559, 145-51	55
1213	On the mechanism of SPP-catalysed intramembrane proteolysis; conformational control of peptide bond hydrolysis in the plane of the membrane. 2004 , 564, 213-8	36
1212	Structure and function of the glycine receptor and related nicotinicoid receptors. 2004 , 279, 19383-6	60
1211	Membrane model for the G-protein-coupled receptor rhodopsin: hydrophobic interface and dynamical structure. 2004 , 86, 2078-100	124
1210	Liquid domains in vesicles investigated by NMR and fluorescence microscopy. 2004 , 86, 2910-22	385
1209	Applications of Small Molecule Crystallography and the Cambridge Structural Database in Drug Design. 2004 , 1, 595-606	
1208	The Triple Layer Model: A Different Perspective on Lipid Bilayers. 2004 , 51, 1183-1191	2

1207	Structure prediction of membrane proteins. 2004 , 2, 1-5	7
1206	Looking chloride channels straight in the eye: bestrophins, lipofuscinosis, and retinal degeneration. 2005 , 20, 292-302	66
1205	The Photoreceptor Membrane as a Model System in the Study of Biological Signal Transduction. 2005 , 1, 181-206	
1204	Transmembrane Domains in Membrane Protein Folding, Oligomerization, and Function. 876-918	3
1203	[Fundamental studies on membrane protein folding using model transmembrane helices]. 2005 , 125, 725-32	1
1202	A new amphipathy scale I. Determination of the scale from molecular dynamics data. 2005 , 1747, 35-46	10
1201	Investigations of the structure and dynamics of membrane-associated peptides by magic angle spinning NMR. 2005 , 46, 79-107	54
1200	Modeling and predicting all-. 2005 , 335, 67-92	14
1199	Forster resonance energy transfer in liposomes: measurements of transmembrane helix dimerization in the native bilayer environment. 2005 , 340, 154-64	100
1198	How proteins come together in the plasma membrane and function in macromolecular assemblies: focus on receptor mosaics. 2005 , 26, 133-54	25
1197	Cell-penetrating peptides: mechanism and kinetics of cargo delivery. 2005 , 57, 529-45	660
1196	In or out?. 2005 , 6, 192-192	
1195	Actin' out of control. 2005 , 6, 192-192	
1194	Cloning and functional characterization of two cDNAs encoding NADPH-dependent 3-ketoacyl-CoA reductases from developing cotton fibers. 2005 , 15, 465-73	33
1193	Recognition of transmembrane helices by the endoplasmic reticulum translocon. 2005 , 433, 377-81	801
1192	Solving the membrane protein folding problem. 2005 , 438, 581-9	372
1191	Plasma membrane phosphoinositide organization by protein electrostatics. 2005 , 438, 605-11	707
1190	Cell biology: border crossing. 2005 , 433, 367-9	11

1189	Materials science: build your own superlattice. 2005 , 433, 369-70		104
1188	The membrane-water interface region of membrane proteins: structural bias and the anti-snorkeling effect. 2005 , 30, 355-7		29
1187	Antimicrobial peptides: new candidates in the fight against bacterial infections. 2005 , 80, 717-35		244
1186	Lipid-coated nanocrystals as multifunctionalized luminescent scaffolds for supramolecular biological assemblies. <i>Angewandte Chemie - International Edition</i> , 2005 , 44, 1388-92	16.4	52
1185	Lipid-Coated Nanocrystals as Multifunctionalized Luminescent Scaffolds for Supramolecular Biological Assemblies. <i>Angewandte Chemie</i> , 2005 , 117, 1412-1416	3.6	6
1184	Modeling of receptor mimics that inhibit superantigen pathogenesis. 2005 , 18, 73-83		6
1183	Partitioning of tetrachlorophenol into lipid bilayers and sarcoplasmic reticulum: effect of length of acyl chains, carbonyl group of lipids and biomembrane structure. <i>Journal of Membrane Biology</i> , 2005 , 203, 127-42	2.3	4
1182	The influenza virus ion channel and maturation cofactor M2 is a cholesterol-binding protein. 2005 , 34, 52-66		94
1181	Thermodynamics of alpha-lactalbumin-DL-alpha-dipalmitoylphosphatidylcholine interactions and effect of the antioxidant nicotinamide on these interactions. 2005 , 114, 157-67		2
1180	An investigation into the ability to define transmembrane protein spans using the biophysical properties of amino acid residues. 2005 , 275, 189-97		2
1179	Computer simulation of partitioning of ten pentapeptides Ace-WLXLL at the cyclohexane/water and phospholipid/water interfaces. 2005 , 6, 30		36
1178	Properties of integral membrane protein structures: derivation of an implicit membrane potential. 2005 , 59, 252-65		162
1177	Understanding the energetics of helical peptide orientation in membranes. 2005 , 58, 913-22		33
1176	Empirical lipid propensities of amino acid residues in multispans alpha helical membrane proteins. 2005 , 59, 496-509		84
1175	Folding is not required for bilayer insertion: replica exchange simulations of an alpha-helical peptide with an explicit lipid bilayer. 2005 , 59, 783-90		94
1174	Energetics and stability of transmembrane helix packing: a replica-exchange simulation with a knowledge-based membrane potential. 2006 , 62, 539-52		15
1173	Multipass membrane protein structure prediction using Rosetta. 2006 , 62, 1010-25		260
1172	Amphiphilic alpha-helical antimicrobial peptides and their structure/function relationships. 2005 , 12, 31-9		136

1171	Folding of Membrane Proteins. 998-1031		0
1170	. 2005,		23
1169	A peptide pertaining to the loop segment of human immunodeficiency virus gp41 binds and interacts with model biomembranes: implications for the fusion mechanism. 2005, 79, 5142-52		42
1168	Identification of the membrane-active regions of the severe acute respiratory syndrome coronavirus spike membrane glycoprotein using a 16/18-mer peptide scan: implications for the viral fusion mechanism. 2005, 79, 1743-52		66
1167	How hydrogen bonds shape membrane protein structure. 2005, 72, 157-72		36
1166	The identification of a minimal dimerization motif QXXS that enables homo- and hetero-association of transmembrane helices in vivo. 2005, 280, 27449-57		51
1165	Viral Membrane Proteins: Structure, Function, and Drug Design. 2005,		6
1164	NMR experiments on aligned samples of membrane proteins. 2005, 394, 350-82		66
1163	Conservation of statistical results under the reduction of pair-contact interactions to solvation interactions. <i>Physical Review E</i> , 2005, 72, 061915	2.4	3
1162	Transmembrane helix prediction: a comparative evaluation and analysis. 2005, 18, 295-308		103
1161	The epidermal growth factor receptor family. 2005, 12 Suppl 1, S17-27		162
1160	Fusogenic domains in herpes simplex virus type 1 glycoprotein H. 2005, 280, 28632-43		83
1159	Interfacial folding and membrane insertion of designed peptides studied by molecular dynamics simulations. 2005, 102, 6771-6		157
1158	Destabilization of the transmembrane domain induces misfolding in a phenotypic mutant of cystic fibrosis transmembrane conductance regulator. 2005, 280, 4968-74		21
1157	Double-spanning plant viral movement protein integration into the endoplasmic reticulum membrane is signal recognition particle-dependent, translocon-mediated, and concerted. 2005, 280, 25907-12		37
1156	Transmembrane peptides from tyrosine kinase receptor. Mutation-related behavior in a lipid bilayer investigated by molecular dynamics simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2005, 23, 91-100	3.6	10
1155	ALLD: An object-oriented mesoscopic simulation program for polar biomolecules in hydrophobic chromatography or biomembranes. 2005, 31, 623-636		3
1154	Identification and characterization of the putative fusion peptide of the severe acute respiratory syndrome-associated coronavirus spike protein. 2005, 79, 7195-206		100

1153	A simple statistical method for discriminating outer membrane proteins with better accuracy. 2005 , 21, 961-8	91
1152	Rational combinatorial design of pore-forming beta-sheet peptides. 2005 , 102, 10511-5	61
1151	A dual function for SecA in the assembly of single spanning membrane proteins in Escherichia coli. 2005 , 280, 39077-85	41
1150	NMR Structure Determination of Proteins in Bilayer Lipid Membranes: The FXVD Family Proteins. 2005 , 2, 77-93	2
1149	The T cell receptor: critical role of the membrane environment in receptor assembly and function. 2005 , 23, 101-25	157
1148	Cholesterol-dependent cytolysins, a family of versatile pore-forming toxins. 2005 , 73, 6199-209	372
1147	Lipid membranes modulate the structure of islet amyloid polypeptide. 2005 , 44, 12113-9	225
1146	Headgroup organization and hydration of methylated phosphatidylethanolamines in Langmuir monolayers. 2005 , 7, 150-6	26
1145	Investigation of the binding geometry of a peripheral membrane protein. 2005 , 44, 16064-71	31
1144	Mesoscopic simulation of adsorption of peptides in a hydrophobic chromatography system. 2005 , 77, 1243-52	11
1143	Effect of lipid composition on the "membrane response" induced by a fusion peptide. 2005 , 44, 14626-37	27
1142	Determination of peptide oligomerization in lipid bilayers using ¹⁹ F spin diffusion NMR. 2005 , 127, 4477-83	91
1141	Capping transmembrane helices of MscL with aromatic residues changes channel response to membrane stretch. 2005 , 44, 12589-97	28
1140	Environmental Effects on Glycophorin A Folding and Structure Examined through Molecular Simulations. 2005 , 1, 375-88	3
1139	Barriers to folding of the transmembrane domain of the Escherichia coli autotransporter adhesin involved in diffuse adherence. 2005 , 44, 4533-45	28
1138	Archiving and absolute quantitation of solutes separated by single charged droplet coulomb explosion. 2005 , 77, 3461-5	4
1137	Identifying interactions between transmembrane helices from the adenosine A2A receptor. 2005 , 44, 16239-45	23
1136	Single molecule studies of antibody-antigen interaction strength versus intra-molecular antigen stability. 2005 , 347, 597-606	97

1135	Synergistic interactions between aqueous and membrane domains of a designed protein determine its fold and stability. 2005 , 348, 1225-33		19
1134	Defining the structural basis for assembly of a transmembrane cytochrome. 2005 , 350, 744-56		30
1133	Structural analysis of residues involving cation-pi interactions in different folding types of membrane proteins. 2005 , 35, 55-62		29
1132	Connexins and their environment: effects of lipids composition on ion channels. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2005 , 1711, 142-53	3.8	36
1131	Membrane association and activity of 15/16-membered peptide antibiotics: zervamicin IIB, ampullosporin A and antiameobin I. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2005 , 1715, 6-18	3.8	20
1130	Influence of hydrophobic matching on association of model transmembrane fragments containing a minimised glycophorin A dimerisation motif. 2005 , 579, 1633-8		30
1129	Proteins, chlorophylls and lipids: X-ray analysis of a three-way relationship. 2005 , 10, 275-82		26
1128	Membrane-protein interactions in mechanosensitive channels. 2005 , 88, 880-902		144
1127	Interaction of human apolipoprotein A-I with model membranes exhibiting lipid domains. 2005 , 89, 285-95		26
1126	Molecular packing and packing defects in helical membrane proteins. 2005 , 88, 1970-7		37
1125	Melittin-induced bilayer leakage depends on lipid material properties: evidence for toroidal pores. 2005 , 88, 1828-37		199
1124	Probing conformational disorder in neurotensin by two-dimensional solid-state NMR and comparison to molecular dynamics simulations. 2005 , 89, 2113-20		46
1123	An experiment-based algorithm for predicting the partitioning of unfolded peptides into phosphatidylcholine bilayer interfaces. 2005 , 44, 12614-9		42
1122	The aromatic domain of the coronavirus class I viral fusion protein induces membrane permeabilization: putative role during viral entry. 2005 , 44, 947-58		48
1121	Life As a Matter of Fat. 2005 ,		232
1120	Membrane-bound conformation and topology of the antimicrobial peptide tachyplesin I by solid-state NMR. 2006 , 45, 13323-30		34
1119	Folding and stability of alpha-helical integral membrane proteins. 2006 , 106, 1931-77		181
1118	Interaction of the neurotransmitter, neuropeptide Y, with phospholipid membranes: film balance and fluorescence microscopy studies. 2006 , 110, 22143-51		27

1117	The N-terminal domain of Bcl-xL reversibly binds membranes in a pH-dependent manner. 2006 , 45, 14533-42	31
1116	The position of the Gly-xxx-Gly motif in transmembrane segments modulates dimer affinity. 2006 , 84, 1006-12	20
1115	Evaluating tilt angles of membrane-associated helices: comparison of computational and NMR techniques. 2006 , 90, 1650-60	45
1114	Kinetic analysis of the thermal stability of the photosynthetic reaction center from <i>Rhodobacter sphaeroides</i> . 2006 , 90, 4155-66	39
1113	Redesigning channel-forming peptides: amino acid substitutions that enhance rates of supramolecular self-assembly and raise ion transport activity. 2006 , 90, 2138-50	25
1112	Molecular dynamics simulations of model trans-membrane peptides in lipid bilayers: a systematic investigation of hydrophobic mismatch. 2006 , 90, 2326-43	148
1111	Indole localization in lipid membranes revealed by molecular simulation. 2006 , 91, 2046-54	95
1110	Three-dimensional structure of the transmembrane domain of Vpu from HIV-1 in aligned phospholipid bicelles. 2006 , 91, 3032-42	101
1109	Neutron diffraction studies of fluid bilayers with transmembrane proteins: structural consequences of the achondroplasia mutation. 2006 , 91, 3736-47	29
1108	Amino-acid solvation structure in transmembrane helices from molecular dynamics simulations. 2006 , 91, 4450-63	66
1107	Continuous membrane-cytoskeleton adhesion requires continuous accommodation to lipid and cytoskeleton dynamics. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2006 , 35, 417-34	231
1106	Sequence analysis of the cbb3 oxidases and an atomic model for the <i>Rhodobacter sphaeroides</i> enzyme. 2006 , 45, 5754-65	39
1105	Chapter 1 Piercing Lipid Bilayers with Peptides. 2006 , 5, 1-23	2
1104	Roles of bilayer material properties in function and distribution of membrane proteins. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2006 , 35, 177-98	200
1103	Structure prediction of helical transmembrane proteins at two length scales. 2006 , 4, 317-33	6
1102	Probing folded and unfolded states of outer membrane protein a with steady-state and time-resolved tryptophan fluorescence. 2006 , 110, 17656-62	22
1101	Structural and functional effects of tryptophans inserted into the membrane-binding and substrate-binding sites of human group IIA phospholipase A2. 2006 , 45, 12448-60	17
1100	Irreversible misfolding of diacylglycerol kinase is independent of aggregation and occurs prior to trimerization and membrane association. 2006 , 45, 10072-84	16

1099	Lipid solvation effects contribute to the affinity of Gly-xxx-Gly motif-mediated helix-helix interactions. 2006 , 45, 8507-15	25
1098	Size and orientation of the lipid II headgroup as revealed by AFM imaging. 2006 , 45, 6195-202	26
1097	Interactions of tryptophan, tryptophan peptides, and tryptophan alkyl esters at curved membrane interfaces. 2006 , 45, 11713-26	40
1096	Conserved and cooperative assembly of membrane-bound alpha-helical states of islet amyloid polypeptide. 2006 , 45, 9496-508	271
1095	Measurement of thermodynamic parameters for hydrophobic mismatch 1: self-association of a transmembrane helix. 2006 , 45, 3370-8	44
1094	The membrane-active regions of the hepatitis C virus E1 and E2 envelope glycoproteins. 2006 , 45, 3755-68	63
1093	Phlorizin- and 6-ketocholestanol-mediated antagonistic modulation of alamethicin activity in phospholipid planar membranes. 2006 , 22, 8452-7	36
1092	Energetics of membrane protein folding and stability. 2006 , 453, 32-53	43
1091	Specific phospholipid recognition by human immunodeficiency virus type-1 neutralizing anti-gp41 2F5 antibody. 2006 , 580, 2395-99	42
1090	The transmembrane domain provides nucleotide binding specificity to the bacterial conjugation protein TrwB. 2006 , 580, 3075-82	21
1089	Role of the membrane interface on the conformation of the caveolin scaffolding domain: a CD and NMR study. 2006 , 580, 5301-5	22
1088	Protein-protein interactions: modeling the hepatitis C virus ion channel p7. 2006 , 49, 648-55	87
1087	Observing folding pathways and kinetics of a single sodium-proton antiporter from Escherichia coli. 2006 , 355, 2-8	46
1086	Characterizing molecular interactions in different bacteriorhodopsin assemblies by single-molecule force spectroscopy. 2006 , 355, 640-50	87
1085	Bacteriorhodopsin folds into the membrane against an external force. 2006 , 357, 644-54	89
1084	Transmembrane helix heterodimerization in lipid bilayers: probing the energetics behind autosomal dominant growth disorders. 2006 , 358, 1-7	35
1083	The stability of transmembrane helix interactions measured in a biological membrane. 2006 , 358, 1221-8	54
1082	Evidence that membrane insertion of the cytosolic domain of Bcl-xL is governed by an electrostatic mechanism. 2006 , 359, 1045-58	43

1081	Self-association of the transmembrane domain of an anthrax toxin receptor. 2006 , 360, 145-56	23
1080	Sequence motifs and antimotifs in beta-barrel membrane proteins from a genome-wide analysis: the Ala-Tyr dichotomy and chaperone binding motifs. 2006 , 363, 611-23	23
1079	In meso structure of the cobalamin transporter, BtuB, at 1.95 Å resolution. 2006 , 364, 716-34	88
1078	Sequence dependence of BNIP3 transmembrane domain dimerization implicates side-chain hydrogen bonding and a tandem GxxxG motif in specific helix-helix interactions. 2006 , 364, 974-90	55
1077	Inhibition of severe acute respiratory syndrome-associated coronavirus (SARS-CoV) infectivity by peptides analogous to the viral spike protein. 2006 , 120, 146-55	59
1076	Imaging and detecting molecular interactions of single transmembrane proteins. 2006 , 27, 546-61	38
1075	Lipid Bilayers, Translocons and the Shaping of Polypeptide Structure. 2006 , 1-25	1
1074	Post-integration Misassembly of Membrane Proteins and Disease. 2006 , 81-94	
1073	Membrane Recognition and Pore Formation by Bacterial Pore-forming Toxins. 2006 , 163-186	2
1072	Subcellular pH and predicted pH-dependent features of proteins. 2006 , 6, 3494-501	30
1071	Discrimination of outer membrane proteins using machine learning algorithms. 2006 , 63, 1031-7	42
1070	Analysis and prediction of helix-helix interactions in membrane channels and transporters. 2006 , 64, 253-62	28
1069	Interactions of the C2 domain of human factor V with a model membrane. 2006 , 64, 363-75	9
1068	Assembly of transmembrane helices of simple polytopic membrane proteins from sequence conservation patterns. 2006 , 64, 895-905	13
1067	Origin of functional diversity among tetrameric voltage-gated channels. 2007 , 66, 136-46	13
1066	Interaction of indole derivatives and tryptophan peptides with interfaces of sodium dodecyl sulfate micelles. 2006 , 12, 403-11	4
1065	Membrane-protein topology. 2006 , 7, 909-18	364
1064	Characterization of phospholipid-protein interactions by capillary isoelectric focusing with whole-column imaging detection. 2006 , 350, 91-8	15

