

Yaakov Levy

List of Publications by Year in descending order

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107
papers

6,917
citations

71102

41
h-index

62596

80
g-index

109
all docs

109
docs citations

109
times ranked

7200
citing authors

#	ARTICLE	IF	CITATIONS
1	WATER MEDIATION IN PROTEIN FOLDING AND MOLECULAR RECOGNITION. Annual Review of Biophysics and Biomolecular Structure, 2006, 35, 389-415.	18.3	884
2	Effect of glycosylation on protein folding: A close look at thermodynamic stabilization. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8256-8261.	7.1	490
3	Protein topology determines binding mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 511-516.	7.1	318
4	Conformational Transitions of Adenylate Kinase: Switching by Cracking. Journal of Molecular Biology, 2007, 366, 1661-1671.	4.2	272
5	P versus Q: Structural reaction coordinates capture protein folding on smooth landscapes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 586-591.	7.1	215
6	Folding of glycoproteins: toward understanding the biophysics of the glycosylation code. Current Opinion in Structural Biology, 2009, 19, 524-533.	5.7	206
7	A Survey of Flexible Protein Binding Mechanisms and their Transition States Using Native Topology Based Energy Landscapes. Journal of Molecular Biology, 2005, 346, 1121-1145.	4.2	205
8	Fly-Casting in Protein-DNA Binding: Frustration between Protein Folding and Electrostatics Facilitates Target Recognition. Journal of the American Chemical Society, 2007, 129, 738-739.	13.7	199
9	Protein Sliding along DNA: Dynamics and Structural Characterization. Journal of Molecular Biology, 2009, 385, 1087-1097.	4.2	199
10	Intrinsically disordered regions as affinity tuners in protein-DNA interactions. Molecular BioSystems, 2012, 8, 47-57.	2.9	176
11	Water and proteins: A love-hate relationship. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 3325-3326.	7.1	168
12	Domain swapping is a consequence of minimal frustration. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13786-13791.	7.1	164
13	Searching DNA via a "Monkey Bar" Mechanism: The Significance of Disordered Tails. Journal of Molecular Biology, 2010, 396, 674-684.	4.2	135
14	Nonnative Electrostatic Interactions Can Modulate Protein Folding: Molecular Dynamics with a Grain of Salt. Journal of Molecular Biology, 2009, 393, 527-542.	4.2	128
15	DNA search efficiency is modulated by charge composition and distribution in the intrinsically disordered tail. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21004-21009.	7.1	110
16	Frustration in protein-DNA binding influences conformational switching and target search kinetics. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17957-17962.	7.1	109
17	Electronic Transport via Homopeptides: The Role of Side Chains and Secondary Structure. Journal of the American Chemical Society, 2015, 137, 9617-9626.	13.7	101
18	Asymmetrical roles of zinc fingers in dynamic DNA-scanning process by the inducible transcription factor Egr-1. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1724-E1732.	7.1	90

