

Nir Ben-Tal

List of Publications by Year in descending order

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169
papers

16,646
citations

28274

55
h-index

17592

121
g-index

191
all docs

191
docs citations

191
times ranked

21312
citing authors

#	ARTICLE	IF	CITATIONS
1	The copper-linked Escherichia coli AZY operon: Structure, metal binding, and a possible physiological role in copper delivery. <i>Journal of Biological Chemistry</i> , 2022, 298, 101445.	3.4	1
2	Potential Antigenic Cross-reactivity Between Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and Dengue Viruses. <i>Clinical Infectious Diseases</i> , 2021, 73, e2444-e2449.	5.8	137
3	Structural motifs in protein cores and at protein-protein interfaces are different. <i>Protein Science</i> , 2021, 30, 381-390.	7.6	8
4	C5 conserved region of hydrophilic C-terminal part of <i>Saccharomyces cerevisiae</i> Nha1 antiporter determines its requirement of Erv14 COPII cargo receptor for plasma membrane targeting. <i>Molecular Microbiology</i> , 2021, 115, 41-57.	2.5	3
5	Bridging Themes: Short Protein Segments Found in Different Architectures. <i>Molecular Biology and Evolution</i> , 2021, 38, 2191-2208.	8.9	32
6	Global Dynamics Renders Protein Sites with High Functional Response. <i>Journal of Physical Chemistry B</i> , 2021, 125, 4734-4745.	2.6	5
7	PredictProtein - Predicting Protein Structure and Function for 29 Years. <i>Nucleic Acids Research</i> , 2021, 49, W535-W540.	14.5	135
8	Editorial overview: Sequences and topology: paths from sequence to structure™. <i>Current Opinion in Structural Biology</i> , 2021, 68, vi-viii.	5.7	2
9	Structure of plant photosystem I-plastocyanin complex reveals strong hydrophobic interactions. <i>Biochemical Journal</i> , 2021, 478, 2371-2384.	3.7	15
10	Gram-negative outer-membrane proteins with multiple β -barrel domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	10
11	Integrative Structural Biology in the Era of Accurate Structure Prediction. <i>Journal of Molecular Biology</i> , 2021, 433, 167127.	4.2	36
12	Titrateable transmembrane residues and a hydrophobic plug are essential for manganese import via the <i>Bacillus anthracis</i> ABC transporter MntBC-A. <i>Journal of Biological Chemistry</i> , 2021, 297, 101087.	3.4	1
13	Using ConSurf to Detect Functionally Important Regions in RNA. <i>Current Protocols</i> , 2021, 1, e270.	2.9	3
14	The Sigma-1 receptor is an ER-localized type II membrane protein. <i>Journal of Biological Chemistry</i> , 2021, 297, 101299.	3.4	18
15	Dimeric and high-resolution structures of <i>Chlamydomonas</i> Photosystem I from a temperature-sensitive Photosystem II mutant. <i>Communications Biology</i> , 2021, 4, 1380.	4.4	6
16	ConSurf®: An accessible repository for the evolutionary conservation patterns of the majority of PDB proteins. <i>Protein Science</i> , 2020, 29, 258-267.	7.6	98
17	Distinct Allosteric Networks Underlie Mechanistic Speciation of ABC Transporters. <i>Structure</i> , 2020, 28, 651-663.e5.	3.3	17
18	Substrate recognition and ATPase activity of the <i>E. coli</i> cysteine/cystine ABC transporter YecSC-FliY. <i>Journal of Biological Chemistry</i> , 2020, 295, 5245-5256.	3.4	12