1063	Modelling of proteins in membranes. 2006 , 141, 2-29	61
1062	NMR of membrane proteins in solution. 2006 , 48, 201-210	60
1061	Positioning of proteins in membranes: a computational approach. 2006 , 15, 1318-33	192
1060	Recognition of GPCRs by peptide ligands and membrane compartments theory: structural studies of endogenous peptide hormones in membrane environment. 2006 , 26, 131-58	29
1059	Comprehensive evaluation of solution nuclear magnetic resonance spectroscopy sample preparation for helical integral membrane proteins. 2006 , 7, 51-64	74
1058	NMR spectroscopy of basic/aromatic amino acid clusters in membrane proteins. 2006 , 48, 183-199	7
1057	Anchoring mechanisms of membrane-associated M13 major coat protein. 2006 , 141, 83-93	36
1056	Stereoselectivity of 8-OH-DPAT toward the serotonin 5-HT1A receptor: biochemical and molecular modeling study. 2006 , 72, 498-511	16
1055	Progress in structure prediction of alpha-helical membrane proteins. 2006 , 16, 496-504	55
1054	Has the code for protein translocation been broken?. 2006 , 31, 192-6	17
1053	Environmental effects on a prion's helix II domain: copper(II) and membrane interactions with PrP180-193 and its analogues. 2005 , 12, 537-47	31
1052	How strongly do sequence conservation patterns and empirical scales correlate with exposure patterns of transmembrane helices of membrane proteins?. 2006 , 83, 389-99	14
1051	Dynamic process of phospholipid-protein interaction studied by capillary isoelectric focusing with whole-column imaging detection. 2006 , 27, 852-8	13
1050	Membrane binding and structure of de novo designed alpha-helical cationic coiled-coil-forming peptides. 2006 , 7, 1361-71	21
1049	Solution NMR of membrane proteins: practice and challenges. 2006 , 44 Spec No, S24-40	193
1048	Enhanced recognition of protein transmembrane domains with prediction-based structural profiles. 2006 , 22, 303-9	78
1047	ZPRED: predicting the distance to the membrane center for residues in alpha-helical membrane proteins. 2006 , 22, e191-6	47
1046	The biological significance of lipid-protein interactions. 2006 , 18, S1281-91	22

1045	Topology of the porin MspA in the outer membrane of <i>Mycobacterium smegmatis</i> . 2006 , 281, 5908-15	38
1044	Translocation of amino acyl residues from the membrane interface to the hydrophobic core: thermodynamic model and experimental analysis using ATR-FTIR spectroscopy. 2006 , 23, 363-74	21
1043	Towards genome-scale structure prediction for transmembrane proteins. 2006 , 361, 465-75	33
1042	Topography of the prostaglandin endoperoxide H2 synthase-2 in membranes. 2006 , 281, 28354-64	18
1041	Cooperative adsorption of proteins onto lipid membranes. 2006 , 18, S1257-70	15
1040	Directed assembly of surface-supported bilayers with transmembrane helices. 2006 , 22, 1247-53	38
1039	Aggregation of polyalanine in a hydrophobic environment. 2006 , 124, 134904	26
1038	Interactions involved in the realignment of membrane-associated helices. An investigation using oriented solid-state NMR and attenuated total reflection Fourier transform infrared spectroscopies. 2006 , 281, 7708-16	35
1037	Membrane association and epitope recognition by HIV-1 neutralizing anti-gp41 2F5 and 4E10 antibodies. 2006 , 22, 998-1006	61
1036	Computational Methods for Protein Structure Prediction and Modeling. 2007 ,	3
1035	The GABAA receptor alpha1 subunit epilepsy mutation A322D inhibits transmembrane helix formation and causes proteasomal degradation. 2007 , 104, 12999-3004	86
1034	From interactions of single transmembrane helices to folding of alpha-helical membrane proteins: analyzing transmembrane helix-helix interactions in bacteria. 2007 , 8, 45-61	37
1033	Membrane protein insertion: the biology-physics nexus. 2007 , 129, 363-9	57
1032	Formation of transmembrane helices in vivo--is hydrophobicity all that matters?. 2007 , 129, 353-6	32
1031	On the derivation of propensity scales for predicting exposed transmembrane residues of helical membrane proteins. 2007 , 23, 701-8	28
1030	Crystal structure of YegS, a homologue to the mammalian diacylglycerol kinases, reveals a novel regulatory metal binding site. 2007 , 282, 19644-52	29
1029	Accurate prediction of deleterious protein kinase polymorphisms. 2007 , 23, 2918-25	56
1028	Experimental measures of amino acid hydrophobicity and the topology of transmembrane and globular proteins. 2007 , 129, 357-62	88

1027	NMR of membrane proteins in micelles and bilayers: the FXVD family proteins. 2007 , 41, 398-408		31
1026	Detergents for the stabilization and crystallization of membrane proteins. 2007 , 41, 388-97		377
1025	Gating of the ATP-sensitive K ⁺ channel by a pore-lining phenylalanine residue. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 39-51	3.8	11
1024	G-protein coupled receptor structure. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 808-24	3.8	40
1023	Transmembrane helices of membrane proteins may flex to satisfy hydrophobic mismatch. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 530-7	3.8	45
1022	The predicted transmembrane fragment 17 of the human multidrug resistance protein 1 (MRP1) behaves as an interfacial helix in membrane mimics. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 538-52	3.8	10
1021	Identification of a segment in the precursor of pulmonary surfactant protein SP-B, potentially involved in pH-dependent membrane assembly of the protein. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 1059-69	3.8	9
1020	Conformation of a double-membrane-spanning fragment of a G protein-coupled receptor: effects of hydrophobic environment and pH. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 1199-210	3.8	8
1019	Membrane interaction of islet amyloid polypeptide. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 2002-9	3.8	144
1018	Structure of the C-terminal domain of the pro-apoptotic protein Hrk and its interaction with model membranes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 1659-70	3.8	26
1017	Conformational changes of chicken liver bile acid-binding protein bound to anionic lipid membrane are coupled to the lipid phase transitions. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 1583-91	3.8	11
1016	Interactions of the Australian tree frog antimicrobial peptides aurein 1.2, citropin 1.1 and maculatin 1.1 with lipid model membranes: differential scanning calorimetric and Fourier transform infrared spectroscopic studies. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 2787-800	3.8	54
1015	Discontinuous membrane helices in transport proteins and their correlation with function. 2007 , 159, 261-7		117
1014	E(z), a depth-dependent potential for assessing the energies of insertion of amino acid side-chains into membranes: derivation and applications to determining the orientation of transmembrane and interfacial helices. 2007 , 366, 436-48		130
1013	Janus model of the Na,K-ATPase beta-subunit transmembrane domain: distinct faces mediate alpha/beta assembly and beta-beta homo-oligomerization. 2007 , 365, 706-14		44
1012	Beyond dimerization: a membrane-dependent activation model for interleukin-4 receptor-mediated signalling. 2007 , 366, 1365-73		20
1011	Folding amphipathic helices into membranes: amphiphilicity trumps hydrophobicity. 2007 , 370, 459-70		129
1010	The N-terminal helix is a post-assembly clamp in the bacterial outer membrane protein PagP. 2007 , 373, 529-40		52

1009	Deciphering molecular interactions of native membrane proteins by single-molecule force spectroscopy. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2007 , 36, 233-60		113
1008	Amino acid hydrophobicity and accessible surface area. <i>Physical Review E</i> , 2007 , 75, 011920	2.4	86
1007	Phosphate-mediated arginine insertion into lipid membranes and pore formation by a cationic membrane peptide from solid-state NMR. 2007 , 129, 11438-46		158
1006	Behavior of the N-terminal helices of the diphtheria toxin T domain during the successive steps of membrane interaction. 2007 , 46, 1878-87		36
1005	Beta-sheet pore-forming peptides selected from a rational combinatorial library: mechanism of pore formation in lipid vesicles and activity in biological membranes. 2007 , 46, 12124-39		65
1004	Aromatic and cation-pi interactions enhance helix-helix association in a membrane environment. 2007 , 46, 9208-14		83
1003	In silico screening of mutational effects on transmembrane helix dimerization: insights from rigid-body docking and molecular dynamics simulations. 2007 , 111, 9114-24		20
1002	Molecular dynamics simulations of rhodopsin in different one-component lipid bilayers. 2007 , 111, 7052-63		43
1001	Studies of the minimum hydrophobicity of alpha-helical peptides required to maintain a stable transmembrane association with phospholipid bilayer membranes. 2007 , 46, 1042-54		16
1000	How protein transmembrane segments sense the lipid environment. 2007 , 46, 1457-65		134
999	Lipid interaction converts prion protein to a PrP ^{Sc} -like proteinase K-resistant conformation under physiological conditions. 2007 , 46, 7045-53		88
998	Design of a functional membrane protein by engineering a heme-binding site in glycophorin A. 2007 , 129, 512-8		48
997	Improving the accuracy of transmembrane protein topology prediction using evolutionary information. 2007 , 23, 538-44		355
996	Self-assembling of peptide/membrane complexes by atomistic molecular dynamics simulations. 2007 , 92, 903-12		45
995	Structure of the first transmembrane domain of the neuronal acetylcholine receptor beta2 subunit. 2007 , 92, 1616-22		9
994	Free energy of membrane protein unfolding derived from single-molecule force measurements. 2007 , 93, 930-7		41
993	Contact-induced structure transformation in transmembrane prion propagation. 2007 , 92, 2704-10		4
992	2,2,2-Trifluoroethanol changes the transition kinetics and subunit interactions in the small bacterial mechanosensitive channel MscS. 2007 , 92, 2771-84		26

991	Mechanism of the cell-penetrating peptide transportan 10 permeation of lipid bilayers. 2007 , 92, 2434-44	138
990	Tetracaine-membrane interactions: effects of lipid composition and phase on drug partitioning, location, and ionization. 2007 , 92, 3988-4001	54
989	NMR studies in dodecylphosphocholine of a fragment containing the seventh transmembrane helix of a G-protein-coupled receptor from <i>Saccharomyces cerevisiae</i> . 2007 , 93, 467-82	29
988	Interactions of cationic-hydrophobic peptides with lipid bilayers: a Monte Carlo simulation method. 2007 , 93, 1858-71	30
987	Multistructure 3D-QSAR studies on a series of conformationally constrained butyrophenones docked into a new homology model of the 5-HT _{2A} receptor. 2007 , 50, 3242-55	19
986	Multi-property fitting and parameterization of a coarse grained model for aqueous surfactants. 2007 , 33, 27-36	353
985	Evidence for a role of the membrane-proximal region of herpes simplex virus type 1 glycoprotein H in membrane fusion and virus inhibition. 2007 , 8, 885-95	47
984	Peptides as transmembrane segments: decrypting the determinants for helix-helix interactions in membrane proteins. 2007 , 88, 217-32	26
983	Molecular dynamics simulations of Na ⁺ /Cl ⁻ -dependent neurotransmitter transporters in a membrane-aqueous system. 2007 , 2, 827-40	35
982	Monte Carlo folding of trans-membrane helical peptides in an implicit generalized Born membrane. 2007 , 69, 297-308	20
981	Biophysical characterization of Vpu from HIV-1 suggests a channel-pore dualism. 2008 , 70, 1488-97	50
980	A hydrophobic element secures S4 voltage sensor in position in resting Shaker K ⁺ channels. 2007 , 582, 1059-72	10
979	Mechanosensitive channels in bacteria: signs of closure?. 2007 , 5, 431-40	111
978	A novel tripartite motif involved in aquaporin topogenesis, monomer folding and tetramerization. 2007 , 14, 762-9	58
977	The intracellular region of the Notch ligand Jagged-1 gains partial structure upon binding to synthetic membranes. 2007 , 274, 5325-36	21
976	Hydrophobic interactions in complexes of antimicrobial peptides with bacterial polysaccharides. 2007 , 69, 405-12	28
975	Cysteine-string protein isoform beta (Cspbeta) is targeted to the trans-Golgi network as a non-palmitoylated CSP in clonal beta-cells. 2007 , 1773, 109-19	16
974	Small-angle X-ray scattering from RNA, proteins, and protein complexes. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2007 , 36, 307-27	253

973	Solid-state NMR characterization of the putative membrane anchor of TWD1 from <i>Arabidopsis thaliana</i> . 2007 , 36, 393-404		17
972	Molecular dynamics simulation approach for the prediction of transmembrane helix-helix heterodimers assembly. 2007 , 36, 1071-82		16
971	The brain as a system of nested but partially overlapping networks. Heuristic relevance of the model for brain physiology and pathology. 2007 , 114, 3-19		26
970	Biosynthesis and NMR-studies of a double transmembrane domain from the Y4 receptor, a human GPCR. 2008 , 42, 257-69		15
969	Disordered proteins: biological membranes as two-dimensional aggregation matrices. 2008 , 52, 175-89		42
968	Backbone structure of a small helical integral membrane protein: A unique structural characterization. 2009 , 18, 134-46		33
967	Predicting transmembrane helix pair configurations with knowledge-based distance-dependent pair potentials. 2008 , 70, 984-99		7
966	How to lose a kink and gain a helix: pH independent conformational changes of the fusion domains from influenza hemagglutinin in heterogeneous lipid bilayers. 2008 , 72, 299-312		18
965	The identification and characterization of fusogenic domains in herpes virus glycoprotein B molecules. 2008 , 9, 758-67		42
964	Noncovalent keystone interactions controlling biomembrane structure. 2008 , 14, 1690-7		17
963	From valleys to ridges: exploring the dynamic energy landscape of single membrane proteins. 2008 , 9, 954-66		37
962	Use of molecular dynamics data in biochemistry courses: An amphipathy scale to determine protein helix transmembrane segments. 2008 , 36, 129-34		
961	Interactions with hydrophobic clusters in the urea-unfolded membrane protein OmpX. <i>Angewandte Chemie - International Edition</i> , 2008 , 47, 977-81	16.4	20
960	Exogenous agents that target transmembrane domains of proteins. <i>Angewandte Chemie - International Edition</i> , 2008 , 47, 2744-52	16.4	19
959	Wechselwirkungen der hydrophoben Cluster im entfalteten Membranprotein OmpX in Harnstofflösung. <i>Angewandte Chemie</i> , 2008 , 120, 992-996	3.6	6
958	Exogene Wirkstoffe zur Erkennung von Transmembrandomänen von Proteinen. <i>Angewandte Chemie</i> , 2008 , 120, 2784-2793	3.6	3
957	Application of solid-state NMR restraint potentials in membrane protein modeling. 2008 , 193, 68-76		28
956	The effect of entropy on protein hydrogen bonds. 2008 , 462, 1-5		6

955	Stabilization of Membrane Proteins: the Case of G-Protein-Coupled Receptors. 2008 , 8, 207-217	3
954	Mutagenic analysis of membrane protein functional mechanisms: bacteriorhodopsin as a model example. 2008 , 84, 479-515	1
953	Estimating the length of transmembrane helices using Z-coordinate predictions. 2008 , 17, 271-8	23
952	The effect of nucleotide bias upon the composition and prediction of transmembrane helices. 2000 , 9, 505-11	5
951	Effect of ions on a dipalmitoyl phosphatidylcholine bilayer. a molecular dynamics simulation study. 2008 , 112, 1397-408	112
950	The interaction of small molecules with phospholipid membranes studied by 1H NOESY NMR under magic-angle spinning. 2008 , 29, 35-49	77
949	Modest membrane hydrogen bonds deliver rich results. 2008 , 4, 393-4	10
948	Hepatitis C virus core protein binding to lipid membranes: the role of domains 1 and 2. 2008 , 15, 346-56	13
947	Indole and other aromatic compounds activate the yeast TRPY1 channel. 2008 , 582, 1514-8	16
946	Overcoming the challenges of membrane protein crystallography. 2008 , 18, 581-6	298
945	Coarse-grained MD simulations of membrane protein-bilayer self-assembly. 2008 , 16, 621-30	179
944	Transmembrane helix uniformity examined by spectral mapping of torsion angles. 2008 , 16, 787-97	72
943	AFM: a nanotool in membrane biology. 2008 , 47, 7986-98	186
942	Coarse-grained molecular modeling of non-ionic surfactant self-assembly. 2008 , 4, 2454	196
941	Hydrogen-bonding and packing features of membrane proteins: functional implications. 2008 , 94, 1945-53	47
940	Distribution of amino acids in a lipid bilayer from computer simulations. 2008 , 94, 3393-404	434
939	Protein folding in membranes: insights from neutron diffraction studies of a membrane beta-sheet oligomer. 2008 , 94, 492-505	14
938	A method to determine dielectric constants in nonhomogeneous systems: application to biological membranes. 2008 , 94, 1185-93	78

937	A quantitative model for the all-or-none permeabilization of phospholipid vesicles by the antimicrobial peptide cecropin A. 2008 , 94, 1667-80	122
936	The interaction of phospholipase A2 with a phospholipid bilayer: coarse-grained molecular dynamics simulations. 2008 , 95, 1649-57	38
935	Lipid bilayer deformation and the free energy of interaction of a Kv channel gating-modifier toxin. 2008 , 95, 3816-26	26
934	Alpha-helical topology prediction and generation of distance restraints in membrane proteins. 2008 , 95, 5281-95	14
933	Free-energy profiles of membrane insertion of the M2 transmembrane peptide from influenza A virus. 2008 , 95, 5021-9	17
932	Interaction of gramicidin S and its aromatic amino-acid analog with phospholipid membranes. 2008 , 95, 3306-21	39
931	Stable interactions between the transmembrane domains of the adenosine A2A receptor. 2008 , 17, 1188-99	20
930	Membrane adsorption, folding, insertion and translocation of synthetic trans-membrane peptides. 2008 , 25, 245-57	17
929	Mechanical properties of bovine rhodopsin and bacteriorhodopsin: possible roles in folding and function. 2008 , 24, 1330-7	38
928	Packing of transmembrane helices in bacteriorhodopsin folding: structure and thermodynamics. 2008 , 162, 237-47	8
927	Macromolecular crowding at membrane interfaces: adsorption and alignment of membrane peptides. 2008 , 375, 376-85	44
926	Point mutations in membrane proteins reshape energy landscape and populate different unfolding pathways. 2008 , 376, 1076-90	48
925	Rapid incorporation of functional rhodopsin into nanoscale apolipoprotein bound bilayer (NABB) particles. 2008 , 377, 1067-81	101
924	Reversible sheet-turn conformational change of a cell-penetrating peptide in lipid bilayers studied by solid-state NMR. 2008 , 381, 1133-44	36
923	The immunogenic CBD1 peptide corresponding to the caveolin-1 binding domain in HIV-1 envelope gp41 has the capacity to penetrate the cell membrane and bind caveolin-1. 2008 , 45, 1963-75	10
922	The process of folding proteins into membranes: challenges and progress. 2008 , 469, 46-66	80
921	Peptides containing membrane-interacting motifs inhibit herpes simplex virus type 1 infectivity. 2008 , 29, 1461-71	40
920	Solution NMR structures of the antimicrobial peptides phylloseptin-1, -2, and -3 and biological activity: the role of charges and hydrogen bonding interactions in stabilizing helix conformations. 2008 , 29, 1633-44	47