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19	Balancing between affinity and speed in target DNA search by zinc-finger proteins via modulation of dynamic conformational ensemble. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5142-9.	7.1	90
20	The Folding and Dimerization of HIV-1 Protease: Evidence for a Stable Monomer from Simulations. Journal of Molecular Biology, 2004, 340, 67-79.	4.2	89
21	Assessment of CASP8 structure predictions for template free targets. Proteins: Structure, Function and Bioinformatics, 2009, 77, 50-65.	2.6	89
22	Symmetry and frustration in protein energy landscapes: A near degeneracy resolves the Rop dimer-folding mystery. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2373-2378.	7.1	88
23	Mechanisms of Protein Assembly: Lessons from Minimalist Models. Accounts of Chemical Research, 2006, 39, 135-142.	15.6	85
24	Cold denaturation induces inversion of dipole and spin transfer in chiral peptide monolayers. Nature Communications, 2016, 7, 10744.	12.8	83
25	Assembly Mechanism of Mucin and von Willebrand Factor Polymers. Cell, 2020, 183, 717-729.e16.	28.9	79
26	Capillarity theory for the fly-casting mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2746-2750.	7.1	73
27	Ubiquitin not only serves as a tag but also assists degradation by inducing protein unfolding. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2001-2006.	7.1	72
28	Obstacles May Facilitate and Direct DNA Search by Proteins. Biophysical Journal, 2013, 104, 2042-2050.	0.5	72
29	Confinement effects on the kinetics and thermodynamics of protein dimerization. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5517-5522.	7.1	69
30	Context-Dependent Effects of Asparagine Glycosylation on Pin WW Folding Kinetics and Thermodynamics. Journal of the American Chemical Society, 2010, 132, 15359-15367.	13.7	69
31	Facilitated DNA Search by Multidomain Transcription Factors: Cross Talk via a Flexible Linker. Biophysical Journal, 2010, 99, 1202-1211.	0.5	67
32	Quantitative criteria for native energetic heterogeneity influences in the prediction of protein folding kinetics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 434-439.	7.1	64
33	Stabilization of a protein conferred by an increase in folded state entropy. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10628-10633.	7.1	64
34	Disordered Tails of Homeodomains Facilitate DNA Recognition by Providing a Trade-Off between Folding and Specific Binding. Journal of the American Chemical Society, 2009, 131, 15084-15085.	13.7	61
35	Sliding of p53 along DNA Can Be Modulated by Its Oligomeric State and by Cross-Talks between Its Constituent Domains. Journal of Molecular Biology, 2011, 408, 335-355.	4.2	60
36	Simulations of proteins with inhomogeneous degrees of freedom: The effect of thermostats. Journal of Computational Chemistry, 2008, 29, 1992-1998.	3.3	59

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37	Criteria for Selecting PEGylation Sites on Proteins for Higher Thermodynamic and Proteolytic Stability. <i>Journal of the American Chemical Society</i> , 2014, 136, 17547-17560.	13.7	54
38	Mutations as trapdoors to two competing native conformations of the Rop-dimer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17674-17679.	7.1	53
39	Intrinsic Disorder in Ubiquitination Substrates. <i>Journal of Molecular Biology</i> , 2011, 412, 319-324.	4.2	52
40	Charge pattern affects the structure and dynamics of polyampholyte condensates. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 19368-19375.	2.8	51
41	Structure, stability and specificity of the binding of ssDNA and ssRNA with proteins. <i>PLoS Computational Biology</i> , 2019, 15, e1006768.	3.2	49
42	Search by proteins for their DNA target site: 1. The effect of DNA conformation on protein sliding. <i>Nucleic Acids Research</i> , 2014, 42, 12404-12414.	14.5	47
43	Overcoming residual frustration in domain-swapping: the roles of disulfide bonds in dimerization and aggregation. <i>Physical Biology</i> , 2005, 2, S44-S55.	1.8	45
44	Glycosylation May Reduce Protein Thermodynamic Stability by Inducing a Conformational Distortion. <i>Journal of Physical Chemistry Letters</i> , 2015, 6, 3572-3577.	4.6	43
45	Biophysics of Phase Separation of Disordered Proteins Is Governed by Balance between Short- And Long-Range Interactions. <i>Journal of Physical Chemistry B</i> , 2021, 125, 2202-2211.	2.6	42
46	Weak Frustration Regulates Sliding and Binding Kinetics on Rugged Protein-DNA Landscapes. <i>Journal of Physical Chemistry B</i> , 2013, 117, 13005-13014.	2.6	39
47	Folding of multidomain proteins: Biophysical consequences of tethering even in apparently independent folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2780-2798.	2.6	37
48	Molecular determinants of the interactions between proteins and ssDNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5033-5038.	7.1	37
49	On the coupling between the dynamics of protein and water. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 8243-8257.	2.8	33
50	Proteins: molecules defined by their trade-offs. <i>Current Opinion in Structural Biology</i> , 2020, 60, 50-56.	5.7	32
51	Search by proteins for their DNA target site: 2. The effect of DNA conformation on the dynamics of multidomain proteins. <i>Nucleic Acids Research</i> , 2014, 42, 12415-12424.	14.5	31
52	Asymmetric DNA-Search Dynamics by Symmetric Dimeric Proteins. <i>Biochemistry</i> , 2013, 52, 5335-5344.	2.5	30
53	Nonnative interactions regulate folding and switching of myristoylated protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17839-17844.	7.1	29
54	Shortening a loop can increase protein native state entropy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 2137-2146.	2.6	27

