Nir Ben-Tal

List of Publications by Year
in descending order

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	ConSurf 2016: an improved methodology to estimate and visualize evolutionary conservation in macromolecules. Nucleic Acids Research, 2016, 44, W344-W350.	14.5	2,395
2	ConSurf 2010: calculating evolutionary conservation in sequence and structure of proteins and nucleic acids. Nucleic Acids Research, 2010, 38, W529-W533.	14.5	1,592
3	ConSurf 2005: the projection of evolutionary conservation scores of residues on protein structures. Nucleic Acids Research, 2005, 33, W299-W302.	14.5	1,255
4	ConSurf: Identification of Functional Regions in Proteins by Surface-Mapping of Phylogenetic Information. Bioinformatics, 2003, 19, 163-164.	4.1	1,082
5	PredictProtein—an open resource for online prediction of protein structural and functional features. Nucleic Acids Research, 2014, 42, W337-W343.	14.5	589
6	Rate4Site: an algorithmic tool for the identification of functional regions in proteins by surface mapping of evolutionary determinants within their homologues. Bioinformatics, 2002, 18, S71-S77.	4.1	536
7	ConSurf: Using Evolutionary Data to Raise Testable Hypotheses about Protein Function. Israel Journal of Chemistry, 2013, 53, 199-206.	2.3	459
8	ConSeq: the identification of functionally and structurally important residues in protein sequences. Bioinformatics, 2004, 20, 1322-1324.	4.1	458
9	ConSurf: an algorithmic tool for the identification of functional regions in proteins by surface mapping of phylogenetic information. Journal of Molecular Biology, 2001, 307, 447-463.	4.2	451
10	Comparison of Site-Specific Rate-Inference Methods for Protein Sequences: Empirical Bayesian Methods Are Superior. Molecular Biology and Evolution, 2004, 21, 1781-1791.	8.9	405
11	Residue frequencies and pairing preferences at protein-protein interfaces. Proteins: Structure, Function and Bioinformatics, 2001, 43, 89-102.	2.6	359
12	Mutations in the gene encoding pejvakin, a newly identified protein of the afferent auditory pathway, cause DFNB59 auditory neuropathy. Nature Genetics, 2006, 38, 770-778.	21.4	262
13	A putative molecular-activation switch in the transmembrane domain of erbB2. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15937-15940.	7.1	247
14	Electrostatic interaction of myristoylated proteins with membranes: simple physics, complicated biology. Structure, 1997, 5, 985-989.	3.3	216
15	The ConSurf-DB: pre-calculated evolutionary conservation profiles of protein structures. Nucleic Acids Research, 2009, 37, D323-D327.	14.5	178
16	Electrostatic Properties of Membranes Containing Acidic Lipids and Adsorbed Basic Peptides: Theory and Experiment. Biophysical Journal, 1999, 77, 3176-3188.	0.5	173
17	Electrostatics and the Membrane Association of Src: Theory and Experiment€. Biochemistry, 1998, 37, 2145-2159.	2.5	172
18	Free Energy of Amide Hydrogen Bond Formation in Vacuum, in Water, and in Liquid Alkane Solution. Journal of Physical Chemistry B, 1997, 101, 450-457.	2.6	143

#	ARTICLE	IF	CITATIONS
19	Potential Antigenic Cross-reactivity Between Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and Dengue Viruses. Clinical Infectious Diseases, 2021, 73, e2444-e2449.	5.8	137
20	PredictProtein - Predicting Protein Structure and Function for 29 Years. Nucleic Acids Research, 2021, 49, W535-W540.	14.5	135
21	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
22	Interactions of Cholesterol with Lipid Bilayers: The Preferred Configuration and Fluctuations. Biophysical Journal, 2001, 81, 643-658.	0.5	115