919	Interfacial pre-transmembrane domains in viral proteins promoting membrane fusion and fission. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2008 , 1778, 1624-39	3.8	57
918	Biophysical characterization and membrane interaction of the most membranotropic region of the HIV-1 gp41 endodomain. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2008 , 1778, 1298-307	3.8	10
917	Binding and interactions of L-BABP to lipid membranes studied by molecular dynamic simulations. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2008 , 1778, 1390-7	3.8	21
916	Partitioning of amino-acid analogues in a five-slab membrane model. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2008 , 1778, 2234-43	3.8	23
915	Secondary structure transitions and aggregation induced in dynorphin neuropeptides by the detergent sodium dodecyl sulfate. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2008 , 1778, 2580-7	3.8	16
914	How translocons select transmembrane helices. 2008 , 37, 23-42		164
913	Probing melittin helix-coil equilibria in solutions and vesicles. 2008 , 112, 3202-7		8
912	Enhanced membrane protein topology prediction using a hierarchical classification method and a new scoring function. 2008 , 7, 487-96		35
911	Formation of an unfolding intermediate state of soluble chloride intracellular channel protein CLIC1 at acidic pH. 2008 , 47, 11674-81		38
910	Effects of tryptophan microenvironment, soluble domain, and vesicle size on the thermodynamics of membrane protein folding: lessons from the transmembrane protein OmpA. 2008 , 47, 12844-52		40
909	Small changes in the primary structure of transportan 10 alter the thermodynamics and kinetics of its interaction with phospholipid vesicles. 2008 , 47, 3051-60		35
908	Modulation of the spontaneous curvature and bending rigidity of lipid membranes by interfacially adsorbed amphipathic peptides. 2008 , 112, 6988-96		76
907	The membrane lateral pressure-perturbing capacity of parabens and their effects on the mechanosensitive channel directly correlate with hydrophobicity. 2008 , 47, 10540-50		21
906	Ultraviolet resonance Raman spectroscopy of folded and unfolded states of an integral membrane protein. 2008 , 112, 9507-11		36
905	Membrane Insertion Profiles of Peptides Probed by Molecular Dynamics Simulations. 2008 ,		
904	Biomolecular engineering by combinatorial design and high-throughput screening: small, soluble peptides that permeabilize membranes. 2008 , 130, 9849-58		110
903	Stability of the glycerol facilitator in detergent solutions. 2008 , 47, 3513-24		32
902	Prediction of membrane-protein topology from first principles. 2008 , 105, 7177-81		246

901	Ion channels in microbes. 2008 , 88, 1449-90	145
900	Molecular architecture of the bipartite fusion loops of vesicular stomatitis virus glycoprotein G, a class III viral fusion protein. 2008 , 283, 6418-27	49
899	Chapter 5 Implicit Modeling of Membranes. 2008 , 131-157	13
898	The broadly neutralizing anti-human immunodeficiency virus type 1 4E10 monoclonal antibody is better adapted to membrane-bound epitope recognition and blocking than 2F5. 2008 , 82, 8986-96	39
897	Transmembrane domain length of viral K ⁺ channels is a signal for mitochondria targeting. 2008 , 105, 12313-8	35
896	Prediction of the translocon-mediated membrane insertion free energies of protein sequences. 2008 , 24, 1271-7	7
895	Identification of the membrane-active regions of hepatitis C virus p7 protein: biophysical characterization of the loop region. 2008 , 283, 8089-101	30
894	Vertebrate membrane proteins: structure, function, and insights from biophysical approaches. 2008 , 60, 43-78	83
893	Forster resonance energy transfer measurements of transmembrane helix dimerization energetics. 2008 , 450, 107-27	27
892	A CD study of uncoupling protein-1 and its transmembrane and matrix-loop domains. 2008 , 411, 593-603	11
891	Effects of phosphatidylethanolamine glycation on lipid-protein interactions and membrane protein thermal stability. 2008 , 416, 145-52	31
890	Chapter 7 A New Class of Peptide-Forming Channel. 2008 , 169-202	1
889	Protein Folding and Biogenesis. 160-190	
888	Structural imperatives impose diverse evolutionary constraints on helical membrane proteins. 2009 , 106, 17747-50	50
887	Determinants of aquaporin-4 assembly in orthogonal arrays revealed by live-cell single-molecule fluorescence imaging. 2009 , 122, 813-21	75
886	Mechanism for HIV-1 Tat insertion into the endosome membrane. 2009 , 284, 22736-46	39
885	Three-way interaction between 14-3-3 proteins, the N-terminal region of tyrosine hydroxylase, and negatively charged membranes. 2009 , 284, 32758-69	35
884	Putative re-entrant loop 1 of AE2 transmembrane domain has a major role in acute regulation of anion exchange by pH. 2009 , 284, 6126-39	29

883	Prion protein-detergent micelle interactions studied by NMR in solution. 2009 , 284, 22713-21	23
882	Intrinsic voltage dependence of the epithelial Na ⁺ channel is masked by a conserved transmembrane domain tryptophan. 2009 , 284, 25512-21	9
881	Inferring stabilizing mutations from protein phylogenies: application to influenza hemagglutinin. 2009 , 5, e1000349	50
880	Quantitative determination of skin penetration of PEG-coated CdSe quantum dots in dermabraded but not intact SKH-1 hairless mouse skin. 2009 , 111, 37-48	78
879	Mechanosensitive TRP channels in cardiovascular pathophysiology. 2009 , 123, 371-85	138
878	From 'I' to 'L' and back again: the odyssey of membrane-bound M13 protein. 2009 , 34, 249-55	14
877	Interrogating single proteins through nanopores: challenges and opportunities. 2009 , 27, 333-41	149
876	A mutation within the transmembrane domain of melanosomal protein Silver (Pmel17) changes luminal fragment interactions. 2009 , 88, 653-67	6
875	A comparative study of the COX-1 and COX-2 isozymes bound to lipid membranes. 2009 , 30, 1038-50	8
874	Beta-hairpin restraint potentials for calculations of potentials of mean force as a function of beta-hairpin tilt, rotation, and distance. 2009 , 30, 1334-43	8
873	Ultraviolet resonance Raman spectroscopy of a β -sheet peptide: a model for membrane protein folding. 2009 , 40, 1060-1064	22
872	Dissecting membrane protein architecture: An annotation of structural complexity. 2009 , 91, 815-29	14
871	Interpretable Features for the Activity Prediction of Short Antimicrobial Peptides Using Fuzzy Logic. 2009 , 15, 129-137	13
870	Why hypothetical protein KPN00728 of <i>Klebsiella pneumoniae</i> should be classified as chain C of succinate dehydrogenase?. 2009 , 28, 415-27	4
869	Viewing the bilayer hydrocarbon core using neutron diffraction. <i>Journal of Membrane Biology</i> , 2009 , 227, 123-31	2,3 4
868	Hill coefficient analysis of transmembrane helix dimerization. <i>Journal of Membrane Biology</i> , 2009 , 230, 49-55	2,3 8
867	Activation of Bax by joint action of tBid and mitochondrial outer membrane: Monte Carlo simulations. 2009 , 38, 941-60	13
866	Lipophobicity and the residue environments of the transmembrane alpha-helical bundle. 2009 , 74, 32-49	12

865	A unified hydrophobicity scale for multispans membrane proteins. 2009 , 76, 13-29	39
864	Application of the fuzzy-oil-drop model to membrane protein simulation. 2009 , 77, 378-94	9
863	MPEX: a tool for exploring membrane proteins. 2009 , 18, 2624-8	196
862	Effects of impurities on membrane-protein crystallization in different systems. 2009 , 65, 1062-73	27
861	Toward genomic identification of beta-barrel membrane proteins: composition and architecture of known structures. 2002 , 11, 301-12	178
860	Improved detection of homologous membrane proteins by inclusion of information from topology predictions. 2002 , 11, 652-8	21
859	On transversal hydrophobicity of some proteins and their modules. 2009 , 49, 1821-30	6
858	CO ₂ -formatics: how do proteins bind carbon dioxide?. 2009 , 49, 2111-5	37
857	Benchmark experimental data set and assessment of adsorption free energy for peptide-surface interactions. 2009 , 25, 5637-46	60
856	Structural basis for dimerization of the BNIP3 transmembrane domain. 2009 , 48, 5106-20	53
855	Oriental landscapes of peptides in membranes: prediction of (2)H NMR couplings in a dynamic context. 2009 , 48, 11441-8	16
854	Hydrogen bonds in membrane proteins. 2009 , 113, 5318-26	9
853	Structural constraints imposed by the conserved fusion peptide on the HIV-1 gp41 epitope recognized by the broadly neutralizing antibody 2F5. 2009 , 113, 13626-37	20
852	Roles of arginine and lysine residues in the translocation of a cell-penetrating peptide from (13)C, (31)P, and (19)F solid-state NMR. 2009 , 48, 4587-95	116
851	Wasp mastoparans follow the same mechanism as the cell-penetrating peptide transportan 10. 2009 , 48, 7342-51	34
850	Improved prediction of trans-membrane spans in proteins using an Artificial Neural Network. 2009 , 2009, 68-74	2
849	Peptide Partitioning and Folding into Lipid Bilayers. 2009 , 5, 2202-5	16
848	The RH 421 styryl dye induced, pore model-dependent modulation of antimicrobial peptides activity in reconstituted planar membranes. 2009 , 1790, 809-16	25

847	Membrane binding of lipidated Ras peptides and proteins--the structural point of view. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2009 , 1788, 273-88	3.8	72
846	Effects of arginine density on the membrane-bound structure of a cationic antimicrobial peptide from solid-state NMR. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2009 , 1788, 514-21	3.8	21
845	Chemical modification of Bacillus thuringiensis Cry1Aa toxin single-cysteine mutants reveals the importance of domain I structural elements in the mechanism of pore formation. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2009 , 1788, 575-80	3.8	7
844	Polar residues in transmembrane helices can decrease electrophoretic mobility in polyacrylamide gels without causing helix dimerization. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2009 , 1788, 1321-31	3.8	30
843	Membrane perturbation by the antimicrobial peptide PMAP-23: a fluorescence and molecular dynamics study. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2009 , 1788, 1523-33	3.8	58
842	Kinetics of lipid-membrane binding and conformational change of L-BABP. <i>Biochemical and Biophysical Research Communications</i> , 2009 , 382, 771-5	3.4	7
841	A dual-scale approach toward structure prediction of retinal proteins. 2009 , 165, 37-46		7
840	Utility of surface-supported bilayers in studies of transmembrane helix dimerization. 2009 , 168, 53-60		7
839	Conformational conversion may precede or follow aggregate elongation on alternative pathways of amyloid protofibril formation. 2009 , 385, 1266-76		46
838	Functional analysis of the transmembrane domain in paramyxovirus F protein-mediated membrane fusion. 2009 , 386, 14-36		54
837	Experimental approaches to membrane thermodynamics. 2009 , 5, 3249		7
836	Magainin 2 revisited: a test of the quantitative model for the all-or-none permeabilization of phospholipid vesicles. 2009 , 96, 116-31		96
835	The effect of loops on the structural organization of alpha-helical membrane proteins. 2009 , 96, 2299-312		21
834	The influence of vesicle size and composition on alpha-synuclein structure and stability. 2009 , 96, 2857-70		66
833	Structure of a double transmembrane fragment of a G-protein-coupled receptor in micelles. 2009 , 96, 3187-96		30
832	Tilt and azimuthal angles of a transmembrane peptide: a comparison between molecular dynamics calculations and solid-state NMR data of sarcolipin in lipid membranes. 2009 , 96, 3648-62		32
831	Polymer-Tethered Bimolecular Lipid Membranes. 2009 , 197-233		6
830	Broad-spectrum antimicrobial peptides by rational combinatorial design and high-throughput screening: the importance of interfacial activity. 2009 , 131, 7609-17		222

829	Effect of ring size on conformation and biological activity of cyclic cationic antimicrobial peptides. 2009 , 52, 2090-7		37
828	Gemini surfactant-protein interactions: effect of pH, temperature, and surfactant stereochemistry. 2009 , 10, 2508-14		76
827	Structure and mechanism of beta-hairpin antimicrobial peptides in lipid bilayers from solid-state NMR spectroscopy. 2009 , 5, 317-22		64
826	Transmembrane helix predictions revisited. 2002 , 11, 2774-91		149
825	Optimal bundling of transmembrane helices using sparse distance constraints. 2004 , 13, 2613-27		35
824	Quantification of helix-helix binding affinities in micelles and lipid bilayers. 2004 , 13, 2600-12		26
823	Chapter 1 NMR of Antimicrobial Peptides. 2009 , 65, 1-51		19
822	Hydrogen bonding and solvent polarity markers in the uv resonance raman spectrum of tryptophan: application to membrane proteins. 2009 , 113, 14769-78		45
821	Conserved polar residues stabilize transmembrane domains and promote oligomerization in human nucleoside triphosphate diphosphohydrolase 3. 2009 , 48, 9437-47		11
820	The single transmembrane domains of human receptor tyrosine kinases encode self-interactions. <i>Science Signaling</i> , 2009 , 2, ra56	8.8	92
819	Inter-helical interactions in membrane proteins: analysis based on the local backbone geometry and the side chain interactions. <i>Journal of Biomolecular Structure and Dynamics</i> , 2009 , 26, 719-29	3.6	5
818	Cellular Signaling in Health and Disease. 2009 ,		6
817	Detergent binding explains anomalous SDS-PAGE migration of membrane proteins. 2009 , 106, 1760-5		547
816	Modeling kinetics of subcellular disposition of chemicals. 2009 , 109, 1793-899		59
815	Mechanisms of antimicrobial, cytolytic, and cell-penetrating peptides: from kinetics to thermodynamics. 2009 , 48, 8083-93		219
814	Free-energy relationships for the interactions of tryptophan with phosphocholines. 2009 , 7, 5119-28		23
813	Structures of membrane proteins. 2010 , 43, 65-158		108
812	Role of membrane lipids for the activity of pore forming peptides and proteins. 2010 , 677, 31-55		21

811	Protein misfolding and cellular stress: an overview. 2010 , 648, 3-23		103
810	Protein folding in membranes. 2010 , 67, 1779-98		59
809	The role of extramembranous cytoplasmic termini in assembly and stability of the tetrameric K(+)-channel KcsA. <i>Journal of Membrane Biology</i> , 2010 , 235, 51-61	2.3	13
808	Viruses: incredible nanomachines. New advances with filamentous phages. 2010 , 39, 541-50		56
807	Alpha-helical transmembrane peptides: a "divide and conquer" approach to membrane proteins. 2010 , 163, 1-26		90
806	Influence of assignment on the prediction of transmembrane helices in protein structures. 2010 , 39, 1241-54		6
805	Lipid-induced conformational transition of amyloid beta peptide fragments. 2010 , 41, 368-82		12
804	Divorcing folding from function: how acylation affects the membrane-perturbing properties of an antimicrobial peptide. 2010 , 1804, 806-20		21
803	Construction of an implicit membrane environment for the lattice Monte Carlo simulation of transmembrane protein. 2010 , 147, 35-41		3
802	In vitro association of fragments of a beta-sheet membrane protein. 2010 , 148, 112-20		18
801	Recombinant expression screening of <i>P. aeruginosa</i> bacterial inner membrane proteins. 2010 , 10, 83		7
800	Focus on composition and interaction potential of single-pass transmembrane domains. 2010 , 10, 4196-208		42
799	Dual energy landscape: the functional state of the β -barrel outer membrane protein G molds its unfolding energy landscape. 2010 , 10, 4151-62		14
798	A structural dissection of amino acid substitutions in helical transmembrane proteins. 2010 , 78, 2895-907		9
797	The tension-transmitting 'clutch' in the mechanosensitive channel MscS. 2010 , 17, 451-8		62
796	Phosphatidylinositol-(4,5)-biphosphate enables efficient secretion of HIV-1 Tat by infected T-cells. 2010 , 29, 1348-62		127
795	Protein folding at the membrane interface, the structure of Nogo-66 requires interactions with a phosphocholine surface. 2010 , 107, 6847-51		21
794	Proteins. 2010 , 1-27		7

793	Role of the synaptobrevin C terminus in fusion pore formation. 2010 , 107, 18463-8	69
792	Hydrophobically stabilized open state for the lateral gate of the Sec translocon. 2010 , 107, 5399-404	50
791	Characterization of the beta-D-glucopyranoside binding site of the human bitter taste receptor hTAS2R16. 2010 , 285, 28373-8	73
790	pH (low) insertion peptide (pHLIP) inserts across a lipid bilayer as a helix and exits by a different path. 2010 , 107, 4081-6	110
789	Relationship between antibody 2F5 neutralization of HIV-1 and hydrophobicity of its heavy chain third complementarity-determining region. 2010 , 84, 2955-62	97
788	Protein conducting nanopores. 2010 , 22, 454102	20
787	Present and future of membrane protein structure determination by electron crystallography. 2010 , 81, 33-60	21
786	Understanding functional residues of the cannabinoid CB1. 2010 , 10, 779-98	24
785	Hydration properties of mechanosensitive channel pores define the energetics of gating. 2010 , 22, 454120	51
784	Mechanism and kinetics of peptide partitioning into membranes from all-atom simulations of thermostable peptides. 2010 , 132, 3452-60	70
783	Macromolecules in Solution. 2010 , 485-552	
782	Gramicidin channels are internally gated. 2010 , 98, 1486-93	11
781	Peptide partitioning properties from direct insertion studies. 2010 , 98, L60-2	23
780	NMR structures of the histidine-rich peptide LAH4 in micellar environments: membrane insertion, pH-dependent mode of antimicrobial action, and DNA transfection. 2010 , 99, 2507-15	51
779	Lateral diffusion of membrane proteins: consequences of hydrophobic mismatch and lipid composition. 2010 , 99, 1482-9	44
778	Assembly of the m2 tetramer is strongly modulated by lipid chain length. 2010 , 99, 1810-7	24
777	Effects of curvature and composition on Eynuclein binding to lipid vesicles. 2010 , 99, 2279-88	238
776	Statistical mechanics of integral membrane protein assembly. 2010 , 99, 2217-24	1

775	Actinoporins from the sea anemones, tropical <i>Radianthus macrodactylus</i> and northern <i>Oulactis orientalis</i> : Comparative analysis of structure-function relationships. 2010 , 56, 1299-314		42
774	Influence of the lipid phase state and electrostatic surface potential on the conformations of a peripherally bound membrane protein. 2010 , 114, 15141-50		10
773	MPRAP: an accessibility predictor for α -helical transmembrane proteins that performs well inside and outside the membrane. 2010 , 11, 333		33
772	Secondary structure in de novo designed peptides induced by electrostatic interaction with a lipid bilayer membrane. 2010 , 26, 6437-48		10
771	Measuring the energetics of membrane protein dimerization in mammalian membranes. 2010 , 132, 3628-35	101	
770	Solute Partitioning into Lipid Bilayers: An Implicit Model for Nonuniform and Ordered Environment. 2010 , 6, 2267-80		17
769	Factors that influence helical preferences for singly charged gas-phase peptide ions: the effects of multiple potential charge-carrying sites. 2010 , 114, 809-16		31
768	Membrane-bound dynamic structure of an arginine-rich cell-penetrating peptide, the protein transduction domain of HIV TAT, from solid-state NMR. 2010 , 49, 6009-20		81
767	Polar groups in membrane channels: consequences of replacing alanines with serines in membrane-spanning gramicidin channels. 2010 , 49, 6856-65		6
766	The functionally active Mistic-fused histidine kinase receptor, EnvZ. 2010 , 49, 9089-95		13
765	Membrane interactions and conformational preferences of human and avian prion N-terminal tandem repeats: the role of copper(II) ions, pH, and membrane mimicking environments. 2010 , 114, 13830-8		32
764	Spatial structure of the transmembrane domain heterodimer of ErbB1 and ErbB2 receptor tyrosine kinases. 2010 , 400, 231-43		99
763	Solution structure and phospholipid interactions of the isolated voltage-sensor domain from KvAP. 2010 , 403, 591-606		81
762	A solid-state NMR study of the structure and dynamics of the myristoylated N-terminus of the guanylate cyclase-activating protein-2. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2010 , 1798, 266-74 ^{3,8}		13
761	A membranotropic region in the C-terminal domain of hepatitis C virus protein NS4B interaction with membranes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2010 , 1798, 327-37	3.8	22
760	Probing excited states and activation energy for the integral membrane protein phospholamban by NMR CPMG relaxation dispersion experiments. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2010 , 1798, 77-81	3.8	34
759	Interaction with membrane mimics of transmembrane fragments 16 and 17 from the human multidrug resistance ABC transporter 1 (hMRP1/ABCC1) and two of their tryptophan variants. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2010 , 1798, 401-14	3.8	4
758	The membrane environment modulates self-association of the human GpA TM domain--implications for membrane protein folding and transmembrane signaling. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2010 , 1798, 1899-907	3.8	76