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19	On the evolution of protein-adenine binding. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 4701-4709.	7.1	28
20	Validity of machine learning in biology and medicine increased through collaborations across fields of expertise. Nature Machine Intelligence, 2020, 2, 18-24.	16.0	43
21	An angular motion of a conserved four-helix bundle facilitates alternating access transport in the TtNapA and EcNhaA transporters. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31850-31860.	7.1	6
22	On the emergence of P-Loop NTPase and Rossmann enzymes from a Beta-Alpha-Beta ancestral fragment. ELife, 2020, 9, .	6.0	61
23	DDGun: an untrained method for the prediction of protein stability changes upon single and multiple point variations. BMC Bioinformatics, 2019, 20, 335.	2.6	81
24	Metal Coordination Is Crucial for Geranylgeranyl Diphosphate Synthase-Bisphosphonate Interactions: A Crystallographic and Computational Analysis. Molecular Pharmacology, 2019, 96, 580-588.	2.3	5
25	Protein Databank Survey Hints into the Emergence of Protein-Adenine Recognition in Evolution. Biophysical Journal, 2019, 116, 152a.	0.5	0
26	Using Phylogeny to Decipher Electrogenicity in Cation/Proton Antiporters. Biophysical Journal, 2019, 116, 554a.	0.5	0
27	Navigating Among Known Structures in Protein Space. Methods in Molecular Biology, 2019, 1851, 233-249.	0.9	2
28	A natural upper bound to the accuracy of predicting protein stability changes upon mutations. Bioinformatics, 2019, 35, 1513-1517.	4.1	39
29	Broad phylogenetic analysis of cation/proton antiporters reveals transport determinants. Nature Communications, 2018, 9, 4205.	12.8	74
30	Efflux Pumps Represent Possible Evolutionary Convergence onto the β -Barrel Fold. Structure, 2018, 26, 1266-1274.e2.	3.3	19
31	Single-molecule probing of the conformational homogeneity of the ABC transporter BtuCD. Nature Chemical Biology, 2018, 14, 715-722.	8.0	46
32	Evolutionary pathways of repeat protein topology in bacterial outer membrane proteins. ELife, 2018, 7, .	6.0	36
33	Structural and Dynamics Characterization of the MerR Family Metalloregulator CueR in its Repression and Activation States. Structure, 2017, 25, 988-996.e3.	3.3	38
34	Similarity between the Usher Plug and the Repeating Domain of an Ice Adhesin: Evolution via Surface Reshaping. Israel Journal of Chemistry, 2017, 57, 381-384.	2.3	1
35	Complex evolutionary footprints revealed in an analysis of reused protein segments of diverse lengths. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11703-11708.	7.1	66
36	BcXYG1, a Secreted Xyloglucanase from <i>Botrytis cinerea</i> , Triggers Both Cell Death and Plant Immune Responses. Plant Physiology, 2017, 175, 438-456.	4.8	102