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55	Thermodynamic Protein Destabilization by GFP Tagging: A Case of Interdomain Allostery. <i>Biophysical Journal</i> , 2015, 109, 1157-1162.	0.5	27
56	Cross-linking reveals laminin coiled-coil architecture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13384-13389.	7.1	27
57	Protein Assembly and Building Blocks: Beyond the Limits of the LEGO Brick Metaphor. <i>Biochemistry</i> , 2017, 56, 5040-5048.	2.5	27
58	Coarse-grained models for studying protein diffusion along <scp>DNA</scp>. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2016, 6, 515-531.	14.6	25
59	Quantifying the two-state facilitated diffusion model of protein-DNA interactions. <i>Nucleic Acids Research</i> , 2019, 47, 5530-5538.	14.5	25
60	Tubulin tails and their modifications regulate protein diffusion on microtubules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8876-8883.	7.1	25
61	Diffusion of ring-shaped proteins along DNA: case study of sliding clamps. <i>Nucleic Acids Research</i> , 2018, 46, 5935-5949.	14.5	24
62	ssDNA diffuses along replication protein A via a reptation mechanism. <i>Nucleic Acids Research</i> , 2020, 48, 1701-1714.	14.5	24
63	The origins and evolution of ubiquitination sites. <i>Molecular BioSystems</i> , 2012, 8, 1865.	2.9	23
64	Mechanism of Facilitated Diffusion during a DNA Search in Crowded Environments. <i>Journal of Physical Chemistry B</i> , 2016, 120, 11113-11122.	2.6	23
65	Energy Landscape Analysis of Protein Dimers. <i>Israel Journal of Chemistry</i> , 2004, 44, 281-297.	2.3	22
66	Speed-stability paradox in DNA-scanning by zinc-finger proteins. <i>Transcription</i> , 2013, 4, 58-61.	3.1	22
67	The "Monkey-Bar" Mechanism for Searching for the DNA Target Site: The Molecular Determinants. <i>Israel Journal of Chemistry</i> , 2014, 54, 1374-1381.	2.3	22
68	Arc-Repressor Dimerization on DNA: Folding Rate Enhancement by Colocalization. <i>Biophysical Journal</i> , 2009, 96, 4212-4220.	0.5	21
69	Folding of Elongated Proteins: Conventional or Anomalous?. <i>Journal of the American Chemical Society</i> , 2008, 130, 14253-14262.	13.7	19
70	Negatively Charged Disordered Regions are Prevalent and Functionally Important Across Proteomes. <i>Journal of Molecular Biology</i> , 2022, 434, 167660.	4.2	19
71	Nonspecific yet decisive: Ubiquitination can affect the native-state dynamics of the modified protein. <i>Protein Science</i> , 2015, 24, 1580-1592.	7.6	18
72	Huntingtin's N-Terminus Rearrangements in the Presence of Membranes: A Joint Spectroscopic and Computational Perspective. <i>ACS Chemical Neuroscience</i> , 2019, 10, 472-481.	3.5	18