757	Quantitative assessment of peptide-lipid interactions. Ubiquitous fluorescence methodologies. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2010 , 1798, 1999-2012	3.8	54
756	A comprehensive comparison of transmembrane domains reveals organelle-specific properties. 2010 , 142, 158-69		378
755	Live-cell imaging of aquaporin-4 diffusion and interactions in orthogonal arrays of particles. 2010 , 168, 892-902		25
754	The cholesterol-dependent cytolysin family of gram-positive bacterial toxins. 2010 , 51, 551-77		80
753	Energetics of peptide and protein binding to lipid membranes. 2010 , 677, 14-23		8
752	Crystallographic characterization of N-oxide tripod amphiphiles. 2010 , 132, 1953-9		9
751	Antimicrobial Peptides. 2010 ,		8
750	Design of a soluble transmembrane helix for measurements of water-membrane partitioning. 2010 , 114, 1925-31		8
749	Tandem facial amphiphiles for membrane protein stabilization. 2010 , 132, 16750-2		77
748	Interaction of amino acids with the Au(111) surface: adsorption free energies from molecular dynamics simulations. 2010 , 26, 8347-51		159
747	Deletion of a terminal residue disrupts oligomerization of a transmembrane alpha-helix. 2010 , 88, 339-45		11
746	GeT peptides: a single-domain approach to gene delivery. 2011 , 47, 9045-7		10
745	Host-guest chemistry in the gas phase: complex formation with 18-crown-6 enhances helicity of alanine-based peptides. 2011 , 115, 14215-20		10
744	Effects on membrane lateral pressure suggest permeation mechanisms for bacterial quorum signaling molecules. 2011 , 50, 6983-93		30
743	Spontaneous membrane-translocating peptides by orthogonal high-throughput screening. 2011 , 133, 8995-9004		140
742	Physicochemical mechanism for the enhanced ability of lipid membrane penetration of polyarginine. 2011 , 27, 7099-107		55
741	Paramagnetic-based NMR restraints lift residual dipolar coupling degeneracy in multidomain detergent-solubilized membrane proteins. 2011 , 133, 2232-41		24
740	A thermodynamic approach to the mechanism of cell-penetrating peptides in model membranes. 2011 , 50, 654-62		26

739	Solid-state ^1H NMR shows equivalence of dehydration and osmotic pressures in lipid membrane deformation. 2011 , 100, 98-107		35
738	Membrane insertion of a voltage sensor helix. 2011 , 100, 410-9		14
737	Lipid-controlled peptide topology and interactions in bilayers: structural insights into the synergistic enhancement of the antimicrobial activities of PGLa and magainin 2. 2011 , 100, 1473-80		79
736	Tryptophan-lipid interactions in membrane protein folding probed by ultraviolet resonance Raman and fluorescence spectroscopy. 2011 , 100, 2121-30		63
735	The molecular basis for antimicrobial activity of pore-forming cyclic peptides. 2011 , 100, 2422-31		58
734	Transmembrane helix orientation and dynamics: insights from ensemble dynamics with solid-state NMR observables. 2011 , 100, 2913-21		28
733	Structural plasticity in self-assembling transmembrane β -sheets. 2011 , 101, 828-36		4
732	Regulation of Plant Transporters by Lipids and Microdomains. 2011 , 353-377		
731	In silico partitioning and transmembrane insertion of hydrophobic peptides under equilibrium conditions. 2011 , 133, 15487-95		79
730	High-resolution atomic force microscopy and spectroscopy of native membrane proteins. 2011 , 74, 086601		102
729	Hydrophobic pulses predict transmembrane helix irregularities and channel transmembrane units. 2011 , 12, 135		3
728	Molecular dynamics studies of transportan 10 (tp10) interacting with a POPC lipid bilayer. 2011 , 115, 1188-98		44
727	Cell-Penetrating Peptides. 2011 ,		23
726	Using the Wimley-White Hydrophobicity Scale as a Direct Quantitative Test of Force Fields: The MARTINI Coarse-Grained Model. 2011 , 7, 2316-24		38
725	Opposing structural changes in two symmetrical polypeptides bring about opposing changes to the thermal stability of a complex integral membrane protein. 2011 , 505, 160-70		12
724	The Sec translocase. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011 , 1808, 851-65	3.8	199
723	The prediction and characterization of YshA, an unknown outer-membrane protein from Salmonella typhimurium. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011 , 1808, 287-97	3.8	12
722	An NMR database for simulations of membrane dynamics. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011 , 1808, 818-39	3.8	77

721	Helical integrity and microsolvation of transmembrane domains from Flaviviridae envelope glycoproteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011 , 1808, 1040-9	3.8	4
720	A 35 kDa antigenic protein from <i>Shigella flexneri</i> : in silico structural and functional studies. <i>Biochemical and Biophysical Research Communications</i> , 2011 , 415, 229-34	3.4	4
719	An introduction to membrane proteins. 2011 , 10, 3324-31		47
718	Association of neighboring β -strands of outer membrane protein A in lipid bilayers revealed by site-directed fluorescence quenching. 2011 , 407, 316-32		32
717	SDS-facilitated in vitro formation of a transmembrane B-type cytochrome is mediated by changes in local pH. 2011 , 407, 594-606		16
716	Lipid-mediated folding/unfolding of phospholamban as a regulatory mechanism for the sarcoplasmic reticulum Ca ²⁺ -ATPase. 2011 , 408, 755-65		45
715	Kinetic folding mechanism of an integral membrane protein examined by pulsed oxidative labeling and mass spectrometry. 2011 , 410, 146-58		28
714	cAMP-dependent protein kinase A selects the excited state of the membrane substrate phospholamban. 2011 , 412, 155-64		54
713	Roles of carboxyl groups in the transmembrane insertion of peptides. 2011 , 413, 359-71		47
712	Thermodynamics of insertion and self-association of a transmembrane helix: a lipophobic interaction by phosphatidylethanolamine. 2011 , 50, 6806-14		13
711	Efficient expression screening of human membrane proteins in transiently transfected Human Embryonic Kidney 293S cells. 2011 , 55, 273-80		26
710	Structural analysis of the Na ⁺ /H ⁺ exchanger isoform 1 (NHE1) using the divide and conquer approach. 2011 , 89, 189-99		20
709	Surfactants and Alcohols as Inducers of Protein Amyloid: Aggregation Chaperones or Membrane Simulators?. 2011 , 57-92		
708	AcrB trimer stability and efflux activity, insight from mutagenesis studies. 2011 , 6, e28390		23
707	Membrane-transferring regions of gp41 as targets for HIV-1 fusion inhibition and viral neutralization. 2011 , 11, 2985-96		5
706	The Mesomorphic Phase Behavior of Lipid Bilayers. 2011 , 19-89		6
705	Membrane protein integration into the endoplasmic reticulum. 2011 , 278, 3846-58		26
704	Membrane protein folding: how important are hydrogen bonds?. 2011 , 21, 42-9		128

703	The effect of lipids on the enzymatic activity of 6-phosphofructo-1-kinase from <i>B. stearothermophilus</i> . 2011 , 164, 713-21		9
702	What determines the activity of antimicrobial and cytolytic peptides in model membranes. 2011 , 50, 7919-32		25
701	In vitro folding of KvAP, a voltage-gated K ⁺ channel. 2011 , 50, 10442-50		17
700	Membrane protein insertion at the endoplasmic reticulum. 2011 , 27, 25-56		207
699	Simulation of amino acid diffusion across water/hydrophobic interfaces. 2011 , 13, 11579-82		11
698	Physicochemical properties of pore residues predict activation gating of Ca V1.2: a correlation mutation analysis. 2011 , 461, 53-63		6
697	A look at arginine in membranes. <i>Journal of Membrane Biology</i> , 2011 , 239, 49-56	2.3	84
696	Determining peptide partitioning properties via computer simulation. <i>Journal of Membrane Biology</i> , 2011 , 239, 15-26	2.3	21
695	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
694	The presence of membranes or micelles induces structural changes of the myristoylated guanylate-cyclase activating protein-2. 2011 , 40, 565-76		17
693	A lipocentric view of peptide-induced pores. 2011 , 40, 399-415		94
692	Transverse and tangential orientation of predicted transmembrane fragments 4 and 10 from the human multidrug resistance protein (hMRP1/ABCC1) in membrane mimics. 2011 , 40, 1043-60		7
691	A new in-silico method for determination of helical transmembrane domains based on the PepLook scan: application to IL-2R β and IL-2R γ receptor chains. 2011 , 11, 26		1
690	Not all transmembrane helices are born equal: Towards the extension of the sequence homology concept to membrane proteins. 2011 , 6, 57		26
689	Molecular mechanism of β -sheet self-organization at water-hydrophobic interfaces. 2011 , 79, 1-22		42
688	Why are polar residues within the membrane core evolutionary conserved?. 2011 , 79, 79-91		36
687	Conserved conformational dynamics of membrane fusion protein transmembrane domains and flanking regions indicated by sequence statistics. 2011 , 79, 2418-27		10
686	Insights into the mechanisms of action of host defence peptides from biophysical and structural investigations. 2011 , 17, 306-14		70

685	Structure and dynamics of cationic membrane peptides and proteins: insights from solid-state NMR. 2011 , 20, 641-55	79
684	A new paradigm in molecular recognition? Specific antibody binding to membrane-inserted HIV-1 epitopes. 2011 , 24, 642-6	9
683	First implication of STRA6 mutations in isolated anophthalmia, microphthalmia, and coloboma: a new dimension to the STRA6 phenotype. 2011 , 32, 1417-26	62
682	Statistical analysis and exposure status classification of transmembrane beta barrel residues. 2011 , 35, 96-107	5
681	The optimization of polymeric acid peptide copolymers for endosomolytic drug delivery. 2011 , 32, 5269-78	43
680	Biomimetic fabrication of gold nanoparticles on templated indole-3-acetic acid based nanofibers. 2011 , 31, 620-628	5
679	Structural and functional studies of a 50 kDa antigenic protein from Salmonella enterica serovar Typhi. 2011 , 29, 834-42	10
678	Bilayer hydrophobic thickness and integral membrane protein function. 2011 , 12, 760-6	33
677	FXFD proteins stabilize Na,K-ATPase: amplification of specific phosphatidylserine-protein interactions. 2011 , 286, 9699-712	65
676	Transmembrane segments of nascent polytopic membrane proteins control cytosol/ER targeting during membrane integration. 2011 , 195, 41-54	29
675	Misalignment of PLP/DM20 transmembrane domains determines protein misfolding in Pelizaeus-Merzbacher disease. 2011 , 31, 14961-71	47
674	An in vivo screen reveals protein-lipid interactions crucial for gating a mechanosensitive channel. 2011 , 25, 694-702	20
673	Amino acid interaction preferences in helical membrane proteins. 2011 , 24, 579-88	6
672	Highly conserved structural properties of the C-terminal tail of HIV-1 gp41 protein despite substantial sequence variation among diverse clades: implications for functions in viral replication. 2011 , 286, 27156-66	34
671	Sensing bilayer tension: bacterial mechanosensitive channels and their gating mechanisms. 2011 , 39, 733-40	22
670	Membrane texture induced by specific protein binding and receptor clustering: active roles for lipids in cellular function. 2011 , 108, 6975-80	59
669	We choose to go to the membrane. 2011 , 108, 10027-8	1
668	Stable folding core in the folding transition state of an alpha-helical integral membrane protein. 2011 , 108, 14133-8	43

667	Side-chain hydrophobicity scale derived from transmembrane protein folding into lipid bilayers. 2011 , 108, 10174-7	218
666	Interactions of benzo[a]pyrene and diesel exhaust particulate matter with the lung surfactant system. 2011 , 55, 329-38	17
665	Construction and maintenance of randomized retroviral expression libraries for transmembrane protein engineering. 2011 , 24, 311-20	6
664	Transmembrane helix: simple or complex. 2012 , 40, W370-5	15
663	Membrane physical properties influence transmembrane helix formation. 2012 , 109, 14422-7	55
662	The Study of Lyotropic Liquid Crystal Structure Using the Molecular Dynamics Simulation Method. 2012 , 561, 155-169	2
661	The rational design of a synthetic polymer nanoparticle that neutralizes a toxic peptide in vivo. 2012 , 109, 33-8	152
660	Structural basis for the acyltransferase activity of lecithin:retinol acyltransferase-like proteins. 2012 , 287, 23790-807	49
659	On the origin of multiphasic kinetics in peptide binding to phospholipid vesicles. 2012 , 116, 951-7	6
658	Functional determinants of human enteric β -defensin HD5: crucial role for hydrophobicity at dimer interface. 2012 , 287, 21615-27	57
657	The polymorphic nature of membrane-active peptides from biophysical and structural investigations. 2012 , 13, 602-10	20
656	Physicochemical Mechanism for the Lipid Membrane Binding of Polyarginine: The Favorable Enthalpy Change with Structural Transition from Random Coil to β -Helix. 2012 , 41, 1374-1376	1
655	Isotope labeling for solution and solid-state NMR spectroscopy of membrane proteins. 2012 , 992, 35-62	57
654	Analytical approaches for studying transporters, channels and porins. 2012 , 112, 6227-49	40
653	Membrane association of the PTEN tumor suppressor: electrostatic interaction with phosphatidylserine-containing bilayers and regulatory role of the C-terminal tail. 2012 , 180, 394-408	34
652	Dynamics of the L-fucose/H ⁺ symporter revealed by fluorescence spectroscopy. 2012 , 109, 14847-51	18
651	Polymersome surface decoration by an EGFP fusion protein employing Cecropin A as peptide "anchor". 2012 , 157, 31-7	27
650	Membrane protein structural bioinformatics. 2012 , 179, 327-37	33

649	Anchoring proteins to Escherichia coli cell membranes using hydrophobic anchors derived from a Bacillus subtilis integral membrane protein. 2012 , 85, 60-5		3
648	Enhanced activity of cyclic transporter sequences driven by phase behavior of peptide-lipid complexes. 2012 , 8, 6430-6433		14
647	The importance of the shape of the protein-water interface of a kinesin motor domain for dynamics of the surface atoms of the protein. 2012 , 14, 5561-9		14
646	Interaction of cetyltrimethylammonium bromide and its gemini homologue bis(cetyldimethylammonium)butane dibromide with xanthine oxidase. 2012 , 116, 5711-8		35
645	Role of lipids in the interaction of antimicrobial peptides with membranes. 2012 , 51, 149-77		443
644	Overexpressing human membrane proteins in stably transfected and clonal human embryonic kidney 293S cells. 2012 , 7, 453-66		55
643	Studying plant salt tolerance with the voltage clamp technique. 2012 , 913, 19-33		
642	Shifting hydrogen bonds may produce flexible transmembrane helices. 2012 , 109, 8121-6		61
641	Statistical analyses and computational prediction of helical kinks in membrane proteins. 2012 , 26, 1171-85		13
640	Protein structure in membrane domains. 2012 , 41, 135-55		24
639	Thermodynamic measurements of bilayer insertion of a single transmembrane helix chaperoned by fluorinated surfactants. 2012 , 416, 328-34		16
638	Functional and topological analysis of phosphatidylcholine synthase from Sinorhizobium meliloti. 2012 , 1821, 573-81		15
637	Hydrogen-bond energetics drive helix formation in membrane interfaces. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 178-82	3.8	40
636	Biophysics of Eynuclein membrane interactions. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 162-71	3.8	141
635	Transmembrane helix-helix interactions are modulated by the sequence context and by lipid bilayer properties. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 963-73	3.8	86
634	Membrane assembly of the cholesterol-dependent cytolysin pore complex. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 1028-38	3.8	135
633	Probing ground and excited states of phospholamban in model and native lipid membranes by magic angle spinning NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 146-53	3.8	41
632	An ensemble dynamics approach to decipher solid-state NMR observables of membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 252-62	3.8	21

631	Föster resonance energy transfer as a probe of membrane protein folding. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 154-61	3.8	15
630	Transmembrane helix dimerization: beyond the search for sequence motifs. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 183-93	3.8	117
629	Computational studies of membrane proteins: models and predictions for biological understanding. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 927-41	3.8	32
628	Structural basis for misfolding at a disease phenotypic position in CFTR: comparison of TM3/4 helix-loop-helix constructs with TM4 peptides. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 49-54	3.8	5
627	The amphipathic helix of an enzyme that regulates phosphatidylcholine synthesis remodels membranes into highly curved nanotubules. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 1173-86	3.8	28
626	Efficiency of detergents at maintaining membrane protein structures in their biologically relevant forms. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 1351-8	3.8	46
625	Hydrophobic mismatch of mobile transmembrane helices: Merging theory and experiments. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 1242-9	3.8	78
624	Autonomous transmembrane segment S4 of the voltage sensor domain partitions into the lipid membrane. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 1698-705	3.8	2
623	Binding of the three-repeat domain of tau to phospholipid membranes induces an aggregated-like state of the protein. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 2302-13	3.8	49
622	Structural and thermodynamic insight into the process of "weak" dimerization of the ErbB4 transmembrane domain by solution NMR. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 2158-70	3.8	50
621	Single-molecule force spectroscopy from nanodiscs: an assay to quantify folding, stability, and interactions of native membrane proteins. 2012 , 6, 961-71		44
620	Curvature forces in membrane lipid-protein interactions. 2012 , 51, 9782-95		112
619	Structural insights into the common E-chain family of cytokines and receptors from the interleukin-7 pathway. 2012 , 250, 303-16		41
618	Assembly and Stability of α -Helical Membrane Proteins. 2012 , 8, 7742-7752		24
617	5.8 Structure and Folding of Outer Membrane Proteins. 2012 , 139-163		6
616	5.10 Interactions of Antimicrobial Peptides with Lipid Bilayers. 2012 , 189-222		11
615	5.11 Membrane Recruitment of Signaling Domains. 2012 , 223-244		0
614	NS4A and NS4B proteins from dengue virus: membranotropic regions. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 2818-30	3.8	28

613	The membrane spanning domains of protein NS4B from hepatitis C virus. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 2958-66	3.8	7
612	Modulation of the pHLIP transmembrane helix insertion pathway. 2012 , 102, 1846-55		44
611	Stabilizing effect of solvent and guest residue amino acids on a model alpha-helix peptide. 2012 , 998, 80-86		1
610	Out but not in: the large transmembrane β -barrel protein FhuA unfolds but cannot refold via β -hairpins. 2012 , 20, 2185-90		40
609	Quantifying interactions of β -synuclein and β -synuclein with model membranes. 2012 , 423, 528-39		22
608	1.11 The Hybrid Solution/Solid-State NMR Method for Membrane Protein Structure Determination. 2012 , 182-198		4
607	Identifying and measuring transmembrane helix-helix interactions by FRET. 2012 , 914, 87-106		2
606	Structure-based and multiple potential three-dimensional quantitative structure-activity relationship (SB-MP-3D-QSAR) for inhibitor design. 2012 , 52, 996-1004		7
605	Cross-talk between amino acid residues and flavonoid derivatives: insights into their chemical recognition. 2012 , 14, 15682-92		8
604	Prokaryotic diacylglycerol kinase and undecaprenol kinase. 2012 , 41, 81-101		52
603	Spectroscopic and computational study of melittin, cecropin A, and the hybrid peptide CM15. 2012 , 116, 10600-8		31
602	Characterization of adenosine receptor in its native environment: insights from molecular dynamics simulations of palmitoylated/glycosylated, membrane-integrated human A(2B) adenosine receptor. 2012 , 18, 4309-24		15
601	Replica exchange Monte-Carlo simulations of helix bundle membrane proteins: rotational parameters of helices. 2012 , 26, 363-74		8
600	Construction of covalent membrane protein complexes and high-throughput selection of membrane mimics. 2012 , 134, 9030-3		11
599	Protein Transduction Domain Mimics: The Role of Aromatic Functionality. <i>Angewandte Chemie</i> , 2012 , 124, 1004-1007	3.6	7
598	A new class of amphiphiles bearing rigid hydrophobic groups for solubilization and stabilization of membrane proteins. 2012 , 18, 9485-90		87
597	Structure-Directing L-Tryptophan for Supported DPPC Helices and Fractals: An Alkyl-Chain Tilt-Angle Dependence. 2012 , 77, 898-907		4
596	Synthetic mimics of antimicrobial peptides with immunomodulatory responses. 2012 , 134, 11088-91		87