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37	The uncoupled ATPase activity of the ABC transporter BtuC2D2 leads to a hysteretic conformational change, conformational memory and improved activity. <i>Scientific Reports</i> , 2016, 6, 21696.	3.3	18
38	ConSurf 2016: an improved methodology to estimate and visualize evolutionary conservation in macromolecules. <i>Nucleic Acids Research</i> , 2016, 44, W344-W350.	14.5	2,395
39	Systems-Wide Prediction of Enzyme Promiscuity Reveals a New Underground Alternative Route for Pyridoxal 5â€™-Phosphate Production in <i>E. coli</i> . <i>PLoS Computational Biology</i> , 2016, 12, e1004705.	3.2	20
40	The Na ⁺ /H ⁺ Exchanger NHE6 Links Endosomal pH to Amyloid Pathologies in Alzheimer's Disease. <i>Biophysical Journal</i> , 2015, 108, 308a.	0.5	0
41	Changes to the dynamic nature of hemagglutinin and the emergence of the 2009 pandemic H1N1 influenza virus. <i>Scientific Reports</i> , 2015, 5, 12828.	3.3	10
42	Using ConTemplate and the PDB to explore conformational space: on the detection of rare protein conformations. <i>BMC Bioinformatics</i> , 2015, 16, .	2.6	1
43	Navigating in the Protein Universe. <i>Biophysical Journal</i> , 2015, 108, 203a.	0.5	0
44	DynaFace: Discrimination between Obligatory and Non-obligatory Protein-Protein Interactions Based on the Complexâ€™s Dynamics. <i>PLoS Computational Biology</i> , 2015, 11, e1004461.	3.2	9
45	Metal binding spectrum and model structure of the <i>Bacillus anthracis</i> virulence determinant MntA. <i>Metallomics</i> , 2015, 7, 1407-1419.	2.4	20
46	CyToStruct: Augmenting the Network Visualization of Cytoscape with the Power of Molecular Viewers. <i>Structure</i> , 2015, 23, 941-948.	3.3	20
47	NhaA antiporter functions using 10 helices, and an additional 2 contribute to assembly/stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5575-82.	7.1	17
48	ConTemplate Suggests Possible Alternative Conformations for a Query Protein of Known Structure. <i>Structure</i> , 2015, 23, 2162-2170.	3.3	13
49	Structure, Dynamics and Implied Gating Mechanism of a Human Cyclic Nucleotide-Gated Channel. <i>PLoS Computational Biology</i> , 2014, 10, e1003976.	3.2	9
50	PredictProteinâ€™ an open resource for online prediction of protein structural and functional features. <i>Nucleic Acids Research</i> , 2014, 42, W337-W343.	14.5	589
51	Representation of the Protein Universe using Classifications, Maps, and Networks. <i>Israel Journal of Chemistry</i> , 2014, 54, 1286-1292.	2.3	10
52	Herp coordinates compartmentalization and recruitment of HRD1 and misfolded proteins for ERAD. <i>Molecular Biology of the Cell</i> , 2014, 25, 1050-1060.	2.1	64
53	ConTemplate: exploiting the protein databank to propose ensemble of conformations of a query protein of known structure. <i>BMC Bioinformatics</i> , 2014, 15, .	2.6	2
54	Global view of the protein universe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11691-11696.	7.1	69

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55	Functional Evaluation of NHE6 Mutation Associated with Syndromic Autism and Tau Deposition. <i>Biophysical Journal</i> , 2014, 106, 366a.	0.5	0
56	Emergence and Transmission of Arbovirus Evolutionary Intermediates with Epidemic Potential. <i>Cell Host and Microbe</i> , 2014, 15, 706-716.	11.0	107
57	Novel activating mutations lacking cysteine in type I cytokine receptors in acute lymphoblastic leukemia. <i>Blood</i> , 2014, 124, 106-110.	1.4	50
58	Lifting the lid on pilus assembly. <i>ELife</i> , 2014, 3, .	6.0	4
59	Functional Evaluation of Autism Associated Mutations in Slc9A9 (NHE9). <i>Biophysical Journal</i> , 2013, 104, 22a.	0.5	0
60	ConSurf: Using Evolutionary Data to Raise Testable Hypotheses about Protein Function. <i>Israel Journal of Chemistry</i> , 2013, 53, 199-206.	2.3	459
61	Functional evaluation of autism-associated mutations in NHE9. <i>Nature Communications</i> , 2013, 4, 2510.	12.8	87
62	Editorial. <i>Bioinformatics</i> , 2013, 29, i1-i2.	4.1	3
63	The Î±-Helical Structure of Prodomains Promotes Translocation of Intrinsically Disordered Neuropeptide Hormones into the Endoplasmic Reticulum. <i>Journal of Biological Chemistry</i> , 2013, 288, 13961-13973.	3.4	14
64	Monte Carlo simulations of peptide-membrane interactions with the MCPep web server. <i>Nucleic Acids Research</i> , 2012, 40, W358-W363.	14.5	28
65	A Model-Structure of a Periplasm-facing State of the NhaA Antiporter Suggests the Molecular Underpinnings of pH-induced Conformational Changes. <i>Journal of Biological Chemistry</i> , 2012, 287, 18249-18261.	3.4	29
66	Membrane integration of a mitochondrial signal-anchored protein does not require additional proteinaceous factors. <i>Biochemical Journal</i> , 2012, 442, 381-389.	3.7	23
67	New Model of Cystic Fibrosis Transmembrane Conductance Regulator Proposes Active Channel-like Conformation. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 1842-1853.	5.4	73
68	The Transmembrane Helix Tilt May Be Determined by the Balance between Precession Entropy and Lipid Perturbation. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 2896-2904.	5.3	16
69	How Does KCNE1 Regulate the Kv7.1 Potassium Channel? Model-Structure, Mutations, and Dynamics of the Kv7.1-KCNE1 Complex. <i>Structure</i> , 2012, 20, 1343-1352.	3.3	34
70	A structural model of the copper ATPase ATP7B to facilitate analysis of Wilson disease-causing mutations and studies of the transport mechanism. <i>Metallomics</i> , 2012, 4, 669.	2.4	56
71	Structure and Flexibility of the C-Ring in the Electromotor of Rotary FoF1-ATPase of Pea Chloroplasts. <i>PLoS ONE</i> , 2012, 7, e43045.	2.5	28
72	Functional Evaluation of Autism-Related Mutations in the Na ⁺ (k+)/ H ⁺ Exchanger NHE9. <i>Biophysical Journal</i> , 2011, 100, 247a-248a.	0.5	0