23	The ConSurf-HSSP database: The mapping of evolutionary conservation among homologs onto PDB structures. Proteins: Structure, Function and Bioinformatics, 2004, 58, 610-617.	2.6	115
24	Quasi-symmetry in the Cryo-EM Structure of EmrE Provides the Key to Modeling its Transmembrane Domain. Journal of Molecular Biology, 2006, 364, 54-67.	4.2	114
25	Model Structure of the Na+/H+ Exchanger 1 (NHE1). Journal of Biological Chemistry, 2007, 282, 37854-37863.	3.4	111
26	Calculation of Alkane to Water Solvation Free Energies Using Continuum Solvent Models. The Journal of Physical Chemistry, 1996, 100, 2744-2752.	2.9	110
27	A CÎ± Model for the Transmembrane Î± Helices of Gap Junction Intercellular Channels. Molecular Cell, 2004, 15, 879-888.	9.7	107
28	Emergence and Transmission of Arbovirus Evolutionary Intermediates with Epidemic Potential. Cell Host and Microbe, 2014, 15, 706-716.	11.0	107
29	Stress-protective signalling of prion protein is corrupted by scrapie prions. EMBO Journal, 2008, 27, 1974-1984.	7.8	106
30	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
31	ConSurfâ€ÐB: An accessible repository for the evolutionary conservation patterns of the majority of PDB proteins. Protein Science, 2020, 29, 258-267.	7.6	98
32	Association Entropy in Adsorption Processes. Biophysical Journal, 2000, 79, 1180-1187.	0.5	96
33	Free Diffusion of Steroid Hormones Across Biomembranes: A Simplex Search with Implicit Solvent Model Calculations. Biophysical Journal, 2004, 87, 768-779.	0.5	93
34	Functional evaluation of autism-associated mutations in NHE9. Nature Communications, 2013, 4, 2510.	12.8	87
35	Transmembrane protein structures without X-rays. Trends in Biochemical Sciences, 2006, 31, 106-113.	7.5	84
36	Targeting the voltage sensor of Kv7.2 voltage-gated K ⁺ channels with a new gating-modifier. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15637-15642.	7.1	81

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37	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
38	A Myo6 Mutation Destroys Coordination between the Myosin Heads, Revealing New Functions of Myosin VI in the Stereocilia of Mammalian Inner Ear Hair Cells. PLoS Genetics, 2008, 4, e1000207.	3.5	79
39	Disruption of the Aspergillus fumigatus ECM33 homologue results in rapid conidial germination, antifungal resistance and hypervirulence. Microbiology (United Kingdom), 2006, 152, 1919-1928.	1.8	78
40	KPROT: A knowledge-based scale for the propensity of residue orientation in transmembrane segments. Application to membrane protein structure prediction. Journal of Molecular Biology, 1999, 294, 921-935.	4.2	77
41	iDBPs: a web server for the identification of DNA binding proteins. Bioinformatics, 2010, 26, 692-693.	4.1	76
42	Identification of DNA-binding Proteins Using Structural, Electrostatic and Evolutionary Features. Journal of Molecular Biology, 2009, 387, 1040-1053.	4.2	75
43	A Novel Scoring Function for Predicting the Conformations of Tightly Packed Pairs of Transmembrane α-Helices. Journal of Molecular Biology, 2002, 321, 363-378.	4.2	74
44	Broad phylogenetic analysis of cation/proton antiporters reveals transport determinants. Nature Communications, 2018, 9, 4205.	12.8	74
45	Continuum Solvent Model Calculations of Alamethicin-Membrane Interactions: Thermodynamic Aspects. Biophysical Journal, 2000, 78, 571-583.	0.5	73
46	A mutation in GJB3 is associated with recessive erythrokeratodermia variabilis (EKV) and leads to defective trafficking of the connexin 31 protein. Human Molecular Genetics, 2002, 11, 1311-1316.	2.9	73
47	New Model of Cystic Fibrosis Transmembrane Conductance Regulator Proposes Active Channel-like Conformation. Journal of Chemical Information and Modeling, 2012, 52, 1842-1853.	5.4	73