595	Comparative study on the interaction of cell-penetrating polycationic polymers with lipid membranes. 2012 , 165, 51-8	31
594	The transmembrane protein KpOmpA anchoring the outer membrane of <i>Klebsiella pneumoniae</i> unfolds and refolds in response to tensile load. 2012 , 20, 121-7	33
593	Protein transduction domain mimics: the role of aromatic functionality. <i>Angewandte Chemie - International Edition</i> , 2012 , 51, 980-3	16.4 67
592	In silico investigations of possible routes of assembly of ORF 3a from SARS-CoV. 2012 , 18, 501-14	24
591	Structure-based statistical analysis of transmembrane helices. 2013 , 42, 199-207	50
590	Competition between homodimerization and cholesterol binding to the C99 domain of the amyloid precursor protein. 2013 , 52, 5051-64	84
589	Structural changes in the mitochondrial Tim23 channel are coupled to the proton-motive force. 2013 , 20, 965-72	53
588	Mechanistic explanation of different unfolding behaviors observed for transmembrane and soluble β -barrel proteins. 2013 , 21, 1317-24	14
587	Effect of particle diameter and surface composition on the spontaneous fusion of monolayer-protected gold nanoparticles with lipid bilayers. 2013 , 13, 4060-7	192
586	Polyoxometalate macroion induced phase and morphology instability of lipid membrane. 2013 , 4, 3818	29
585	Surface-Modified Anisotropic TiO ₂ Nanocrystals Immobilized in Membranes: A Biologically Inspired Solar Fuel Catalyst. 2013 , 263-278	
584	On the role of NMR spectroscopy for characterization of antimicrobial peptides. 2013 , 1063, 159-80	26
583	Measuring transmembrane helix interaction strengths in lipid bilayers using steric trapping. 2013 , 1063, 37-56	17
582	Cationic membrane peptides: atomic-level insight of structure-activity relationships from solid-state NMR. 2013 , 44, 821-33	48
581	Membrane protein thermodynamic stability may serve as the energy sink for sorting in the periplasm. 2013 , 110, 4285-90	91
580	Cysteine scanning of CFTR's first transmembrane segment reveals its plausible roles in gating and permeation. 2013 , 104, 786-97	40
579	Translocation of cationic amphipathic peptides across the membranes of pure phospholipid giant vesicles. 2013 , 135, 16517-25	62
578	Antimicrobial peptides and induced membrane curvature: geometry, coordination chemistry, and molecular engineering. 2013 , 17, 151-163	125

577	Characterization of a membrane-active peptide from the Bordetella pertussis CyaA toxin. 2013 , 288, 32585-32598		36
576	Membrane partitioning of the pore-forming domain of colicin A. Role of the hydrophobic helical hairpin. 2013 , 105, 1432-43		3
575	Engineering antimicrobial peptides with improved antimicrobial and hemolytic activities. 2013 , 53, 3280-96		66
574	Lipid-induced conformational changes within the cytochrome b6f complex of oxygenic photosynthesis. 2013 , 52, 2649-54		27
573	Ab initio and all-atom modeling of detergent organization around Aquaporin-0 based on SAXS data. 2013 , 117, 13588-94		20
572	Modulating the structure and interactions of lipid-peptide complexes by varying membrane composition and solution conditions. 2013 , 9, 7117		14
571	Correction factors for membrane protein molecular weight readouts on sodium dodecyl sulfate-polyacrylamide gel electrophoresis. 2013 , 434, 67-72		23
570	The structure of cross-β-tapes and tubes formed by an octapeptide, S ₁₁ . <i>Angewandte Chemie - International Edition</i> , 2013 , 52, 2279-83	16.4	45
569	Novel tripod amphiphiles for membrane protein analysis. 2013 , 19, 15645-51		35
568	Reversible folding of human peripheral myelin protein 22, a tetraspan membrane protein. 2013 , 52, 3229-41		27
567	Cells and cell lysates: a direct approach for engineering antibodies against membrane proteins using yeast surface display. 2013 , 60, 27-37		40
566	Detergent-mediated protein aggregation. 2013 , 169, 72-84		13
565	Structure and expression of a novel compact myelin protein - small VCP-interacting protein (SVIP). <i>Biochemical and Biophysical Research Communications</i> , 2013 , 440, 173-8	3.4	13
564	Glucose-neopentyl glycol (GNG) amphiphiles for membrane protein study. 2013 , 49, 2287-9		67
563	Carbohydrate-containing Triton X-100 analogues for membrane protein solubilization and stabilization. 2013 , 9, 626-9		19
562	Thermal unfolding of a mammalian pentameric ligand-gated ion channel proceeds at consecutive, distinct steps. 2013 , 288, 5756-69		16
561	Membrane protein native state discrimination by implicit membrane models. 2013 , 34, 731-8		23
560	Validation of depth-dependent fluorescence quenching in membranes by molecular dynamics simulation of tryptophan octyl ester in POPC bilayer. 2013 , 117, 4770-8		13

559	Aspartate embedding depth affects pHLIP's insertion pKa. 2013 , 52, 4595-604		34
558	Membrane depth-dependent energetic contribution of the tryptophan side chain to the stability of integral membrane proteins. 2013 , 52, 4413-21		23
557	Coarse-grained simulations of the salt dependence of the radius of gyration of polyelectrolytes as models for biomolecules in aqueous solution. 2013 , 42, 661-72		22
556	The devil and holy water: protein and carbon nanotube hybrids. 2013 , 46, 2454-63		120
555	Synthetic molecular evolution of pore-forming peptides by iterative combinatorial library screening. 2013 , 8, 823-31		24
554	Cell-penetrating peptides: 20 years later, where do we stand?. 2013 , 587, 1693-702		606
553	UV resonance Raman and DFT studies of arginine side chains in peptides: insights into arginine hydration. 2013 , 117, 7145-56		14
552	Effects of a polar amino acid substitution on helix formation and aggregate size along the detergent-induced peptide folding pathway. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013 , 1828, 373-81	3.8	8
551	Lipid exposure prediction enhances the inference of rotational angles of transmembrane helices. 2013 , 14, 304		8
550	Lipid-specific β -sheet formation in a mussel byssus protein domain. 2013 , 14, 3238-45		7
549	Membrane mimetics induce helix formation and oligomerization of the chloride intracellular channel protein 1 transmembrane domain. 2013 , 52, 2739-49		6
548	Glycophorin A transmembrane domain dimerization in plasma membrane vesicles derived from CHO, HEK 293T, and A431 cells. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013 , 1828, 1829-33	3.8	25
547	Dissecting the function of a protruding loop in AcrB trimerization. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013 , 31, 385-92	3.6	7
546	A critical evaluation of random copolymer mimesis of homogeneous antimicrobial peptides. 2013 , 46, 1908-1915		64
545	The importance of being kinked: role of Pro residues in the selectivity of the helical antimicrobial peptide P5. 2013 , 19, 758-69		40
544	Amino acid capture by aqueous interfaces. Implications for biological uptake. 2013 , 117, 12469-74		14
543	Effects of flanking loops on membrane insertion of transmembrane helices: a role for peptide conformational equilibrium. 2013 , 117, 8330-9		4
542	ADAM8 in asthma. Friend or foe to airway inflammation?. 2013 , 49, 875-84		9

541	Membrane lipid saturation activates endoplasmic reticulum unfolded protein response transducers through their transmembrane domains. 2013 , 110, 4628-33		389
540	Recent Progress in Advanced Nanobiological Materials for Energy and Environmental Applications. 2013 , 6, 5821-5856		12
539	Rampant exchange of the structure and function of extramembrane domains between membrane and water soluble proteins. 2013 , 9, e1002997		8
538	Antibody affinity maturation using yeast display with detergent-solubilized membrane proteins as antigen sources. 2013 , 26, 101-12		17
537	Evolutionary mix-and-match with MFS transporters II. 2013 , 110, E4831-8		23
536	Polar residues and their positional context dictate the transmembrane domain interactions of influenza A neuraminidases. 2013 , 288, 10652-60		19
535	Structure of the YajR transporter suggests a transport mechanism based on the conserved motif A. 2013 , 110, 14664-9		121
534	Quantitative residue-level structure-evolution relationships in the yeast membrane proteome. 2013 , 5, 734-44		9
533	Simultaneous prediction of protein secondary structure and transmembrane spans. 2013 , 81, 1127-40		42
532	Multiscale multiphysics and multidomain models--flexibility and rigidity. 2013 , 139, 194109		56
531	Stochastic model for protein flexibility analysis. <i>Physical Review E</i> , 2013 , 88, 062709	2.4	14
530	Polar transmembrane interactions drive formation of ligand-specific and signal pathway-biased family B G protein-coupled receptor conformations. 2013 , 110, 5211-6		158
529	Crystalline polymorphism induced by charge regulation in ionic membranes. 2013 , 110, 16309-14		30
528	Modulation of human mitochondrial voltage-dependent anion channel 2 (hVDAC-2) structural stability by cysteine-assisted barrel-lipid interactions. 2013 , 288, 25584-25592		35
527	Direct cytosolic delivery of polar cargo to cells by spontaneous membrane-translocating peptides. 2013 , 288, 29974-86		41
526	Peptide transporter DtpA has two alternate conformations, one of which is promoted by inhibitor binding. 2013 , 110, E3978-86		17
525	The Structure of Cross- β -Tapes and Tubes Formed by an Octapeptide, 5 β 1. <i>Angewandte Chemie</i> , 2013 , 125, 2335-2339	3.6	8
524	Hemifluorinated maltose-neopentyl glycol (HF-MNG) amphiphiles for membrane protein stabilisation. 2013 , 14, 452-5		30

523	How round is a protein? Exploring protein structures for globularity using conformal mapping. 2014 , 1, 26		7
522	. 2014 ,		4
521	Scaling and alpha-helix regulation of protein relaxation in a lipid bilayer. 2014 , 141, 225101		4
520	Fast and anisotropic flexibility-rigidity index for protein flexibility and fluctuation analysis. 2014 , 140, 234105		45
519	Model for coupled insertion and folding of membrane-spanning proteins. <i>Physical Review E</i> , 2014 , 90, 022707	2.4	
518	Calibrated Langevin-dynamics simulations of intrinsically disordered proteins. <i>Physical Review E</i> , 2014 , 90, 042709	2.4	15
517	Bioinformatics approaches for functional annotation of membrane proteins. 2014 , 15, 155-68		29
516	Electrostatic Forces on Charged Surfaces of Bilayer Lipid Membranes. 2014 , 74, 1-21		7
515	Hydrophobic variations of N-oxide amphiphiles for membrane protein manipulation: importance of non-hydrocarbon groups in the hydrophobic portion. 2014 , 9, 110-6		7
514	More than the sum of its parts: coarse-grained peptide-lipid interactions from a simple cross-parametrization. 2014 , 140, 115101		33
513	The effect of triple glutamic mutations E9Q/E194Q/E204Q on the structural stability of bacteriorhodopsin. 2014 , 281, 1181-95		3
512	Molecular nonlinear dynamics and protein thermal uncertainty quantification. 2014 , 24, 013103		15
511	Structure and dynamics of G-protein coupled receptors. 2014 , 796, 37-54		22
510	Peptides with the same composition, hydrophobicity, and hydrophobic moment bind to phospholipid bilayers with different affinities. 2014 , 118, 12462-70		15
509	Assessing the effect of dynamics on the closed-loop protein-folding hypothesis. 2014 , 11, 20130935		5
508	Bindings of hMRP1 transmembrane peptides with dodecylphosphocholine and dodecyl- β -D-maltoside micelles: a molecular dynamics simulation study. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014 , 1838, 493-509	3.8	5
507	Membrane-active peptides: binding, translocation, and flux in lipid vesicles. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014 , 1838, 2216-27	3.8	31
506	The C2 domains of granuphilin are high-affinity sensors for plasma membrane lipids. 2014 , 182, 29-37		10

505	Structural basis for PI(4)P-specific membrane recruitment of the Legionella pneumophila effector DrrA/SidM. 2014 , 22, 397-408		37
504	EmrE dimerization depends on membrane environment. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014 , 1838, 1817-22	3.8	10
503	Toward the de novo design of antimicrobial peptides: Lack of correlation between peptide permeabilization of lipid vesicles and antimicrobial, cytolytic, or cytotoxic activity in living cells. 2014 , 102, 1-6		22
502	Structural basis of the proinflammatory signaling complex mediated by TSLP. 2014 , 21, 375-82		35
501	Computational prediction of kink properties of helices in membrane proteins. 2014 , 28, 99-109		6
500	Helix kinks are equally prevalent in soluble and membrane proteins. 2014 , 82, 1960-70		52
499	Channelrhodopsins: a bioinformatics perspective. 2014 , 1837, 643-55		11
498	Antimicrobial peptides against <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> and <i>Erwinia amylovora</i> : Chemical synthesis, secondary structure, efficacy, and mechanistic investigations. 2014 , 102, 88-96		9
497	A critical evaluation of in silico methods for detection of membrane protein intrinsic disorder. 2014 , 106, 1638-49		15
496	The three lives of viral fusion peptides. 2014 , 181, 40-55		65
495	Identification of proteins associated with ion homeostasis and salt tolerance in barley. 2014 , 14, 1381-92		45
494	Absorption and folding of melittin onto lipid bilayer membranes via unbiased atomic detail microsecond molecular dynamics simulation. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014 , 1838, 2243-9	3.8	36
493	PEG-peptide conjugates. 2014 , 15, 1543-59		209
492	Structural plasticity in the topology of the membrane-interacting domain of HIV-1 gp41. 2014 , 106, 610-20		20
491	Theoretical approach to the innovative mutation of naphthalene 1,2-dioxygenase: a molecular dynamics and docking study. 2014 , 20, 2354		2
490	Molecular understanding of a potential functional link between antimicrobial and amyloid peptides. 2014 , 10, 7425-51		73
489	Unexpected structural features of the hepatitis C virus envelope protein 2 ectodomain. 2014 , 88, 10280-8		25
488	Polar interactions trump hydrophobicity in stabilizing the self-inserting membrane protein Mistic. 2014 , 136, 13761-8		19

487	Free energy change for insertion of charged, monolayer-protected nanoparticles into lipid bilayers. 2014 , 10, 648-58	53
486	Spontaneous transmembrane helix insertion thermodynamically mimics translocon-guided insertion. 2014 , 5, 4863	79
485	Heavy atom-bearing tripod amphiphiles for the membrane protein study. 2014 , 38, 2354	2
484	New ganglio-tripod amphiphiles (TPAs) for membrane protein solubilization and stabilization: implications for detergent structure-property relationships. 2014 , 12, 8480-7	10
483	Fusion of ligand-coated nanoparticles with lipid bilayers: effect of ligand flexibility. 2014 , 118, 5848-56	39
482	Life at the border: adaptation of proteins to anisotropic membrane environment. 2014 , 23, 1165-96	19
481	Membrane interactions of phylloseptin-1, -2, and -3 peptides by oriented solid-state NMR spectroscopy. 2014 , 107, 901-11	35
480	Structure-function relationships of membrane-associated GT-B glycosyltransferases. 2014 , 24, 108-24	63
479	Adamantane-based amphiphiles (ADAs) for membrane protein study: importance of a detergent hydrophobic group in membrane protein solubilisation. 2014 , 50, 12300-3	8
478	Toward understanding driving forces in membrane protein folding. 2014 , 564, 297-313	40
477	Characterization of membrane protein interactions by isothermal titration calorimetry. 2014 , 426, 3670-80	22
476	Membranotropic regions of the dengue virus prM protein. 2014 , 53, 5280-9	4
475	Size-to-charge dispersion of collision-induced dissociation product ions for enhancement of structural information and product ion identification. 2014 , 86, 4791-8	5
474	A Lys-Trp cation- π interaction mediates the dimerization and function of the chloride intracellular channel protein 1 transmembrane domain. 2014 , 53, 57-67	19
473	Membrane interacting regions of Dengue virus NS2A protein. 2014 , 118, 10142-55	11
472	Structure-activity relationship of the antimicrobial peptide gomesin: the role of peptide hydrophobicity in its interaction with model membranes. 2014 , 30, 3513-21	33
471	Effect of the aspartic acid D2 on the affinity of Polybia-MP1 to anionic lipid vesicles. 2014 , 43, 121-30	12
470	A conserved cationic motif enhances membrane binding and insertion of the chloride intracellular channel protein 1 transmembrane domain. 2014 , 43, 405-14	5

469	Increased immunoaccessibility of MOMP epitopes in a vaccine formulated with amphipols may account for the very robust protection elicited against a vaginal challenge with <i>Chlamydia muridarum</i> . 2014 , 192, 5201-13		41
468	Peptide entry inhibitors of enveloped viruses: the importance of interfacial hydrophobicity. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014 , 1838, 2180-97	3.8	93
467	Prediction of linear cationic antimicrobial peptides based on characteristics responsible for their interaction with the membranes. 2014 , 54, 1512-23		37
466	Lipid interactions of LAH4, a peptide with antimicrobial and nucleic acid transfection activities. 2014 , 43, 499-507		24
465	All-atom molecular dynamics simulation of a photosystem i/detergent complex. 2014 , 118, 11633-45		10
464	On permuted super-secondary structures of transmembrane β -barrel proteins. 2014 , 540-541, 133-142		
463	Free energy analysis of conductivity and charge selectivity of M2GlyR-derived synthetic channels. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014 , 1838, 2319-25	3.8	1
462	Implicit membrane treatment of buried charged groups: application to peptide translocation across lipid bilayers. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014 , 1838, 2149-59	3.8	10
461	Hydrophobic variants of ganglio-tripod amphiphiles for membrane protein manipulation. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014 , 1838, 278-86	3.8	28
460	Improved glucose-neopentyl glycol (GNG) amphiphiles for membrane protein solubilization and stabilization. 2014 , 9, 632-8		25
459	Structural heterogeneity in transmembrane amyloid precursor protein homodimer is a consequence of environmental selection. 2014 , 136, 9619-26		31
458	Terminal residue hydrophobicity modulates transmembrane helix-helix interactions. 2014 , 53, 3747-57		3
457	Energetics of membrane protein folding. 2014 , 43, 233-55		49
456	The use of soluble protein structures in modeling helical proteins in a layered membrane. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014 , 32, 308-18	3.6	1
455	Structures and Dynamics of Proteins Probed by UV Resonance Raman Spectroscopy. 2014 , 243-268		1
454	Drug Formulations Based on Self-Assembled Liquid Crystalline Nanostructures. 2014 , 358-377		
453	Extractant Molecules as Hosts in Surfactant Monolayers or Bilayers. 2014 , 66-85		
452	Optimal conditions for opening of membrane pore by amphiphilic peptides. 2015 , 143, 243115		15

