

Eugene Shakhnovich

List of Publications by Year in descending order

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35
papers

3,443
citations

471371

17
h-index

434063

31
g-index

40
all docs

40
docs citations

40
times ranked

2517
citing authors

#	ARTICLE	IF	CITATIONS
1	How does a protein fold?. Nature, 1994, 369, 248-251.	13.7	934
2	Kinetics of Protein Folding. Journal of Molecular Biology, 1994, 235, 1614-1636.	2.0	513
3	Protein Folding Thermodynamics and Dynamics:Â Where Physics, Chemistry, and Biology Meet. Chemical Reviews, 2006, 106, 1559-1588.	23.0	332
4	Protein Folding Theory: From Lattice to All-Atom Models. Annual Review of Biophysics and Biomolecular Structure, 2001, 30, 361-396.	18.3	326
5	Enumeration of all compact conformations of copolymers with random sequence of links. Journal of Chemical Physics, 1990, 93, 5967-5971.	1.2	240
6	The interface of protein structure, protein biophysics, and molecular evolution. Protein Science, 2012, 21, 769-785.	3.1	188
7	On the origin and highly likely completeness of single-domain protein structures. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2605-2610.	3.3	182
8	Evolutionary conservation of the folding nucleus1 Edited by A. R. Fersht. Journal of Molecular Biology, 2001, 308, 123-129.	2.0	116
9	Topology of protein interaction network shapes protein abundances and strengths of their functional and nonspecific interactions. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4258-4263.	3.3	94
10	Protein structure and evolutionary history determine sequence space topology. Genome Research, 2005, 15, 385-392.	2.4	82
11	Statistical mechanics of proteins with "evolutionary selected"™™ sequences. Physical Review E, 1994, 50, 1303-1312.	0.8	69
12	A strategy for detecting the conservation of folding-nucleus residues in protein superfamilies. Folding & Design, 1998, 3, 239-251.	4.5	49
13	Factors that affect the folding ability of proteins. , 1999, 35, 34-40.		45
14	Cotranslational folding allows misfolding-prone proteins to circumvent deep kinetic traps. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1485-1495.	3.3	44
15	Benchmarking Inverse Statistical Approaches for Protein Structure and Design with Exactly Solvable Models. PLoS Computational Biology, 2016, 12, e1004889.	1.5	43
16	Stability of the Influenza Virus Hemagglutinin Protein Correlates with Evolutionary Dynamics. MSphere, 2018, 3, .	1.3	31
17	On the role of conformational geometry in protein folding. Journal of Chemical Physics, 1999, 111, 10375-10380.	1.2	28
18	Searching the Sequence Space for Potent Aptamers Using SELEX in Silico. Journal of Chemical Theory and Computation, 2015, 11, 5939-5946.	2.3	27

#	ARTICLE	IF	CITATIONS
19	Rational Design of Novel Allosteric Dihydrofolate Reductase Inhibitors Showing Antibacterial Effects on Drug-Resistant <i>Escherichia coli</i> Escape Variants. ACS Chemical Biology, 2017, 12, 1848-1857.	1.6	22
20	Development of antibacterial compounds that constrain evolutionary pathways to resistance. ELife, 2021, 10, .	2.8	12
21	Exploring the Mutational Robustness of Nucleic Acids by Searching Genotype Neighborhoods in Sequence Space. Journal of Physical Chemistry Letters, 2017, 8, 407-414.	2.1	11
22	Validation of DBFOLD: An efficient algorithm for computing folding pathways of complex proteins. PLoS Computational Biology, 2020, 16, e1008323.	1.5	11
23	Freezing in polyampholytes globules: Influence of the long-range nature of the interaction. Journal of Chemical Physics, 1999, 111, 772-785.	1.2	8
24	Frozen phases with re-entrant transition for random heteropolymers with composition specific and annealed cross-links. Journal of Chemical Physics, 1997, 107, 1247-1258.	1.2	7
25	Phase diagram analysis of random heteropolymers with composition specific and quenched cross-links. Journal of Chemical Physics, 1998, 109, 2947-2958.	1.2	7
26	Protein Dynamics: From the Native to the Unfolded State and Back Again. Jerusalem Symposia on Quantum Chemistry and Biochemistry, 1995, , 69-84.	0.2	5
27	Disordered heteropolymers with cross-links $\hat{\epsilon}^{\epsilon}$ phase diagram and conformational transitions. Chemical Physics Letters, 1999, 303, 355-362.	1.2	4
28	Orientational ordering in sequence-disordered liquid crystalline polymers. Chemical Physics Letters, 2000, 325, 323-329.	1.2	4
29	Protein folding roller coaster, one molecule at a time. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11823-11824.	3.3	4
30	Exotic phase transitions in disordered globular networks. Journal of Chemical Physics, 2001, 114, 10968-10976.	1.2	2
31	Protein dynamics: From the native to the unfolded state and back again. Molecular Engineering, 1995, 5, 55-70.	0.2	1
32	Field theory and segmental alignment analysis for a solution of sequence disordered liquid crystalline polymers. Journal of Chemical Physics, 2002, 116, 3134-3140.	1.2	1
33	Soluble oligomerization provides a beneficial fitness effect on destabilizing mutations.. Nature Precedings, 2011, , .	0.1	0
34	Phase Transformations and Orientational Ordering in Chemically Disordered Polymers $\hat{\epsilon}^{\epsilon}$ a Modern Primer. , 2004, , 455-484.		0
35	Protein Dynamics. , 1996, , 113-126.		0