48	Global view of the protein universe. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11691-11696.	7.1	69
49	A Putative Mechanism for Downregulation of the Catalytic Activity of the EGF Receptor via Direct Contact between Its Kinase and C-Terminal Domains. Structure, 2004, 12, 2265-2275.	3.3	66
50	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
51	Co-evolving residues in membrane proteins. Bioinformatics, 2007, 23, 3312-3319.	4.1	65
52	Type I chaperonins: not all are created equal. FEBS Letters, 2002, 529, 1-5.	2.8	64
53	Herp coordinates compartmentalization and recruitment of HRD1 and misfolded proteins for ERAD. Molecular Biology of the Cell, 2014, 25, 1050-1060.	2.1	64
54	Detection of Functionally Important Regions in "Hypothetical Proteins" of Known Structure. Structure, 2008, 16, 1755-1763.	3.3	63

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55	Progress in structure prediction of α-helical membrane proteins. Current Opinion in Structural Biology, 2006, 16, 496-504.	5.7	61
56	On the emergence of P-Loop NTPase and Rossmann enzymes from a Beta-Alpha-Beta ancestral fragment. ELife, 2020, 9, .	6.0	61
57	An Evolutionarily Conserved Network of Amino Acids Mediates Gating in Voltage-dependent Potassium Channels. Journal of Molecular Biology, 2004, 340, 307-318.	4.2	59
58	The Conserved Carboxy Terminus of the Capsid Domain of Human Immunodeficiency Virus Type 1 Gag Protein Is Important for Virion Assembly and Release. Journal of Virology, 2004, 78, 9675-9688.	3.4	57
59	A structural model of the copper ATPase ATP7B to facilitate analysis of Wilson disease-causing mutations and studies of the transport mechanism. Metallomics, 2012, 4, 669.	2.4	56
60	Increased Concentration of Polyvalent Phospholipids in the Adsorption Domain of a Charged Protein. Biophysical Journal, 2004, 86, 2165-2178.	0.5	55
61	Introduction to Proteins. , 0, , .		55
62	Model-Guided Mutagenesis Drives Functional Studies of Human NHA2, Implicated in Hypertension. Journal of Molecular Biology, 2010, 396, 1181-1196.	4.2	53
63	An Automatic Method for Predicting Transmembrane Protein Structures Using Cryo-EM and Evolutionary Data. Biophysical Journal, 2004, 87, 3448-3459.	0.5	51
64	In silico identification of functional regions in proteins. Bioinformatics, 2005, 21, i328-i337.	4.1	51
65	Protein stability: a single recorded mutation aids in predicting the effects of other mutations in the same amino acid site. Bioinformatics, 2011, 27, 3286-3292.	4.1	51
66	Novel activating mutations lacking cysteine in type I cytokine receptors in acute lymphoblastic leukemia. Blood, 2014, 124, 106-110.	1.4	50
67	Free energy determinants of peptide association with lipid bilayers. Current Topics in Membranes, 2002, 52, 205-253.	0.9	49
68	Cα-trace model of the transmembrane domain of human copper transporter 1, motion and functional implications. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10908-10913.	7.1	48
69	Interactions of Hydrophobic Peptides with Lipid Bilayers: Monte Carlo Simulations with M2δ. Biophysical Journal, 2003, 85, 3431-3444.	0.5	46
70	Quality assessment of protein model-structures using evolutionary conservation. Bioinformatics, 2010, 26, 1299-1307.	4.1	46
71	Structural and Functional Analysis of Tomosyn Identifies Domains Important in Exocytotic Regulation. Journal of Biological Chemistry, 2011, 286, 14542-14553.	3.4	46
72	Single-molecule probing of the conformational homogeneity of the ABC transporter BtuCD. Nature Chemical Biology, 2018, 14, 715-722.	8.0	46