451	Modeling the structure of SARS 3a transmembrane protein using a minimum unfavorable contact approach. 2015 , 127, 2159-2169		3
450	Fabrication of Chiral Materials via Self-Assembly and Biomineralization of Peptides. 2015 , 15, 665-74		4
449	Novel Xylene-Linked Maltoside Amphiphiles (XMAS) for Membrane Protein Stabilisation. 2015 , 21, 10008-13		14
448	Clustering and visualizing similarity networks of membrane proteins. 2015 , 83, 1450-61		7
447	Deoxycholate-Based Glycosides (DCGs) for Membrane Protein Stabilisation. 2015 , 16, 1454-9		5
446	Design of aromatic-containing cell-penetrating peptide mimics with structurally modified π electronics. 2015 , 21, 3013-9		31
445	Marginally hydrophobic transmembrane β -helices shaping membrane protein folding. 2015 , 24, 1057-74		16
444	Implications of aromatic-aromatic interactions: From protein structures to peptide models. 2015 , 24, 1920-33		98
443	Phase Behavior of a Designed Cyclopropyl Analogue of Monoolein: Implications for Low-Temperature Membrane Protein Crystallization. <i>Angewandte Chemie</i> , 2015 , 127, 1041-1045	3.6	4
442	Development of a machine learning method to predict membrane protein-ligand binding residues using basic sequence information. 2015 , 2015, 843030		10
441	Viroporins, Examples of the Two-Stage Membrane Protein Folding Model. 2015 , 7, 3462-82		8
440	Coil-helix transition of polypeptide at water-lipid interface. 2015 , 2015,		6
439	Scanning Mscl Channels with Targeted Post-Translational Modifications for Functional Alterations. 2015 , 10, e0137994		18
438	The Hydrophobic Effect Contributes to the Closed State of a Simplified Ion Channel through a Conserved Hydrophobic Patch at the Pore-Helix Crossing. 2015 , 6, 284		8
437	The Use of Liposomes to Shape Epitope Structure and Modulate Immunogenic Responses of Peptide Vaccines Against HIV MPER. 2015 , 99, 15-54		14
436	Peptide Folding in Translocon-Like Pores. <i>Journal of Membrane Biology</i> , 2015 , 248, 407-17	2.3	3
435	Optimal Force Mismatch for Fluctuation-Activated Transition in a System of Two Coupled Bistable Oscillators. 2015 , 63, 575-580		
434	Mechanism Matters: A Taxonomy of Cell Penetrating Peptides. 2015 , 40, 749-764		198

433	Accessible glyco-tripod amphiphiles for membrane protein analysis. 2015 , 7, 5808-5813		1
432	Determining the Secondary Structure of Membrane Proteins and Peptides Via Electron Spin Echo Envelope Modulation (ESEEM) Spectroscopy. 2015 , 564, 289-313		11
431	Conformational Fine-Tuning of Pore-Forming Peptide Potency and Selectivity. 2015 , 137, 16144-52		48
430	Membrane Interaction of the Glycosyltransferase WaaG. 2015 , 109, 552-63		8
429	Cholesterol-induced lipophobic interaction between transmembrane helices using ensemble and single-molecule fluorescence resonance energy transfer. 2015 , 54, 1371-9		19
428	Computational design and experimental characterization of peptides intended for pH-dependent membrane insertion and pore formation. 2015 , 10, 1082-93		18
427	Phase behavior of a designed cyclopropyl analogue of monoolein: implications for low-temperature membrane protein crystallization. <i>Angewandte Chemie - International Edition</i> , 2015 , 54, 1027-31	16.4	26
426	Testing the limits of rational design by engineering pH sensitivity into membrane-active peptides. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015 , 1848, 951-7	3.8	25
425	Helix-helix interactions: is the medium the message?. 2015 , 23, 437-438		5
424	Maltose neopentyl glycol-3 (MNG-3) analogues for membrane protein study. 2015 , 140, 3157-63		38
423	A Practical Implicit Membrane Potential for NMR Structure Calculations of Membrane Proteins. 2015 , 109, 574-85		18
422	Insights into Protein Structure and Dynamics by Ultraviolet and Visible Resonance Raman Spectroscopy. 2015 , 54, 4770-83		19
421	Anomalous behavior of water inside the SecY translocon. 2015 , 112, 9016-21		34
420	β-synuclein interactions with phospholipid model membranes: Key roles for electrostatic interactions and lipid-bilayer structure. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015 , 1848, 2002-12	3.8	33
419	Perfringolysin O: The Underrated <i>Clostridium perfringens</i> Toxin?. 2015 , 7, 1702-21		36
418	Role of Lipids in Folding, Misfolding and Function of Integral Membrane Proteins. 2015 , 855, 1-31		7
417	Repressive mutations restore function-loss caused by the disruption of trimerization in <i>Escherichia coli</i> multidrug transporter AcrB. 2015 , 6, 4		6
416	Branched dimerization of Tat peptide improves permeability to HeLa and hippocampal neuronal cells. 2015 , 51, 5463-6		23

415	Polymer Adsorbed Bilayer Membranes Form Self-Healing Hydrogels with Tunable Superstructure. 2015 , 48, 2277-2282		23
414	Amphipathic agents for membrane protein study. 2015 , 557, 57-94		21
413	Phospholipid Ether Linkages Significantly Modulate the Membrane Affinity of the Antimicrobial Peptide Novicidin. <i>Journal of Membrane Biology</i> , 2015 , 248, 487-96	2.3	1
412	Continuum electrostatic approach for evaluating positions and interactions of proteins in a bilayer membrane. 2015 , 59, 81-91		4
411	Single-molecule force spectroscopy of membrane proteins from membranes freely spanning across nanoscopic pores. 2015 , 15, 3624-33		24
410	Development of protein mimics for intracellular delivery. 2015 , 104, 265-80		34
409	Partially induced transition from horizontal to vertical orientation of helical peptides at the air-water interface and the structure of their monolayers transferred on the solid substrates. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015 , 1848, 967-75	3.8	7
408	Folding of β -barrel membrane proteins in lipid bilayers - Unassisted and assisted folding and insertion. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015 , 1848, 1927-43	3.8	63
407	Amphipathic solvation of indole: implications for the role of tryptophan in membrane proteins. 2015 , 119, 5979-87		31
406	Can proteins be intrinsically disordered inside a membrane?. 2015 , 3, e984570		8
405	Reversible Transformation of a One-Handed Helical Foldamer Utilizing a Planarity-Switchable Spacer and C2-Chiral Spirobifluorene Units. 2015 , 4, 462-466		16
404	The negative charge of the membrane has opposite effects on the membrane entry and exit of pH-low insertion peptide. 2015 , 54, 1709-12		21
403	Comparative Sequence-Function Analysis of the Major Facilitator Superfamily: The "Mix-and-Match" Method. 2015 , 557, 521-49		2
402	A Novel Soluble Peptide with pH-Responsive Membrane Insertion. 2015 , 54, 6567-75		37
401	The Unique Molecular Choreography of Giant Pore Formation by the Cholesterol-Dependent Cytolysins of Gram-Positive Bacteria. 2015 , 69, 323-40		60
400	On predicting transport proteins and their substrates for the reconstruction of metabolic networks. 2015 ,		1
399	Using fluorescence for studies of biological membranes: a review. 2015 , 3, 042003		25
398	Cell-Membrane-Mimicking Lipid-Coated Nanoparticles Confer Raman Enhancement to Membrane Proteins and Reveal Membrane-Attached Amyloid- β Conformation. 2015 , 9, 9070-7		62

397	Development of Guanidinium-Rich Protein Mimics for Efficient siRNA Delivery into Human T Cells. 2015 , 16, 3172-9		20
396	Specific ion effects on the hydrophobic interaction of benzene self-assembled monolayers. 2015 , 17, 21432-41		7
395	The efficacy of trivalent cyclic hexapeptides to induce lipid clustering in PG/PE membranes correlates with their antimicrobial activity. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015 , 1848, 2998-3006	3.8	24
394	The consideration of indolicidin modification to balance its hemocompatibility and delivery efficiency. 2015 , 494, 498-505		6
393	Supramolecular self-assembly of 14-helical nanorods with tunable linear and dendritic hierarchical morphologies. 2015 , 39, 3280-3287		20
392	Mistic's membrane association and its assistance in overexpression of a human GPCR are independent processes. 2015 , 24, 38-48		6
391	The SMART model: Soft Membranes Adapt and Respond, also Transiently, in the presence of antimicrobial peptides. 2015 , 21, 346-55		61
390	Translocation mechanism(s) of cell-penetrating peptides: biophysical studies using artificial membrane bilayers. 2015 , 54, 194-207		96
389	Elastic deformation and area per lipid of membranes: atomistic view from solid-state deuterium NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015 , 1848, 246-59	3.8	37
388	Probing coiled-coil assembly by paramagnetic NMR spectroscopy. 2015 , 13, 1159-68		13
387	SecA drives transmembrane insertion of RodZ, an unusual single-span membrane protein. 2015 , 427, 1023-37		21
386	Understanding dengue virus capsid protein disordered N-Terminus and pep14-23-based inhibition. 2015 , 10, 517-26		36
385	Dynamics of the Plasma Membrane Proton Pump. <i>Journal of Membrane Biology</i> , 2015 , 248, 443-53	2.3	11
384	Mechanisms of integral membrane protein insertion and folding. 2015 , 427, 999-1022		221
383	Mechanism for transforming cytosolic SOD1 into integral membrane proteins of organelles by ALS-causing mutations. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015 , 1848, 1-7	3.8	20
382	Exploration and Utilization of Salt-Tolerant Barley Germplasm. 2016 , 75-113		
381	In-Situ Observation of Membrane Protein Folding during Cell-Free Expression. 2016 , 11, e0151051		23
380	Measuring Membrane Protein Dimerization Equilibrium in Lipid Bilayers by Single-Molecule Fluorescence Microscopy. 2016 , 581, 53-82		10

379	Examining the Conservation of Kinks in Alpha Helices. 2016 , 11, e0157553	17
378	Direct Monitoring of β -Sheet Formation in the Outer Membrane Protein TtoA Assisted by TtOmp85. 2016 , 55, 4333-43	3
377	Structure Effect of Some New Anticancer Pt(II) Complexes of Amino Acid Derivatives with Small Branched or Linear Hydrocarbon Chains on Their DNA Interaction. 2016 , 88, 76-87	23
376	Accessible Mannitol-Based Amphiphiles (MNAs) for Membrane Protein Solubilisation and Stabilisation. 2016 , 22, 7068-73	26
375	Free backbone carbonyls mediate rhodopsin activation. 2016 , 23, 738-43	11
374	Perturbed rhythmic activation of signaling pathways in mice deficient for Sterol Carrier Protein 2-dependent diurnal lipid transport and metabolism. 2016 , 6, 24631	5
373	Simplification of complexity in protein molecular systems by grouping amino acids: a view from physics. 2016 , 1, 444-466	3
372	Structural basis for broad neutralization of HIV-1 through the molecular recognition of 10E8 helical epitope at the membrane interface. 2016 , 6, 38177	25
371	Biological insertion of computationally designed short transmembrane segments. 2016 , 6, 23397	14
370	Concatemers of Outer Membrane Protein A Take Detours in the Folding Landscape. 2016 , 55, 7123-7140	3
369	ALB3 Insertase Mediates Cytochrome b Co-translational Import into the Thylakoid Membrane. 2016 , 6, 34557	11
368	Molecular Basis of Membrane Association by the Phosphatidylinositol Mannosyltransferase PimA Enzyme from Mycobacteria. 2016 , 291, 13955-13963	11
367	Memdock: an β helical membrane protein docking algorithm. 2016 , 32, 2444-50	24
366	Alpha-synuclein and familial variants affect the chain order and the thermotropic phase behavior of anionic lipid vesicles. 2016 , 1864, 1206-1214	13
365	Effect of lipid head group interactions on membrane properties and membrane-induced cationic β hairpin folding. 2016 , 18, 17836-50	15
364	Coarse-grained simulations of hemolytic peptide β lysin interacting with a POPC bilayer. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016 , 1858, 3182-3194	3.8 4
363	Approaches for Preparation and Biophysical Characterization of Transmembrane β Barrels. 2016 , 49-116	1
362	50 years of amino acid hydrophobicity scales: revisiting the capacity for peptide classification. 2016 , 49, 31	39

361	Antimicrobial activities of phosphonium containing polynorbornenes. 2016 , 6, 86151-86157	28
360	Interplay between hydrophobicity and the positive-inside rule in determining membrane-protein topology. 2016 , 113, 10340-5	26
359	Important roles for membrane lipids in haloarchaeal bioenergetics. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016 , 1858, 2940-2956	3.8 22
358	The Single Transmembrane Segment of Minimal Sensor DesK Senses Temperature via a Membrane-Thickness Caliper. 2016 , 198, 2945-2954	13
357	Structural basis for selective recognition of acyl chains by the membrane-associated acyltransferase PatA. 2016 , 7, 10906	17
356	Single-molecule visualization of dynamic transitions of pore-forming peptides among multiple transmembrane positions. 2016 , 7, 12906	22
355	Coarse-Grained Simulations of Membrane Insertion and Folding of Small Helical Proteins Using the CABS Model. 2016 , 56, 2207-2215	12
354	Nanoyeast and Other Cell Envelope Compositions for Protein Studies and Biosensor Applications. 2016 , 8, 30649-30664	13
353	Charge Distribution Fine-Tunes the Translocation of α -Helical Amphipathic Peptides across Membranes. 2016 , 111, 1738-1749	17
352	Novel pH-Sensitive Cyclic Peptides. 2016 , 6, 31322	18
351	Membrane Proteins. 2016 , 219-268	5
350	Hydrophobic CDR3 residues promote the development of self-reactive T cells. 2016 , 17, 946-55	84
349	Delipidation of cytochrome c oxidase from <i>Rhodobacter sphaeroides</i> destabilizes its quaternary structure. 2016 , 125, 23-31	2
348	Protein-Backbone Thermodynamics across the Membrane Interface. 2016 , 120, 6391-400	6
347	The physics of pulling polyproteins: a review of single molecule force spectroscopy using the AFM to study protein unfolding. 2016 , 79, 076601	72
346	Strategies for Exploring Electrostatic and Nonelectrostatic Contributions to the Interaction of Helical Antimicrobial Peptides with Model Membranes. 2016 , 43-73	5
345	Efficient DNP NMR of membrane proteins: sample preparation protocols, sensitivity, and radical location. 2016 , 64, 223-37	52
344	Self-Assembly of Telechelic Tyrosine End-Capped PEO and Poly(alanine) Polymers in Aqueous Solution. 2016 , 17, 1186-97	8

343	Aromaticity/Bulkiness of Surface Ligands to Promote the Interaction of Anionic Amphiphilic Gold Nanoparticles with Lipid Bilayers. 2016 , 32, 1601-10		16
342	Mechanism of biological denitrification inhibition: procyanidins induce an allosteric transition of the membrane-bound nitrate reductase through membrane alteration. 2016 , 92, fiw034		22
341	Fully quantified spectral imaging reveals in vivo membrane protein interactions. 2016 , 8, 216-29		64
340	A Class of Rigid Linker-bearing Glucosides for Membrane Protein Structural Study. 2016 , 7, 1933-1939		25
339	A general overview on outer membrane protein (Omp) simulations. 2016 , 17, 285-291		1
338	5-Lipoxygenase-activating protein rescues activity of 5-lipoxygenase mutations that delay nuclear membrane association and disrupt product formation. 2016 , 30, 1892-900		26
337	Alanine scan and (2)H NMR analysis of the membrane-active peptide BP100 point to a distinct carpet mechanism of action. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016 , 1858, 1328-38	3.8	22
336	A Guide to Differential Scanning Calorimetry of Membrane and Soluble Proteins in Detergents. 2016 , 567, 319-58		13
335	Mechanism of Reversible Peptide-Bilayer Attachment: Combined Simulation and Experimental Single-Molecule Study. 2016 , 32, 810-21		12
334	LIFE - AS A MATTER OF FAT. 2016 ,		26
333	GXXXG-Mediated Parallel and Antiparallel Dimerization of Transmembrane Helices and Its Inhibition by Cholesterol: Single-Pair FRET and 2D IR Studies. <i>Angewandte Chemie - International Edition</i> , 2017 , 56, 1756-1759	16.4	13
332	GXXXG-Mediated Parallel and Antiparallel Dimerization of Transmembrane Helices and Its Inhibition by Cholesterol: Single-Pair FRET and 2D IR Studies. <i>Angewandte Chemie</i> , 2017 , 129, 1782-1785 ^{3.6}		1
331	Peripheral Membrane Interactions Boost the Engagement by an Anti-HIV-1 Broadly Neutralizing Antibody. 2017 , 292, 5571-5583		9
330	Conformationally Preorganized Diastereomeric Norbornane-Based Maltosides for Membrane Protein Study: Implications of Detergent Kink for Micellar Properties. 2017 , 139, 3072-3081		32
329	Investigations into the potential anticancer activity of Maximin H5. 2017 , 137, 29-34		8
328	Computational Approaches for Revealing the Structure of Membrane Transporters: Case Study on Bilitranslocase. 2017 , 15, 232-242		14
327	Estimating the Lipophobic Contributions in Model Membranes. 2017 , 121, 2111-2120		5
326	Fluorescence Applications for Structural and Thermodynamic Studies of Membrane Protein Insertion. 2017 , 243-274		3

325	Transmembrane helices containing a charged arginine are thermodynamically stable. 2017 , 46, 627-637		15
324	Interactions stabilizing the C-terminal helix of human phospholipid scramblase 1 in lipid bilayers: A computational study. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017 , 1859, 1200-1210	3.8	7
323	In vivo selection of heterotypically interacting transmembrane helices: Complementary helix surfaces, rather than conserved interaction motifs, drive formation of transmembrane hetero-dimers. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017 , 1859, 245-256	3.8	4
322	Conformational Plasticity of the Cell-Penetrating Peptide SAP As Revealed by Solid-State F-NMR and Circular Dichroism Spectroscopies. 2017 , 121, 6479-6491		14
321	Design of self-assembling transmembrane helical bundles to elucidate principles required for membrane protein folding and ion transport. 2017 , 372,		17
320	Soft Matter in Lipid-Protein Interactions. 2017 , 46, 379-410		68
319	Membrane Proteins: Chemical Synthesis and Ligation. 2017 , 269-284		2
318	The Nature and Relevance of Solvent Stress in Microbes and Mechanisms of Tolerance. 2017 , 201-213		3
317	DNA as a Target for Anticancer Phen-Imidazole Pd(II) Complexes. 2017 , 182, 110-127		17
316	Dendronic trimaltoside amphiphiles (DTMs) for membrane protein study. 2017 , 8, 8315-8324		15
315	ALS-causing profilin-1-mutant forms a non-native helical structure in membrane environments. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017 , 1859, 2161-2170	3.8	12
314	Transmembrane β -barrels: Evolution, folding and energetics. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017 , 1859, 2467-2482	3.8	30
313	Distinct Effects of Multivalent Macroion and Simple Ion on the Structure and Local Electric Environment of a Weak Polyelectrolyte in Aqueous Solution. 2017 , 121, 8829-8837		8
312	Reaction rates of glutathione and ascorbate with alkyl radicals are too slow for protection against protein peroxidation in vivo. 2017 , 633, 118-123		8
311	Kinetic stability of membrane proteins. 2017 , 9, 563-572		8
310	Ultrasensitive Quantitation of Plasma Membrane Proteins via isRTA. 2017 , 89, 10776-10782		23
309	Scrutiny of electrostatic-driven conformational ordering of polypeptide chains in DMSO: a study with a model oligopeptide. 2017 , 7, 27981-27991		5
308	Structural studies of amyloid- β peptides: Unlocking the mechanism of aggregation and the associated toxicity. 2017 , 140, 176-192		42