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73	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. <i>Journal of Molecular Biology</i> , 2011, 414, 289-302.	4.2	131
74	Structural and Functional Analysis of Tomosyn Identifies Domains Important in Exocytotic Regulation. <i>Journal of Biological Chemistry</i> , 2011, 286, 14542-14553.	3.4	46
75	Putative amino acid determinants of the emergence of the 2009 influenza A (H1N1) virus in the human population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13522-13527.	7.1	12
76	Two Conflicting NHE1 Model Structures: Compatibility with Experimental Data and Implications for the Transport Mechanism. <i>Journal of Biological Chemistry</i> , 2011, 286, le9.	3.4	11
77	Protein stability: a single recorded mutation aids in predicting the effects of other mutations in the same amino acid site. <i>Bioinformatics</i> , 2011, 27, 3286-3292.	4.1	51
78	MuD: an interactive web server for the prediction of non-neutral substitutions using protein structural data. <i>Nucleic Acids Research</i> , 2010, 38, W523-W528.	14.5	34
79	Targeting the voltage sensor of Kv7.2 voltage-gated K ⁺ channels with a new gating-modifier. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 15637-15642.	7.1	81
80	Quality assessment of protein model-structures using evolutionary conservation. <i>Bioinformatics</i> , 2010, 26, 1299-1307.	4.1	46
81	C \pm -trace model of the transmembrane domain of human copper transporter 1, motion and functional implications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10908-10913.	7.1	48
82	iDBPs: a web server for the identification of DNA binding proteins. <i>Bioinformatics</i> , 2010, 26, 692-693.	4.1	76
83	Model-Structure, Mutagenesis and Functional Characteristics of the Human Transporter, NHA2. <i>Biophysical Journal</i> , 2010, 98, 684a.	0.5	0
84	Structural Aspects of the Interaction of Nk-2 Derived Peptides with Cancer Cells. <i>Biophysical Journal</i> , 2010, 98, 277a.	0.5	1
85	Monte-Carlo Simulations of Peptide-Membrane Interactions: Web-Server. <i>Biophysical Journal</i> , 2010, 98, 487a.	0.5	1
86	Human Copper Transporter 1: Model-Structure, Function and Motion. <i>Biophysical Journal</i> , 2010, 98, 646a.	0.5	0
87	Non-Toxin Gating Modifiers Reveal the Promiscuous Nature of the Voltage Sensor of Kv7.2 and TRPV1 Channels. <i>Biophysical Journal</i> , 2010, 98, 122a.	0.5	0
88	Independent and Cooperative Motions of the Kv1.2 Channel: Voltage Sensing and Gating. <i>Biophysical Journal</i> , 2010, 98, 2179-2188.	0.5	14
89	ConSurf 2010: calculating evolutionary conservation in sequence and structure of proteins and nucleic acids. <i>Nucleic Acids Research</i> , 2010, 38, W529-W533.	14.5	1,592
90	Membrane Interactions of Novicidin, a Novel Antimicrobial Peptide: Phosphatidylglycerol Promotes Bilayer Insertion. <i>Journal of Physical Chemistry B</i> , 2010, 114, 11053-11060.	2.6	25