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73	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
74	Dynamic equilibrium between multiple active and inactive conformations explains regulation and oncogenic mutations in ErbB receptors. Biochimica Et Biophysica Acta: Reviews on Cancer, 2008, 1785, 12-31.	7.4	42
75	Monte Carlo Studies of Folding, Dynamics, and Stability in Î±-Helices. Biophysical Journal, 2005, 88, 2391-2402.	0.5	39
76	A natural upper bound to the accuracy of predicting protein stability changes upon mutations. Bioinformatics, 2019, 35, 1513-1517.	4.1	39
77	A Combined Pulse EPR and Monte Carlo Simulation Study Provides Molecular Insight on Peptideâ^Membrane Interactions. Journal of Physical Chemistry B, 2009, 113, 12687-12695.	2.6	38
78	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
79	Continuum Solvent Model Studies of the Interactions of an Anticonvulsant Drug with a Lipid Bilayer. Biophysical Journal, 2001, 80, 2536-2545.	0.5	37
80	Integrative Structural Biology in the Era of Accurate Structure Prediction. Journal of Molecular Biology, 2021, 433, 167127.	4.2	36
81	Evolutionary pathways of repeat protein topology in bacterial outer membrane proteins. ELife, 2018, 7, .	6.0	36
82	Implicit Solvent Model Studies of the Interactions of the Influenza Hemagglutinin Fusion Peptide with Lipid Bilayers. Biophysical Journal, 2001, 80, 643-655.	0.5	35
83	QuasiMotiFinder: protein annotation by searching for evolutionarily conserved motif-like patterns. Nucleic Acids Research, 2005, 33, W255-W261.	14.5	35
84	MuD: an interactive web server for the prediction of non-neutral substitutions using protein structural data. Nucleic Acids Research, 2010, 38, W523-W528.	14.5	34
85	How Does KCNE1 Regulate the Kv7.1 Potassium Channel? Model-Structure, Mutations, and Dynamics of the Kv7.1-KCNE1 Complex. Structure, 2012, 20, 1343-1352.	3.3	34
86	Interactions of Cationic-Hydrophobic Peptides with Lipid Bilayers: A Monte Carlo Simulation Method. Biophysical Journal, 2007, 93, 1858-1871.	0.5	32
87	Bridging Themes: Short Protein Segments Found in Different Architectures. Molecular Biology and Evolution, 2021, 38, 2191-2208.	8.9	32
88	Structural Determinants of Transmembrane Helical Proteins. Structure, 2009, 17, 1092-1103.	3.3	30
89	Introduction to Proteins. , 0, , .		30
90	A Model-Structure of a Periplasm-facing State of the NhaA Antiporter Suggests the Molecular Underpinnings of pH-induced Conformational Changes. Journal of Biological Chemistry, 2012, 287, 18249-18261.	3.4	29

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91	Monte Carlo simulations of peptide-membrane interactions with the MCPep web serverÂ. Nucleic Acids Research, 2012, 40, W358-W363.	14.5	28
92	On the evolution of proteinâ€"adenine binding. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 4701-4709.	7.1	28
93	Structure and Flexibility of the C-Ring in the Electromotor of Rotary FoF1-ATPase of Pea Chloroplasts. PLoS ONE, 2012, 7, e43045.	2.5	28
94	Membrane Interactions of Novicidin, a Novel Antimicrobial Peptide: Phosphatidylglycerol Promotes Bilayer Insertion. Journal of Physical Chemistry B, 2010, 114, 11053-11060.	2.6	25
95	Implicit solvent model estimates of the stability of model structures of the alamethicin channel. European Biophysics Journal, 2004, 33, 16-28.	2.2	24
96	Membrane integration of a mitochondrial signal-anchored protein does not require additional proteinaceous factors. Biochemical Journal, 2012, 442, 381-389.	3.7	23
97	Calculations Suggest a Pathway for the Transverse Diffusion of a Hydrophobic Peptide Across a Lipid Bilayer. Biophysical Journal, 2000, 79, 2322-2330.	0.5	21