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73	Dynamic Autoinhibition of the HMGB1 Protein via Electrostatic Fuzzy Interactions of Intrinsically Disordered Regions. <i>Journal of Molecular Biology</i> , 2021, 433, 167122.	4.2	18
74	Asymmetric base-pair opening drives helicase unwinding dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22471-22477.	7.1	15
75	The Folding Energy Landscape of the Dimerization Domain of Escherichia coli Trp Repressor: A Joint Experimental and Theoretical Investigation. <i>Journal of Molecular Biology</i> , 2006, 363, 262-278.	4.2	14
76	Variations in Core Packing of GP2 from Old World Mammarenaviruses in their Post-Fusion Conformations Affect Membrane-Fusion Efficiencies. <i>Journal of Molecular Biology</i> , 2019, 431, 2095-2111.	4.2	14
77	Water organization between oppositely charged surfaces: Implications for protein sliding along DNA. <i>Journal of Chemical Physics</i> , 2015, 142, 085102.	3.0	13
78	Protein diffusion along DNA: on the effect of roadblocks and crowders. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2016, 49, 494003.	2.1	13
79	Entropy-enthalpy compensation in conjugated proteins. <i>Chemical Physics</i> , 2018, 514, 95-105.	1.9	13
80	Protein Diffusion on Charged Biopolymers: DNA versus Microtubule. <i>Biophysical Journal</i> , 2020, 118, 3008-3018.	0.5	13
81	Affinity of disordered protein complexes is modulated by entropy energy reinforcement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	13
82	Stability Effects of Protein Mutations: The Role of Long-Range Contacts. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11450-11459.	2.6	12
83	What Are the Molecular Requirements for Protein Sliding along DNA?. <i>Journal of Physical Chemistry B</i> , 2021, 125, 3119-3131.	2.6	12
84	Analyzing Change in Protein Stability Associated with Single Point Deletions in a Newly Defined Protein Structure Database. <i>Journal of Proteome Research</i> , 2019, 18, 1402-1410.	3.7	11
85	Entropic Contributions to Protein Stability. <i>Israel Journal of Chemistry</i> , 2020, 60, 705-712.	2.3	10
86	Molecular principles of recruitment and dynamics of guest proteins in liquid droplets. <i>Scientific Reports</i> , 2021, 11, 19323.	3.3	10
87	Communication: Folding of glycosylated proteins under confinement. <i>Journal of Chemical Physics</i> , 2011, 135, 141104.	3.0	9
88	Sliding Dynamics Along DNA: A Molecular Perspective. <i>RSC Biomolecular Sciences</i> , 2012, , 236-262.	0.4	8
89	Intersegmental transfer of proteins between DNA regions in the presence of crowding. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 30562-30569.	2.8	8
90	Sliding Mechanism at a Coiled-Coil Interface. <i>Biophysical Journal</i> , 2019, 116, 1228-1238.	0.5	8

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91	Prerecognition Diffusion Mechanism of Human DNA Mismatch Repair Proteins along DNA: Msh2-Msh3 versus Msh2-Msh6. <i>Biochemistry</i> , 2020, 59, 4822-4832.	2.5	7
92	Balance between asymmetry and abundance in multi-domain DNA-binding proteins may regulate the kinetics of their binding to DNA. <i>PLoS Computational Biology</i> , 2020, 16, e1007867.	3.2	7
93	Characterization of the unfolded state of repeat proteins. <i>HFSP Journal</i> , 2008, 2, 405-415.	2.5	6
94	Modulating Microtubules: A Molecular Perspective on the Effects of Tail Modifications. <i>Journal of Molecular Biology</i> , 2021, 433, 166988.	4.2	6
95	Binding of interferon reduces the force of unfolding for interferon receptor 1. <i>PLoS ONE</i> , 2017, 12, e0175413.	2.5	6
96	MODULATING PROTEIN-DNA INTERACTIONS BY POST-TRANSLATIONAL MODIFICATIONS AT DISORDERED REGIONS., 2011, , .		5
97	Mechanism of the formation of the RecA-ssDNA nucleoprotein filament structure: a coarse-grained approach. <i>Molecular BioSystems</i> , 2017, 13, 2697-2703.	2.9	5
98	An NMR Confirmation for Increased Folded State Entropy Following Loop Truncation. <i>Journal of Physical Chemistry B</i> , 2018, 122, 10855-10860.	2.6	5
99	Identification and Rationalization of Kinetic Folding Intermediates for a Low-Density Lipoprotein Receptor Ligand-Binding Module. <i>Biochemistry</i> , 2018, 57, 4776-4787.	2.5	4
100	Does PCNA diffusion on DNA follow a rotation-coupled translation mechanism?. <i>Nature Communications</i> , 2020, 11, 5000.	12.8	4
101	Folding of Conjugated Proteins. <i>Annual Reports in Computational Chemistry</i> , 2010, 6, 263-277.	1.7	3
102	Understanding Hydrogen-Bond Patterns in Proteins using a Novel Statistical Model. <i>Nature Precedings</i> , 2008, , .	0.1	0
103	Inside Cover Image, Volume 6, Issue 5. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2016, 6, ii-ii.	14.6	0
104	Title is missing!. , 2020, 16, e1007867.		0
105	Title is missing!. , 2020, 16, e1007867.		0
106	Title is missing!. , 2020, 16, e1007867.		0
107	Title is missing!. , 2020, 16, e1007867.		0