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91	Model-Guided Mutagenesis Drives Functional Studies of Human NHA2, Implicated in Hypertension. <i>Journal of Molecular Biology</i> , 2010, 396, 1181-1196.	4.2	53
92	Interaction of an Antimicrobial Peptide with Membranes: Experiments and Simulations with NKCS. <i>Journal of Physical Chemistry B</i> , 2010, 114, 4230-4237.	2.6	13
93	Natural constraints, folding, motion, and structural stability in transmembrane helical proteins. , 2010, , 205-229.		0
94	The ConSurf-DB: pre-calculated evolutionary conservation profiles of protein structures. <i>Nucleic Acids Research</i> , 2009, 37, D323-D327.	14.5	178
95	Structural Determinants of Transmembrane Helical Proteins. <i>Structure</i> , 2009, 17, 1092-1103.	3.3	30
96	The Effect of Electrostatic Shielding on H Tunneling in R67 Dihydrofolate Reductase. <i>ChemBioChem</i> , 2009, 10, 2620-2623.	2.6	8
97	Identification of DNA-binding Proteins Using Structural, Electrostatic and Evolutionary Features. <i>Journal of Molecular Biology</i> , 2009, 387, 1040-1053.	4.2	75
98	Study of MDM2 Binding to p53-Analogues: Affinity, Helicity, and Applicability to Drug Design. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 865-876.	5.4	16
99	CTR Structure and Mechanism. <i>Biophysical Journal</i> , 2009, 96, 2a.	0.5	0
100	A Combined Pulse EPR and Monte Carlo Simulation Study Provides Molecular Insight on Peptide~Membrane Interactions. <i>Journal of Physical Chemistry B</i> , 2009, 113, 12687-12695.	2.6	38
101	Targeting The Voltage Sensor of Kv7 channels: Novel Strategies to Cure Hyperexcitability Disorders. <i>Biophysical Journal</i> , 2009, 96, 561a.	0.5	0
102	Stress-protective signalling of prion protein is corrupted by scrapie prions. <i>EMBO Journal</i> , 2008, 27, 1974-1984.	7.8	106
103	Dynamic equilibrium between multiple active and inactive conformations explains regulation and oncogenic mutations in ErbB receptors. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2008, 1785, 12-31.	7.4	42
104	Detection of Functionally Important Regions in "Hypothetical Proteins" of Known Structure. <i>Structure</i> , 2008, 16, 1755-1763.	3.3	63
105	Generation, Comparison, and Merging of Pathways between Protein Conformations: Gating in K-Channels. <i>Biophysical Journal</i> , 2008, 95, 3850-3860.	0.5	19
106	Cooperative Transition between Open and Closed Conformations in Potassium Channels. <i>PLoS Computational Biology</i> , 2008, 4, e1000164.	3.2	19
107	A Myo6 Mutation Destroys Coordination between the Myosin Heads, Revealing New Functions of Myosin VI in the Stereocilia of Mammalian Inner Ear Hair Cells. <i>PLoS Genetics</i> , 2008, 4, e1000207.	3.5	79
108	Prediction and simulation of motion in pairs of transmembrane \hat{A} -helices. <i>Bioinformatics</i> , 2007, 23, e212-e218.	4.1	18