98	Stability of an Ion Channel in Lipid Bilayers:Â Implicit Solvent Model Calculations with Gramicidinâ€. Biochemistry, 2002, 41, 6946-6954.	2.5	21
99	Harmonic generation in ionizing systems by the complex scaled adiabatic-switch method. Physical Review A, 1993, 48, 2437-2442.	2.5	20
100	Metal binding spectrum and model structure of the<i>Bacillus anthracis</i>virulence determinant MntA. Metallomics, 2015, 7, 1407-1419.	2.4	20
101	CyToStruct: Augmenting the Network Visualization of Cytoscape with the Power of Molecular Viewers. Structure, 2015, 23, 941-948.	3.3	20
102	Systems-Wide Prediction of Enzyme Promiscuity Reveals a New Underground Alternative Route for Pyridoxal 5â€™-Phosphate Production in E. coli. PLoS Computational Biology, 2016, 12, e1004705.	3.2	20
103	Multi-Stage Regulation, a Key to Reliable Adaptive Biochemical Pathways. Biophysical Journal, 2001, 81, 3016-3028.	0.5	19
104	Evolutionary analysis reveals collective properties and specificity in the C-type lectin and lectin-like domain superfamily. Proteins: Structure, Function and Bioinformatics, 2003, 53, 44-55.	2.6	19
105	Generation, Comparison, and Merging of Pathways between Protein Conformations: Gating in K-Channels. Biophysical Journal, 2008, 95, 3850-3860.	0.5	19
106	Cooperative Transition between Open and Closed Conformations in Potassium Channels. PLoS Computational Biology, 2008, 4, e1000164.	3.2	19
107	Efflux Pumps Represent Possible Evolutionary Convergence onto the Î²-Barrel Fold. Structure, 2018, 26, 1266-1274.e2.	3.3	19
108	Residue frequencies and pairing preferences at proteinâ€"protein interfaces. Proteins: Structure, Function and Bioinformatics, 2001, 43, 89.	2.6	19

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109	Has the code for protein translocation been broken?. Trends in Biochemical Sciences, 2006, 31, 192-196.	7.5	18
110	Prediction and simulation of motion in pairs of transmembrane Â-helices. Bioinformatics, 2007, 23, e212-e218.	4.1	18
111	The uncoupled ATPase activity of the ABC transporter BtuC2D2 leads to a hysteretic conformational change, conformational memory and improved activity. Scientific Reports, 2016, 6, 21696.	3.3	18
112	The Sigma-1 receptor is an ER-localized type II membrane protein. Journal of Biological Chemistry, 2021, 297, 101299.	3.4	18
113	Energetics of Colloids: Do Oppositely Charged Particles Necessarily Attract Each Other?. The Journal of Physical Chemistry, 1995, 99, 9642-9645.	2.9	17
114	In SilicoIdentification of Functional Protein Interfaces. Comparative and Functional Genomics, 2003, 4, 420-423.	2.0	17
115	Interactions of the M2Î´ Segment of the Acetylcholine Receptor with Lipid Bilayers: A Continuum-Solvent Model Study. Biophysical Journal, 2003, 85, 3687-3695.	0.5	17
116	NhaA antiporter functions using 10 helices, and an additional 2 contribute to assembly/stability. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5575-82.	7.1	17
117	Distinct Allosteric Networks Underlie Mechanistic Speciation of ABC Transporters. Structure, 2020, 28, 651-663.e5.	3.3	17
118	Study of MDM2 Binding to p53-Analogues: Affinity, Helicity, and Applicability to Drug Design. Journal of Chemical Information and Modeling, 2009, 49, 865-876.	5.4	16
119	The Transmembrane Helix Tilt May Be Determined by the Balance between Precession Entropy and Lipid Perturbation. Journal of Chemical Theory and Computation, 2012, 8, 2896-2904.	5.3	16
120	Theoretical calculations of the permeability of monensinâ€"cation complexes in model bio-membranes. Biochimica Et Biophysica Acta - Biomembranes, 2000, 1466, 221-233.	2.6	15