307	Membrane proteins structures: A review on computational modeling tools. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017 , 1859, 2021-2039	3.8	56
306	TRPV1 temperature activation is specifically sensitive to strong decreases in amino acid hydrophobicity. 2017 , 7, 549		16
305	Exploring the dark foldable proteome by considering hydrophobic amino acids topology. 2017 , 7, 41425		16
304	Influence of Protein Scaffold on Side-Chain Transfer Free Energies. 2017 , 113, 597-604		20
303	Aberrantly Large Single-Channel Conductance of Polyhistidine Arm-Containing Protein Nanopores. 2017 , 56, 4895-4905		12
302	Hydrophobic Mismatch in Membranes: When the Tail Matters. 2017 , 375-387		3
301	Determination of Hydrophobic Lengths of Membrane Proteins with the HDGB Implicit Membrane Model. 2017 , 57, 3032-3042		7
300	Fusion pore in exocytosis: More than an exit gate? A β -cell perspective. 2017 , 68, 45-61		10
299	Kinetoplastid membrane protein-11 adopts a four-helix bundle fold in DPC micelle. 2017 , 591, 3793-3804		2
298	Transmembrane Interactions of Full-length Mammalian Bitopic Cytochrome-P450-Cytochrome-b Complex in Lipid Bilayers Revealed by Sensitivity-Enhanced Dynamic Nuclear Polarization Solid-state NMR Spectroscopy. 2017 , 7, 4116		23
297	Protein aggregates: Forms, functions and applications. 2017 , 97, 778-789		17
296	Protonation Enhances the Inherent Helix-Forming Propensity of pHLIP. 2017 , 2, 8536-8542		10
295	Protein-membrane interactions investigated with surface-induced fluorescence attenuation. 2017 , 26, 128708		4
294	Membrane-Active Properties of an Amphitropic Peptide from the CyaA Toxin Translocation Region. 2017 , 9,		13
293	Discovering Novel Succinate Dehydrogenase Inhibitors by Modeling and Virtual Screening Strategies to Combat Early Blight. 2017 , 5, 100		10
292	Strategies for Selecting Membrane Protein-Specific Antibodies using Phage Display with Cell-Based Panning. 2017 , 6,		17
291	T3SS-Independent Uptake of the Short-Trip Toxin-Related Recombinant NleC Effector of Enteropathogenic Leads to NF- κ B p65 Cleavage. 2017 , 7, 119		10
290	Transmembrane Helices Are an Overlooked Source of Major Histocompatibility Complex Class I Epitopes. 2017 , 8, 1118		7

289	Analysis of GXXXG-mediated Association of Transmembrane Helices as Studied by Single-pair Fluorescence and 2D-IR Spectroscopy. 2017 , 57, 205-207		
288	Structurally detailed coarse-grained model for Sec-facilitated co-translational protein translocation and membrane integration. 2017 , 13, e1005427		15
287	Machine learning to design integral membrane channelrhodopsins for efficient eukaryotic expression and plasma membrane localization. 2017 , 13, e1005786		59
286	Charged residues next to transmembrane regions revisited: "Positive-inside rule" is complemented by the "negative inside depletion/outside enrichment rule". 2017 , 15, 66		31
285	Outer membrane protein folding from an energy landscape perspective. 2017 , 15, 123		43
284	And Yet It Moves. 2017 , 113, 759-761		2
283	Helix formation and stability in membranes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018 , 1860, 2108-2117	3.8	23
282	Sculpting nanoparticle dynamics for single-bacteria-level screening and direct binding-efficiency measurement. 2018 , 9, 815		85
281	Watching Three-Dimensional Movements of Single Membrane Proteins in Lipid Bilayers. 2018 , 57, 4735-4740		1
280	A reconstitution method for integral membrane proteins in hybrid lipid-polymer vesicles for enhanced functional durability. 2018 , 147, 142-149		21
279	Functional Optimization of Broadly Neutralizing HIV-1 Antibody 10E8 by Promotion of Membrane Interactions. 2018 , 92,		12
278	Peptide Solubility Limits: Backbone and Side-Chain Interactions. 2018 , 122, 3528-3539		10
277	Balancing Force Field Protein-Lipid Interactions To Capture Transmembrane Helix-Helix Association. 2018 , 14, 1706-1715		24
276	Spatial Position Regulates Power of Tryptophan: Discovery of a Major-Groove-Specific Nuclear-Localizing, Cell-Penetrating Tetrapeptide. 2018 , 140, 1697-1714		23
275	A model-free method for measuring dimerization free energies of CLC-ec1 in lipid bilayers. 2018 , 150, 355-365		7
274	High temperature limit of photosynthetic excitons. 2018 , 9, 99		8
273	Electrostatic Interactions in Protein Structure, Folding, Binding, and Condensation. 2018 , 118, 1691-1741		290
272	Free-Energy Analysis of Peptide Binding in Lipid Membrane Using All-Atom Molecular Dynamics Simulation Combined with Theory of Solutions. 2018 , 122, 3219-3229		15

271	Membrane defect and water leakage caused by passive calcium permeation. 2018 , 270, 227-233	1
270	Synergism of Antimicrobial Frog Peptides Couples to Membrane Intrinsic Curvature Strain. 2018 , 114, 1945-1954	33
269	Transmembrane Domain Recognition during Membrane Protein Biogenesis and Quality Control. 2018 , 28, R498-R511	53
268	Improved free-energy landscape reconstruction of bacteriorhodopsin highlights local variations in unfolding energy. 2018 , 148, 123313	11
267	Effect of Phospholipid Headgroup Charge on the Structure and Dynamics of Water at the Membrane Interface: A Terahertz Spectroscopic Study. 2018 , 122, 5066-5074	10
266	Understanding GPCR Recognition and Folding from NMR Studies of Fragments. 2018 , 8, 9858-9870	4
265	Protein tyrosine phosphatase conjugated with a novel transdermal delivery peptide, astrotactin 1-derived peptide recombinant protein tyrosine phosphatase (AP-rPTP), alleviates both atopic dermatitis-like and psoriasis-like dermatitis. 2018 , 141, 137-151	8
264	Applications of Single-Molecule Methods to Membrane Protein Folding Studies. 2018 , 430, 424-437	20
263	Structure-Function Dissection of Pseudorabies Virus Glycoprotein B Fusion Loops. 2018 , 92,	25
262	Effect of cetyltrimethylammonium bromide and its gemini homologue bis(cetyldimethylammonium)butane dibromide on activity of xanthine oxidase. 2018 , 39, 1121-1125	2
261	Self-Assembly of Telechelic Tyrosine End-Capped PEO Star Polymers in Aqueous Solution. 2018 , 19, 167-177	7
260	Ultrafast Protein Folding in Membrane-Mimetic Environments. 2018 , 430, 554-564	8
259	Uniaxial Diffusional Narrowing of NMR Lineshapes for Membrane Proteins Reconstituted in Magnetically Aligned Bicelles and Macrodiscs. 2018 , 49, 1335-1353	1
258	A Membrane Burial Potential with H-Bonds and Applications to Curved Membranes and Fast Simulations. 2018 , 115, 1872-1884	5
257	Energy landscape underlying spontaneous insertion and folding of an alpha-helical transmembrane protein into a bilayer. 2018 , 9, 4949	16
256	Self-Assembly of ProteinPolymer Conjugates. 2018 , 207-255	
255	Structural Model of the mIgM B-Cell Receptor Transmembrane Domain From Self-Association Molecular Dynamics Simulations. 2018 , 9, 2947	8
254	Cooperative Nonbonded Forces Control Membrane Binding of the pH-Low Insertion Peptide pHLIP. 2018 , 115, 2403-2412	10

253	Transmembrane but not soluble helices fold inside the ribosome tunnel. 2018 , 9, 5246	18
252	Conformational Dynamics Govern the Free-Energy Landscape of a Membrane-Interacting Protein. 2018 , 3, 12026-12032	4
251	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
250	The lipid bilayer membrane and its protein constituents. 2018 , 150, 1472-1483	26
249	Characterizing the Molecular Mechanisms for Flipping Charged Peptide Flanking Loops across a Lipid Bilayer. 2018 , 122, 10337-10348	4
248	Amide I SFG Spectral Line Width Probes the Lipid-Peptide and Peptide-Peptide Interactions at Cell Membrane In Situ and in Real Time. 2018 , 34, 7554-7560	14
247	Embedding a Metal-Binding Motif for Copper Transporter into a Lipid Bilayer by Cu(I) Binding. 2018 , 122, 6364-6370	1
246	Biophysical Analysis of Sec-Mediated Protein Translocation in Nanodiscs. 2018 , 28, 41-85	1
245	Bias-Exchange Metadynamics Simulation of Membrane Permeation of 20 Amino Acids. 2018 , 19,	11
244	An Engineered Lithocholate-Based Facial Amphiphile Stabilizes Membrane Proteins: Assessing the Impact of Detergent Customizability on Protein Stability. 2018 , 24, 9860-9868	9
243	Membrane Proteins and Their Natural Environment. 2018 , 1-57	
242	The impact of ribosomal interference, codon usage, and exit tunnel interactions on translation elongation rate variation. 2018 , 14, e1007166	43
241	Transmembrane Domain Prediction. 2019 , 46-52	
240	Membranproteinfaltung [Kernwissen aus (nicht zu) vereinfachten Systemen. 2019 , 25, 385-387	
239	Structural dynamics of membrane-protein folding from single-molecule FRET. 2019 , 58, 124-137	17
238	Exploring the links between lipid geometry and mitochondrial fission: Emerging concepts. 2019 , 49, 305-313	10
237	Bridge: A Graph-Based Algorithm to Analyze Dynamic H-Bond Networks in Membrane Proteins. 2019 , 15, 6781-6798	16
236	Shaping membranes with disordered proteins. 2019 , 677, 108163	13

235	Obtaining Protein Association Energy Landscape for Integral Membrane Proteins. 2019 , 15, 6444-6455	6
234	Structure Based Prediction of Neoantigen Immunogenicity. 2019 , 10, 2047	34
233	A lipophilicity-based energy function for membrane-protein modelling and design. 2019 , 15, e1007318	16
232	Mathematical Characterization of Membrane Protein Sequences of Homo-Sapiens. 2019 ,	
231	Molecular Determinants of Brevetoxin Binding to Voltage-Gated Sodium Channels. 2019 , 11,	5
230	The rational design of cell-penetrating peptides for application in delivery systems. 2019 , 121, 170149	20
229	Studies on the Interaction of Alyteserin 1c Peptide and Its Cationic Analogue with Model Membranes Imitating Mammalian and Bacterial Membranes. 2019 , 9,	8
228	Asymmetric maltose neopentyl glycol amphiphiles for a membrane protein study: effect of detergent asymmetry on protein stability. 2019 , 10, 1107-1116	18
227	Intrinsically disordered proteins in synaptic vesicle trafficking and release. 2019 , 294, 3325-3342	34
226	Essential Mycoplasma Glycolipid Synthase Adheres to the Cell Membrane by Means of an Amphipathic Helix. 2019 , 9, 7085	1
225	Structural analysis and mode of action of BMAP-27, a cathelicidin-derived antimicrobial peptide. 2019 , 118, 170106	13
224	A symmetric geometry of transmembrane domains inside the B cell antigen receptor complex. 2019 , 116, 13468-13473	4
223	Differential Scanning Calorimetry of Protein-Lipid Interactions. 2019 , 2003, 91-106	0
222	Interaction of the Mechanosensitive Channel, MscS, with the Membrane Bilayer through Lipid Intercalation into Grooves and Pockets. 2019 , 431, 3339-3352	13
221	The Structural and Functional Diversity of Intrinsically Disordered Regions in Transmembrane Proteins. <i>Journal of Membrane Biology</i> , 2019 , 252, 273-292	2.3 8
220	Positive Charge Patterning and Hydrophobicity of Membrane-Active Antimicrobial Peptides as Determinants of Activity, Toxicity, and Pharmacokinetic Stability. 2019 , 62, 6276-6286	20
219	Live-cell imaging of membrane proteins by a coiled-coil labeling method-Principles and applications. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2019 , 1861, 1011-1017	3.8 10
218	Simulation-Guided Rational de Novo Design of a Small Pore-Forming Antimicrobial Peptide. 2019 , 141, 4839-4848	50

217	Visualizing Biological Membrane Organization and Dynamics. 2019 , 431, 1889-1919		9
216	Mechanism of Action of Peptides That Cause the pH-Triggered Macromolecular Poration of Lipid Bilayers. 2019 , 141, 6706-6718		23
215	Canine CD117-Specific Antibodies with Diverse Binding Properties Isolated from a Phage Display Library Using Cell-Based Biopanning. 2019 , 8,		2
214	Phosphatidylserine Asymmetry Promotes the Membrane Insertion of a Transmembrane Helix. 2019 , 116, 1495-1506		17
213	Selectivity of Antimicrobial Peptides: A Complex Interplay of Multiple Equilibria. 2019 , 1117, 175-214		25
212	Using Fluorescence Quenching Titration to Determine the Orientation of a Model Transmembrane Protein in Mimic Membranes. 2019 , 12,		1
211	Biological Membrane Organization and Cellular Signaling. 2019 , 119, 5849-5880		59
210	Parametrization of MARTINI for Modeling Hinging Motions in Membrane Proteins. 2019 , 123, 2254-2269		3
209	The Role of the Small Export Apparatus Protein, SctS, in the Activity of the Type III Secretion System. 2019 , 10, 2551		7
208	A novel amphipathic cell-penetrating peptide based on the N-terminal glycosaminoglycan binding region of human apolipoprotein E. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2019 , 1861, 541-549	3.8	8
207	Investigation onto the correlation between systemic antibodies to surface glycoproteins of infectious laryngotracheitis virus (ILTV) and protective immunity. 2019 , 228, 252-258		2
206	Linking sequence patterns and functionality of alpha-helical antimicrobial peptides. 2019 , 35, 2713-2717		3
205	Preferential Equilibrium Partitioning of Positively Charged Tryptophan into Phosphatidylcholine Bilayer Membranes. 2019 , 123, 170-179		7
204	Folding and Misfolding of Human Membrane Proteins in Health and Disease: From Single Molecules to Cellular Proteostasis. 2019 , 119, 5537-5606		93
203	Mechanistic Landscape of Membrane-Permeabilizing Peptides. 2019 , 119, 6040-6085		91
202	Molecular Modeling of Surfactant Micellization Using Solvent-Accessible Surface Area. 2019 , 35, 2443-2450		22
201	Antimicrobial peptides: Promising alternatives in the post feeding antibiotic era. 2019 , 39, 831-859		162
200	Membrane curvature affects the stability and folding kinetics of bacteriorhodopsin. 2019 , 76, 111-117		3

199	Self-association and folding in membrane determine the mode of action of peptides from the lytic segment of sticholysins. 2019 , 156, 109-117		4
198	The electrostatic core of the outer membrane protein X from E. coli. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020 , 1862, 183031	3.8	5
197	On the nature of the optimal form of the holdase-type chaperone stress response. 2020 , 594, 43-66		9
196	GeTFEP: A general transfer free energy profile of transmembrane proteins. 2020 , 29, 469-479		1
195	NMR Crystallography For Uniformly (¹³ C, ¹⁵ N)-Labeled Oriented Membrane Proteins. <i>Angewandte Chemie</i> , 2020 , 132, 3582-3585	3.6	2
194	NMR "Crystallography" for Uniformly (¹³ C, ¹⁵ N)-Labeled Oriented Membrane Proteins. <i>Angewandte Chemie - International Edition</i> , 2020 , 59, 3554-3557	16.4	2
193	C-terminal sequence deletion effect on antioxidative characteristics of VLPVPQK bioactive peptide from buffalo milk casein. 2020 , 119, 108816		0
192	In vitro antifungal activity of dimethyl trisulfide against <i>Colletotrichum gloeosporioides</i> from mango. 2019 , 36, 4		5
191	Membrane-Protein Unfolding Intermediates Detected with Enhanced Precision Using a Zigzag Force Ramp. 2020 , 118, 667-675		8
190	Molecular Switch between Structural Compaction and Thermodynamic Stability by the Xxx-Pro Interface in Transmembrane β -Barrels. 2020 , 59, 303-314		
189	From Endocytosis to Nonendocytosis: The Emerging Era of Gene Delivery.. 2020 , 3, 2686-2701		22
188	Quantifying the Native Energetics Stabilizing Bacteriorhodopsin by Single-Molecule Force Spectroscopy. 2020 , 125, 068102		5
187	Flanking aromatic residue competition influences transmembrane peptide helix dynamics. 2020 , 594, 4280-4291		0
186	Phage Display Derived Monoclonal Antibodies: From Bench to Bedside. 2020 , 11, 1986		48
185	Broad-Spectrum Antiviral Entry Inhibition by Interfacially Active Peptides. 2020 , 94,		7
184	Affinity for the Interface Underpins Potency of Antibodies Operating In Membrane Environments. 2020 , 32, 108037		3
183	A proximity-exponential hybridization chain reaction (PEHCR) and its application for nondestructive analysis of membrane protein-protein interactions on living cells. 2020 , 1125, 8-18		2
182	Chiroptical Properties and Conformation of Four Lasioepsin-Related Antimicrobial Peptides: Structural Role of Disulfide Bridges. 2020 , 12, 812		

181	Structure of a nascent membrane protein as it folds on the BAM complex. 2020 , 583, 473-478		49
180	How We Came to Understand the "Tumultuous Chemical Heterogeneity" of the Lipid Bilayer Membrane. <i>Journal of Membrane Biology</i> , 2020 , 253, 185-190	2.3	
179	Pendant-bearing glucose-neopentyl glycol (P-GNG) amphiphiles for membrane protein manipulation: Importance of detergent pendant chain for protein stabilization. 2020 , 112, 250-261		5
178	Backbone Hydrogen Bond Energies in Membrane Proteins Are Insensitive to Large Changes in Local Water Concentration. 2020 , 142, 6227-6235		6
177	Effect of Helical Kink on Peptide Translocation across Phospholipid Membranes. 2020 , 124, 5940-5947		5
176	Peptide-Oleate Complexes Create Novel Membrane-Bound Compartments. 2020 , 37, 3083-3093		0
175	Insertion of Bacteriorhodopsin Helix C Variants into Biological Membranes. 2020 , 5, 556-560		3
174	Rapid fabrication of precise high-throughput filters from membrane protein nanosheets. 2020 , 19, 347-354		33
173	Membrane Proteins Have Distinct Fast Internal Motion and Residual Conformational Entropy. <i>Angewandte Chemie</i> , 2020 , 132, 11201-11207	3.6	3
172	Membrane Proteins Have Distinct Fast Internal Motion and Residual Conformational Entropy. <i>Angewandte Chemie - International Edition</i> , 2020 , 59, 11108-11114	16.4	9
171	Physicochemical Characterisation of KEIF-The Intrinsically Disordered N-Terminal Region of Magnesium Transporter A. 2020 , 10,		1
170	Differential Interactions of Piscidins with Phospholipids and Lipopolysaccharides at Membrane Interfaces. 2020 , 36, 5065-5077		3
169	MPTherm: database for membrane protein thermodynamics for understanding folding and stability. 2021 , 22, 2119-2125		4
168	NMR Structure and Dynamics Studies of Yeast Respiratory Supercomplex Factor 2. 2021 , 29, 275-283.e4		5
167	Passive Internalization of Bioactive β -Casein Peptides into Phospholipid (POPC) Bilayers. Free Energy Landscapes from Unbiased Equilibrium MD Simulations at μ s-Time Scale. 2021 , 16, 70-83		
166	Towards a Quantitative Understanding of Protein-Lipid Bilayer Interactions at the Single Molecule Level: Opportunities and Challenges. <i>Journal of Membrane Biology</i> , 2021 , 254, 17-28	2.3	1
165	Electrostatic effects in saturation of membrane binding of cationic cell-penetrating peptide. 2021 , 50, 15-23		4
164	Polarity/charge as a determinant of translocase requirements for membrane protein insertion. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2021 , 1863, 183502	3.8	3