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109	Model Structure of the Na ⁺ /H ⁺ Exchanger 1 (NHE1). <i>Journal of Biological Chemistry</i> , 2007, 282, 37854-37863.	3.4	111
110	Co-evolving residues in membrane proteins. <i>Bioinformatics</i> , 2007, 23, 3312-3319.	4.1	65
111	Interactions of Cationic-Hydrophobic Peptides with Lipid Bilayers: A Monte Carlo Simulation Method. <i>Biophysical Journal</i> , 2007, 93, 1858-1871.	0.5	32
112	The Structural Context of Disease-causing Mutations in Gap Junctions. <i>Journal of Biological Chemistry</i> , 2006, 281, 28958-28963.	3.4	14
113	Quasi-symmetry in the Cryo-EM Structure of EmrE Provides the Key to Modeling its Transmembrane Domain. <i>Journal of Molecular Biology</i> , 2006, 364, 54-67.	4.2	114
114	Mutations in the gene encoding pejkakin, a newly identified protein of the afferent auditory pathway, cause DFNB59 auditory neuropathy. <i>Nature Genetics</i> , 2006, 38, 770-778.	21.4	262
115	Progress in structure prediction of α -helical membrane proteins. <i>Current Opinion in Structural Biology</i> , 2006, 16, 496-504.	5.7	61
116	Transmembrane protein structures without X-rays. <i>Trends in Biochemical Sciences</i> , 2006, 31, 106-113.	7.5	84
117	Has the code for protein translocation been broken?. <i>Trends in Biochemical Sciences</i> , 2006, 31, 192-196.	7.5	18
118	Disruption of the <i>Aspergillus fumigatus</i> ECM33 homologue results in rapid conidial germination, antifungal resistance and hypervirulence. <i>Microbiology (United Kingdom)</i> , 2006, 152, 1919-1928.	1.8	78
119	In silico identification of functional regions in proteins. <i>Bioinformatics</i> , 2005, 21, i328-i337.	4.1	51
120	ConSurf 2005: the projection of evolutionary conservation scores of residues on protein structures. <i>Nucleic Acids Research</i> , 2005, 33, W299-W302.	14.5	1,255
121	QuasiMotiFinder: protein annotation by searching for evolutionarily conserved motif-like patterns. <i>Nucleic Acids Research</i> , 2005, 33, W255-W261.	14.5	35
122	Monte Carlo Studies of Folding, Dynamics, and Stability in α -Helices. <i>Biophysical Journal</i> , 2005, 88, 2391-2402.	0.5	39
123	Comparison of Site-Specific Rate-Inference Methods for Protein Sequences: Empirical Bayesian Methods Are Superior. <i>Molecular Biology and Evolution</i> , 2004, 21, 1781-1791.	8.9	405
124	The Conserved Carboxy Terminus of the Capsid Domain of Human Immunodeficiency Virus Type 1 Gag Protein Is Important for Virion Assembly and Release. <i>Journal of Virology</i> , 2004, 78, 9675-9688.	3.4	57
125	Assigning transmembrane segments to helices in intermediate-resolution structures. <i>Bioinformatics</i> , 2004, 20, i122-i129.	4.1	13
126	ConSeq: the identification of functionally and structurally important residues in protein sequences. <i>Bioinformatics</i> , 2004, 20, 1322-1324.	4.1	458