121	Structure of plant photosystem I-plastocyanin complex reveals strong hydrophobic interactions. Biochemical Journal, 2021, 478, 2371-2384.	3.7	15
122	The Structural Context of Disease-causing Mutations in Gap Junctions. Journal of Biological Chemistry, 2006, 281, 28958-28963.	3.4	14
123	Independent and Cooperative Motions of the Kv1.2 Channel: Voltage Sensing and Gating. Biophysical Journal, 2010, 98, 2179-2188.	0.5	14
124	The Î±-Helical Structure of Prodomains Promotes Translocation of Intrinsically Disordered Neuropeptide Hormones into the Endoplasmic Reticulum. Journal of Biological Chemistry, 2013, 288, 13961-13973.	3.4	14
125	Assigning transmembrane segments to helices in intermediate-resolution structures. Bioinformatics, 2004, 20, i122-i129.	4.1	13
126	Interaction of an Antimicrobial Peptide with Membranes: Experiments and Simulations with NKCS. Journal of Physical Chemistry B, 2010, 114, 4230-4237.	2.6	13

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127	ConTemplate Suggests Possible Alternative Conformations for a Query Protein of Known Structure. Structure, 2015, 23, 2162-2170.	3.3	13
128	Putative amino acid determinants of the emergence of the 2009 influenza A (H1N1) virus in the human population. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13522-13527.	7.1	12
129	Substrate recognition and ATPase activity of the E. coli cysteine/cystine ABC transporter YecSC-FliY. Journal of Biological Chemistry, 2020, 295, 5245-5256.	3.4	12
130	Two Conflicting NHE1 Model Structures: Compatibility with Experimental Data and Implications for the Transport Mechanism. Journal of Biological Chemistry, 2011, 286, le9.	3.4	11
131	On the regulatory role of dipeptidyl peptidase IV (ĩ…CD26ĩ…adenosine deaminase complexing protein) on adenosine deaminase activity. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2002, 1587, 21-30.	3.8	10
132	Representation of the Protein Universe using Classifications, Maps, and Networks. Israel Journal of Chemistry, 2014, 54, 1286-1292.	2.3	10
133	Changes to the dynamic nature of hemagglutinin and the emergence of the 2009 pandemic H1N1 influenza virus. Scientific Reports, 2015, 5, 12828.	3.3	10
134	Gram-negative outer-membrane proteins with multiple β-barrel domains. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	10
135	Structure, Dynamics and Implied Gating Mechanism of a Human Cyclic Nucleotide-Gated Channel. PLoS Computational Biology, 2014, 10, e1003976.	3.2	9
136	DynaFace: Discrimination between Obligatory and Non-obligatory Protein-Protein Interactions Based on the Complex's Dynamics. PLoS Computational Biology, 2015, 11, e1004461.	3.2	9
137	The Effect of Electrostatic Shielding on H Tunneling in R67 Dihydrofolate Reductase. ChemBioChem, 2009, 10, 2620-2623.	2.6	8
138	Structural motifs in protein cores and at protein–protein interfaces are different. Protein Science, 2021, 30, 381-390.	7.6	8
139	Long-range effects on the binding of the influenza HA to receptors are mediated by changes in the stability of a metastable HA conformation. Biochimica Et Biophysica Acta - Biomembranes, 2002, 1565, 81-90.	2.6	7
140	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
141	Dimeric and high-resolution structures of Chlamydomonas Photosystem I from a temperature-sensitive Photosystem II mutant. Communications Biology, 2021, 4, 1380.	4.4	6
142	Metal Coordination Is Crucial for Geranylgeranyl Diphosphate Synthase–Bisphosphonate Interactions: A Crystallographic and Computational Analysis. Molecular Pharmacology, 2019, 96, 580-588.	2.3	5
143	Global Dynamics Renders Protein Sites with High Functional Response. Journal of Physical Chemistry B, 2021, 125, 4734-4745.	2.6	5