163	Letter to the Editor: Distanced Inspiration from the Career of Stephen H. White. <i>Journal of Membrane Biology</i> , 2021 , 254, 1-3	2.3	
162	Analysis of Cancer Cells Based on DNA Signal Amplification and DNA Nanodevices. 2021 , 51, 8-19		2
161	Multivalent lipid targeting by the calcium-independent C2A domain of synaptotagmin-like protein 4/granuphilin. 2021 , 296, 100159		3
160	Transmembrane domains of type III-secreted proteins affect bacterial-host interactions in enteropathogenic. 2021 , 12, 902-917		0
159	as a superior host for overproduction of prokaryotic integral membrane proteins. 2021 , 3, 51-71		2
158	Local Bilayer Hydrophobicity Modulates Membrane Protein Stability. 2021 , 143, 764-772		6
157	pH-triggered pore-forming peptides with strong composition-dependent membrane selectivity. 2021 , 120, 618-630		4
156	OpenAWSEM with Open3SPN2: A fast, flexible, and accessible framework for large-scale coarse-grained biomolecular simulations. 2021 , 17, e1008308		8
155	Tuning of a Membrane-Perforating Antimicrobial Peptide to Selectively Target Membranes of Different Lipid Composition. <i>Journal of Membrane Biology</i> , 2021 , 254, 75-96	2.3	6
154	A photoswitchable helical peptide with light-controllable interface / transmembrane topology in lipidic membranes.		
153	Free-energy changes of bacteriorhodopsin point mutants measured by single-molecule force spectroscopy. 2021 , 118,		7
152	Characterization of the Features of Water Inside the SecY Translocon. <i>Journal of Membrane Biology</i> , 2021 , 254, 133-139	2.3	1
151	Single-Molecule Fluorescence Techniques for Membrane Protein Dynamics Analysis. 2021 , 75, 491-505		3
150	Marker residue types at the structural regions of transmembrane alpha-helical and beta-barrel interfaces. 2021 , 89, 1145-1157		
149	Cotranslational recruitment of ribosomes in protocells recreates a translocon-independent mechanism of proteorhodopsin biogenesis. 2021 , 24, 102429		4
148	Enhanced translocation of amphiphilic peptides across membranes by transmembrane proteins. 2021 , 120, 2296-2305		1
147	Folding of Circularly Permuted and Split Outer Membrane Protein F via Electrostatic Interactions with Terminal Residues. 2021 , 60, 1787-1796		
146	ChrSLoc-Net: Machine Learning-Based Prediction of Channelrhodopsins Proteins within Plasma Membrane. 2021 ,		

145	A photoswitchable helical peptide with light-controllable interface/transmembrane topology in lipidic membranes. 2021 , 24, 102771		0
144	Intramolecular interactions play key role in stabilization of pHLIP at acidic conditions. 2021 , 42, 1809-1816		0
143	Designing Self-Inhibitory fusion peptide analogous to viral spike protein against novel severe acute respiratory syndrome (SARS-CoV-2). <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-16	3.6	
142	Uncoupling Amphipathicity and Hydrophobicity: Role of Charge Clustering in Membrane Interactions of Cationic Antimicrobial Peptides. 2021 , 60, 2586-2592		3
141	Folding and misfolding of potassium channel monomers during assembly and tetramerization. 2021 , 118,		2
140	The Role of the Membrane in Transporter Folding and Activity. 2021 , 433, 167103		2
139	Tryptophan, an Amino-Acid Endowed with Unique Properties and Its Many Roles in Membrane Proteins. 2021 , 11, 1032		2
138	Analyses of the 5' Ends of Escherichia coli ORFs.		
137	The unique genome organization of two novel fusariviruses hosted by the true morel mushroom <i>Morchella esculenta</i> . 2021 , 302, 198486		1
136	Focal accumulation of aromaticity at the CDRH3 loop mitigates 4E10 polyreactivity without altering its HIV neutralization profile. 2021 , 24, 102987		
135	Membrane binding properties of the C-terminal segment of retinol dehydrogenase 8. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2021 , 1863, 183605	3.8	1
134	Deconstructing the transmembrane core of class A G protein-coupled receptors. 2021 , 46, 1017-1029		2
133	The mechanisms of integral membrane protein biogenesis. 2021 ,		10
132	Acetonitrile allows indirect replacement of nondeuterated lipid detergents by deuterated lipid detergents for the nuclear magnetic resonance study of detergent-soluble proteins. 2021 , 30, 2324-2332		2
131	Membrane partitioning and lipid selectivity of the N-terminal amphipathic H0 helices of endophilin isoforms. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2021 , 1863, 183660	3.8	
130	Removal of bovine serum albumin and methylene blue using a hybrid membrane of single walled carbon nanotube-banana peel protein: Fabrication and characterization. 2021 , 24, 101880		0
129	Transmembrane Domains.		2
128	Trichogin Topology and Activity in Model Membranes as Determined by Fluorescence Spectroscopy. 2006 , 47-70		3

127	Gramicidin Channels: Versatile Tools. 2007 , 33-80	11
126	Oligomerization of neurotransmitter transporters: a ticket from the endoplasmic reticulum to the plasma membrane. 2006 , 233-49	40
125	Monoamine Transporters in the Brain. 2007 , 339-362	1
124	Membrane-associated proteins and peptides. 2008 , 443, 161-79	4
123	Computer-based analysis, visualization, and interpretation of antimicrobial peptide activities. 2010 , 618, 287-99	17
122	Tools for predicting binding and insertion of CPPs into lipid bilayers. 2011 , 683, 81-98	3
121	Peptides in Lipid Bilayers: Determination of Location by Absolute-Scale X-ray Refinement. 2001 , 189-206	1
120	Topology prediction of membrane proteins: how distantly related homologs come into play. 2010 , 61-82	1
119	Cholesterol-binding viral proteins in virus entry and morphogenesis. 2010 , 51, 77-108	47
118	Biology. 2014 , 794, 7-40	2
117	Metal Binding to Prion Protein. 2003 , 21-39	1
116	Environment-transformable sequence-structure relationship: a general mechanism for proteotoxicity. 2018 , 10, 503-516	4
115	Chapter 5:Implicit Membrane Models For Peptide Folding and Insertion Studies. 2010 , 91-145	2
114	C-terminal tail of human immunodeficiency virus gp41: functionally rich and structurally enigmatic. 2013 , 94, 1-19	29
113	The impact of ribosomal interference, codon usage, and exit tunnel interactions on translation elongation rate variation.	2
112	GeTFEP: A general transfer free energy profile of transmembrane proteins.	2
111	A unified evolutionary origin for the ubiquitous protein transporters SecY and YidC.	2
110	Crossreactive public TCR sequences undergo positive selection in the human thymic repertoire. 2019 , 129, 2446-2462	28

109	Self-Assembly of Surfactants in Bulk Phases and at Interfaces Using Coarse-Grain Models. 2008 , 329-342	2
108	Biogenesis of Lipids and Proteins within Mitochondrial Membranes. 2011 , 315-377	2
107	Resolving the paradox for protein aggregation diseases: a common mechanism for aggregated proteins to initially attack membranes without needing aggregates. 2013 , 2, 221	7
106	Resolving the paradox for protein aggregation diseases: a common mechanism for aggregated proteins to initially attack membranes without needing aggregates. 2013 , 2, 221	6
105	Why do proteins aggregate? "Intrinsically insoluble proteins" and "dark mediators" revealed by studies on "insoluble proteins" solubilized in pure water. 2013 , 2, 94	29
104	MEPPitope: spatial, electrostatic and secondary structure perturbations in the post-fusion Dengue virus envelope protein highlights known epitopes and conserved residues in the Zika virus. 2016 , 5, 1150	8
103	Computational analysis of perturbations in the post-fusion Dengue virus envelope protein highlights known epitopes and conserved residues in the Zika virus. 2016 , 5, 1150	7
102	Determining the orientation of protegrin-1 in DLPC bilayers using an implicit solvent-membrane model. 2009 , 4, e4799	15
101	Analysis and prediction of the metabolic stability of proteins based on their sequential features, subcellular locations and interaction networks. 2010 , 5, e10972	111
100	A folding pathway-dependent score to recognize membrane proteins. 2011 , 6, e16778	2
99	Context mediates antimicrobial efficacy of kinocidin congener peptide RP-1. 2011 , 6, e26727	16
98	The structural dynamics of the flavivirus fusion peptide-membrane interaction. 2012 , 7, e47596	17
97	Real time observation of single membrane protein insertion events by the Escherichia coli insertase YidC. 2013 , 8, e59023	26
96	Influence of protein-micelle ratios and cysteine residues on the kinetic stability and unfolding rates of human mitochondrial VDAC-2. 2014 , 9, e87701	17
95	iRhom2 is essential for innate immunity to RNA virus by antagonizing ER- and mitochondria-associated degradation of VISA. 2017 , 13, e1006693	31
94	Identifying Native and Non-native Membrane Protein Loops by Using Stabilizing Energetic Terms of Three Popular Force Fields. 2020 , 1, 14-21	1
93	Mutational scanning reveals the determinants of protein insertion and association energetics in the plasma membrane. 2016 , 5,	43
92	The dimerization equilibrium of a ClC Cl(-)/H(+) antiporter in lipid bilayers. 2016 , 5,	27

- 91 The SNAP-25 linker supports fusion intermediates by local lipid interactions. **2019**, 8, 11
- 90 Spiers Memorial Lecture: Analysis and design of membrane-interactive peptides. **2021**, 1
- 89 Intrinsic disorder in integral membrane proteins. **2021**, 183, 101-134 0
- 88 In Silico Structure-Based Design of Antiviral Peptides Targeting the Severe Fever with Thrombocytopenia Syndrome Virus Glycoprotein Gn. **2021**, 13,
- 87 Biologische Membranen und Transport. **2001**, 411-464
- 86 Cell Membranes: Protein Components and Functions. **2002**,
- 85 Helix-Helix Packing Between Transmembrane Fragments. **2004**, 1-14
- 84 Syntactic Approach to Predict Membrane Spanning Regions of Transmembrane Proteins. **2005**, 95-104
- 83 Structure Prediction of Membrane Proteins. **2007**, 65-108
- 82 Transmembrane Domains in Proteins. 876
- 81 Lipid Bilayers, Translocons and the Shaping of Polypeptide Structure. 3
- 80 Folding of Membrane Proteins. 998
- 79 From Structural Genomics to Drug Design: Knowledge Discovery in Crystallographic Databases to Assist Lead Discovery and Optimization. 1769-1788
- 78 Structural studies on large fragments of G protein coupled receptors. **2009**, 611, 309-10
- 77 Resource for structure related information on transmembrane proteins. **2010**, 45-59
- 76 Signaling of IL-4R, a Typical Class I Cytokine Receptor. **2010**, 323-328
- 75 Structural and Functional Discrimination of Membrane Proteins. **2011**, 1-32
- 74 Membrane Protein Biogenesis and Assembly at the Endoplasmic Reticulum Membrane. **2011**, 203-221

- 73 Results and Discussion. **2014**, 29-90
- 72 MscL, a Bacterial Mechanosensitive Channel. 259-290
- 71 Ab Initio Folding of Glycophorin A and Acetylcholine M2 Transmembrane Segments Via Simplified Environment Molecular Simulations. **2015**, 115-139
- 70 Staphylococcal β -barrel Pore-Forming Toxins: Mushrooms That Breach the Greasy Barrier. **2015**, 241-266
- 69 The Use of the Miyazawa-Jernigan Residue Contact Potential in Analyses of Molecular Interaction and Recognition with Complementary Peptides. **2016**, 91-102
- 68 Der Aufbau der Membran. 635-670
- 67 Approaches to ab initio molecular replacement of β helical transmembrane proteins. **2017**, 73, 985-996 3
- 66 Cooperative Non-bonded Forces Control Membrane Binding of the pH-Low Insertion Peptide pHLIP.
- 65 PS membrane asymmetry influences the folding and insertion of a transmembrane helix.
- 64 A lipophilicity-based energy function for membrane-protein modelling and design. 1
- 63 Fusion Peptides: The Claws of the Viral Fusion Glycoproteins. 1-10
- 62 Multivalent lipid targeting by the calcium-independent C2A domain of Slp-4/granuphilin.
- 61 OpenAWSEM with Open3SPN2: a fast, flexible, and accessible framework for large-scale coarse-grained biomolecular simulations.
- 60 Discovery of Dengue Virus Inhibitors. **2020**, 27, 4945-5036 1
- 59 Magic angle spinning NMR of G protein-coupled receptors.. **2022**, 128, 25-43
- 58 Encyclopedia of Biophysics. **2020**, 1-4
- 57 Membrane Proteins Have Distinct Fast Internal Motion and Residual Conformational Entropy.
- 56 Molecular Recognition in the Membrane: Role in the Folding of Membrane Proteins. **2002**, 273-294

55	Influenza A Virus M2 Protein: Proton Selectivity of the Ion Channel, Cytotoxicity, and a Hypothesis on Peripheral Raft Association and Virus Budding. 2005 , 113-130		2
54	Proteins at Lipid Mattresses. 2005 , 137-145		
53	Local Bilayer Hydrophobicity Modulates Membrane Protein Stability.		
52	Rational tuning of a membrane-perforating antimicrobial peptide to selectively target membranes of different lipid composition.		1
51	N-terminal moiety of Antimicrobial peptide Ltc1-k increases its toxicity for eukaryotic cells. 2011 , 3, 68-78		1
50	High-resolution optical tweezers for single-molecule manipulation. 2013 , 86, 367-83		21
49	Plant monounsaturated fatty acids: Diversity, biosynthesis, functions and uses. 2021 , 85, 101138		3
48	Untangling the complexity of membrane protein folding.. 2022 , 72, 237-247		1
47	Architects of their own environment: How membrane proteins shape the Gram-negative cell envelope.. 2022 , 128, 1-34		1
46	Elucidation of Complex Dynamic Intermolecular Interactions in Membranes.. 2022 , 70, 1-9		
45	Studying the Rhodopsin-Like G Protein Coupled Receptors by Atomic Force Microscopy.. 2022 ,		
44	Lipid saturation and head group composition have a pronounced influence on the membrane insertion equilibrium of amphipathic helical polypeptides.. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2021 , 183844	3.8	1
43	Phase separation of the mammalian prion protein: physiological and pathological perspectives.. 2022 ,		0
42	pH-dependent 11 μ FF ATP synthase sub-steps reveal insight into the F torque generating mechanism.. 2021 , 10,		4
41	How lipids affect the energetics of co-translational alpha helical membrane protein folding.. 2022 ,		0
40	Membrane Activity of LL-37 Derived Antimicrobial Peptides against : Superiority of SAAP-148 over OP-145.. 2022 , 12,		1
39	The Function, Structure, and Origins of the ER Membrane Protein Complex.. 2022 ,		2
38	Conserved hydrogen-bond motifs of membrane transporters and receptors.. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2022 , 1864, 183896	3.8	0

37	A unified evolutionary origin for the ubiquitous protein transporters SecY and YidC.. 2021 , 19, 266		2
36	Droplet-based valveless microfluidic system for phage-display screening against spheroids.. 2022 , 16, 024107		
35	The use of vector formalism in the analysis of hydrophobic and electric driving forces in biological assemblies.. 2022 , 1-50		0
34	Data_Sheet_1.PDF. 2019 ,		
33	Data_Sheet_1.pdf. 2018 ,		
32	Data_Sheet_1.PDF. 2019 ,		
31	Insights into Membrane Curvature Sensing and Membrane Remodeling by Intrinsically Disordered Proteins and Protein Regions.. <i>Journal of Membrane Biology</i> , 2022 , 1	2.3	2
30	Tuning Electrostatic and Hydrophobic Surfaces of Aromatic Rings to Enhance Membrane Association and Cell Uptake of Peptides. <i>Angewandte Chemie</i> ,	3.6	
29	Impact of compound mutations I1171N + F1174I and I1171N + L1198H on the structure of ALK in NSCLC pathogenesis: atomistic insights.. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022 , 1-9	3.6	0
28	Tuning Electrostatic and Hydrophobic Surfaces of Aromatic Rings to Enhance Membrane Association and Cell Uptake of Peptides.. <i>Angewandte Chemie - International Edition</i> , 2022 ,	16.4	3
27	Chemical fixation creates nanoscale clusters on the cell surface by aggregating membrane proteins. <i>Communications Biology</i> , 2022 , 5,	6.7	0
26	The perception and response of T cells to a changing environment are based on the law of initial value. <i>Science Signaling</i> , 2022 , 15,	8.8	0
25	Connexins and Pannexins Similarities and Differences According to the FOD-M Model. <i>Biomedicines</i> , 2022 , 10, 1504	4.8	0
24	Effect of lipid saturation on the topology and oligomeric state of helical membrane polypeptides. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2022 , 1864, 184001	3.8	1
23	Free-energy landscapes and insertion pathways for peptides in membrane environment. <i>Physical Review E</i> , 2022 , 106,	2.4	
22	Three-stage model of helical membrane protein folding: Role of membrane-water interface as the intermediate stage vestibule for TM helices during their in membrano assembly. <i>Biochemical and Biophysical Research Communications</i> , 2022 ,	3.4	
21	Impact of bilayer composition on the dimerization properties of the Slg1 stress sensor TMD from a multiscale analysis □		
20	F1FO ATP synthase molecular motor mechanisms. 13,		0

- 19 Transmembrane peptide effects on bacterial membrane integrity and organization. **2022**,
- 18 Tryptophan, more than just an interfacial amino acid in the membrane activity of cationic cell-penetrating and antimicrobial peptides.. 1-49 1
- 17 Effects of Membrane Cholesterol on Stability of Transmembrane Helix Associations. **2022**, 70, 514-518 1
- 16 Functional Delineation of a ProteinMembrane Interaction Hotspot Site on the HIV-1 Neutralizing Antibody 10E8. **2022**, 23, 10767 0
- 15 The Biogenesis of Multipass Membrane Proteins. a041251 0
- 14 Physics of the Cell Membrane. **2022**, 147-172 0
- 13 A Tale of Two Pathways: Tail-Anchored Protein Insertion at the Endoplasmic Reticulum. a041252 0
- 12 Applications of Single-Molecule Vibrational Spectroscopic Techniques for the Structural Investigation of Amyloid Oligomers. **2022**, 27, 6448 0
- 11 Effects of Gly residue and Cholesterol on the GXXXG-Mediated Parallel Association of Transmembrane Helices: A Single-Pair FRET Study. 0
- 10 The impact of bilayer composition on the dimerization properties of the Slg1 stress sensor TMD from a multiscale analysis. 0
- 9 The Contribution of Hydrophobic Interactions to Conformational Changes of Inward/Outward Transmembrane Transport Proteins. **2022**, 12, 1212 0
- 8 Optimization of host cell-compatible, antimicrobial peptides effective against biofilms and clinical isolates of drug-resistant bacteria. 0
- 7 B2LiVe, a label-free 1D-NMR method to quantify the binding of amphitropic peptides or proteins to membrane vesicles. 0
- 6 A selectivity filter in the EMC limits protein mislocalization to the ER. 0
- 5 Mechanism of signal-anchor triage during early steps of membrane protein insertion. **2023**, 83, 961-973.e7 0
- 4 The Formation of β -Strand Nine ($\beta 9$) in the Folding and Insertion of BamA from an Unfolded Form into Lipid Bilayers. **2023**, 13, 247 0
- 3 Saturated fatty acids increase LPI to reduce FUNDC1 dimerization and stability and mitochondrial function. **2023**, 24, 0
- 2 Designing Collagen-Binding Peptide with Enhanced Properties Using Hydropathic Free Energy Predictions. **2023**, 13, 3342 0

- 1 Optimization of Host Cell-Compatible, Antimicrobial Peptides Effective against Biofilms and Clinical Isolates of Drug-Resistant Bacteria. **2023**, 9, 952-965

o