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127	A Putative Mechanism for Downregulation of the Catalytic Activity of the EGF Receptor via Direct Contact between Its Kinase and C-Terminal Domains. <i>Structure</i> , 2004, 12, 2265-2275.	3.3	66
128	Implicit solvent model estimates of the stability of model structures of the alamethicin channel. <i>European Biophysics Journal</i> , 2004, 33, 16-28.	2.2	24
129	The ConSurf-HSSP database: The mapping of evolutionary conservation among homologs onto PDB structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 610-617.	2.6	115
130	Free Diffusion of Steroid Hormones Across Biomembranes: A Simplex Search with Implicit Solvent Model Calculations. <i>Biophysical Journal</i> , 2004, 87, 768-779.	0.5	93
131	An Automatic Method for Predicting Transmembrane Protein Structures Using Cryo-EM and Evolutionary Data. <i>Biophysical Journal</i> , 2004, 87, 3448-3459.	0.5	51
132	A $\hat{C}\hat{I}\hat{\pm}$ Model for the Transmembrane $\hat{I}\hat{\pm}$ Helices of Gap Junction Intercellular Channels. <i>Molecular Cell</i> , 2004, 15, 879-888.	9.7	107
133	An Evolutionarily Conserved Network of Amino Acids Mediates Gating in Voltage-dependent Potassium Channels. <i>Journal of Molecular Biology</i> , 2004, 340, 307-318.	4.2	59
134	Increased Concentration of Polyvalent Phospholipids in the Adsorption Domain of a Charged Protein. <i>Biophysical Journal</i> , 2004, 86, 2165-2178.	0.5	55
135	In Silico Identification of Functional Protein Interfaces. <i>Comparative and Functional Genomics</i> , 2003, 4, 420-423.	2.0	17
136	Evolutionary analysis reveals collective properties and specificity in the C-type lectin and lectin-like domain superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 44-55.	2.6	19
137	Interactions of Hydrophobic Peptides with Lipid Bilayers: Monte Carlo Simulations with M2 \hat{I} . <i>Biophysical Journal</i> , 2003, 85, 3431-3444.	0.5	46
138	Interactions of the M2 \hat{I} Segment of the Acetylcholine Receptor with Lipid Bilayers: A Continuum-Solvent Model Study. <i>Biophysical Journal</i> , 2003, 85, 3687-3695.	0.5	17
139	ConSurf: Identification of Functional Regions in Proteins by Surface-Mapping of Phylogenetic Information. <i>Bioinformatics</i> , 2003, 19, 163-164.	4.1	1,082
140	A putative molecular-activation switch in the transmembrane domain of erbB2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 15937-15940.	7.1	247
141	Stability of an Ion Channel in Lipid Bilayers: An Implicit Solvent Model Calculations with Gramicidin. <i>Biochemistry</i> , 2002, 41, 6946-6954.	2.5	21
142	Free energy determinants of peptide association with lipid bilayers. <i>Current Topics in Membranes</i> , 2002, 52, 205-253.	0.9	49
143	Long-range effects on the binding of the influenza HA to receptors are mediated by changes in the stability of a metastable HA conformation. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2002, 1565, 81-90.	2.6	7
144	Type I chaperonins: not all are created equal. <i>FEBS Letters</i> , 2002, 529, 1-5.	2.8	64

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145	A Novel Scoring Function for Predicting the Conformations of Tightly Packed Pairs of Transmembrane α -Helices. <i>Journal of Molecular Biology</i> , 2002, 321, 363-378.	4.2	74
146	Rate4Site: an algorithmic tool for the identification of functional regions in proteins by surface mapping of evolutionary determinants within their homologues. <i>Bioinformatics</i> , 2002, 18, S71-S77.	4.1	536
147	On the regulatory role of dipeptidyl peptidase IV (\sim ...CD26 \sim ...adenosine deaminase complexing protein) on adenosine deaminase activity. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2002, 1587, 21-30.	3.8	10
148	A mutation in GJB3 is associated with recessive erythrokeratoderma variabilis (EKV) and leads to defective trafficking of the connexin 31 protein. <i>Human Molecular Genetics</i> , 2002, 11, 1311-1316.	2.9	73
149	ConSurf: an algorithmic tool for the identification of functional regions in proteins by surface mapping of phylogenetic information. <i>Journal of Molecular Biology</i> , 2001, 307, 447-463.	4.2	451
150	Interactions of Cholesterol with Lipid Bilayers: The Preferred Configuration and Fluctuations. <i>Biophysical Journal</i> , 2001, 81, 643-658.	0.5	115
151	Multi-Stage Regulation, a Key to Reliable Adaptive Biochemical Pathways. <i>Biophysical Journal</i> , 2001, 81, 3016-3028.	0.5	19
152	Implicit Solvent Model Studies of the Interactions of the Influenza Hemagglutinin Fusion Peptide with Lipid Bilayers. <i>Biophysical Journal</i> , 2001, 80, 643-655.	0.5	35
153	Continuum Solvent Model Studies of the Interactions of an Anticonvulsant Drug with a Lipid Bilayer. <i>Biophysical Journal</i> , 2001, 80, 2536-2545.	0.5	37
154	Residue frequencies and pairing preferences at protein-protein interfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 43, 89-102.	2.6	359
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