144	Lifting the lid on pilus assembly. ELife, 2014, 3, .	6.0	4

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145	Editorial. Bioinformatics, 2013, 29, i1-i2.	4.1	3
146	C5 conserved region of hydrophilic Câ€terminal part of <i>Saccharomyces cerevisiae</i> Nha1 antiporter determines its requirement of Erv14 COPII cargo receptor for plasmaâ€membrane targeting. Molecular Microbiology, 2021, 115, 41-57.	2.5	3
147	Using ConSurf to Detect Functionally Important Regions in RNA. Current Protocols, 2021, 1, e270.	2.9	3
148	ConTemplate: exploiting the protein databank to propose ensemble of conformations of a query protein of known structure. BMC Bioinformatics, 2014, 15, .	2.6	2
149	Navigating Among Known Structures in Protein Space. Methods in Molecular Biology, 2019, 1851, 233-249.	0.9	2
150	Editorial overview: Sequences and topology: â€˜paths from sequence to structureâ€™. Current Opinion in Structural Biology, 2021, 68, vi-viii.	5.7	2
151	Structural Aspects of the Interaction of Nk-2 Derived Peptides with Cancer Cells. Biophysical Journal, 2010, 98, 277a.	0.5	1
152	Monte-Carlo Simulations of Peptide-Membrane Interactions: Web-Server. Biophysical Journal, 2010, 98, 487a.	0.5	1
153	Using ConTemplate and the PDB to explore conformational space: on the detection of rare protein conformations. BMC Bioinformatics, 2015, 16, .	2.6	1
154	Similarity between the Usher Plug and the Repeating Domain of an Iceâ€adhesin: Evolution via Surface Reshaping. Israel Journal of Chemistry, 2017, 57, 381-384.	2.3	1
155	Titratable transmembrane residues and a hydrophobic plug are essential for manganese import via the Bacillus anthracis ABC transporter MntBC-A. Journal of Biological Chemistry, 2021, 297, 101087.	3.4	1
156	The copper-linked Escherichia coli AZY operon: Structure, metal binding, and a possible physiological role in copper delivery. Journal of Biological Chemistry, 2022, 298, 101445.	3.4	1
157	CTR Structure and Mechanism. Biophysical Journal, 2009, 96, 2a.	0.5	0
158	Targeting The Voltage Sensor of Kv7 channels: Novel Strategies to Cure Hyperexcitability Disorders. Biophysical Journal, 2009, 96, 561a.	0.5	0
159	Model-Structure, Mutagenesis and Functional Characteristics of the Human Transporter, NHA2. Biophysical Journal, 2010, 98, 684a.	0.5	0
160	Human Copper Transporter 1: Model-Structure, Function and Motion. Biophysical Journal, 2010, 98, 646a.	0.5	0
161	Non-Toxin Gating Modifiers Reveal the Promiscuous Nature of the Voltage Sensor of Kv7.2 and TRPV1 Channels. Biophysical Journal, 2010, 98, 122a.	0.5	0
162	Functional Evaluation of Autism-Related Mutations in the Na+ (k+)/ H+ Exchanger NHE9. Biophysical Journal, 2011, 100, 247a-248a.	0.5	0

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163	Functional Evaluation of Autism Associated Mutations in Slc9A9 (NHE9). Biophysical Journal, 2013, 104, 22a.	0.5	0
164	Functional Evaluation of NHE6 Mutation Associated with Syndromic Autism and Tau Deposition. Biophysical Journal, 2014, 106, 366a.	0.5	0
165	The Na+/H+ Exchanger NHE6 Links Endosomal pH to Amyloid Pathologies in Alzheimer's Disease. Biophysical Journal, 2015, 108, 308a.	0.5	0
166	Navigating in the Protein Universe. Biophysical Journal, 2015, 108, 203a.	0.5	0
167	Protein Databank Survey Hints into the Emergence of Protein-Adenine Recognition in Evolution. Biophysical Journal, 2019, 116, 152a.	0.5	0
168	Using Phylogeny to Decipher Electrogenicity in Cation/Proton Antiporters. Biophysical Journal, 2019, 116, 554a.	0.5	0
169	Natural constraints, folding, motion, and structural stability in transmembrane helical proteins. , 2010, , 205-229.		0