

Joanna Sulkowski

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

1,392
citations

331259

21
h-index

360668

35
g-index

52
all docs

52
docs citations

52
times ranked

793
citing authors

#	ARTICLE	IF	CITATIONS
1	KnotProt: a database of proteins with knots and slipknots. <i>Nucleic Acids Research</i> , 2015, 43, D306-D314.	6.5	159
2	Topological knots and links in proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3415-3420.	3.3	101
3	Methyl transfer by substrate signaling from a knotted protein fold. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 941-948.	3.6	74
4	Complex lasso: new entangled motifs in proteins. <i>Scientific Reports</i> , 2016, 6, 36895.	1.6	73
5	KnotProt 2.0: a database of proteins with knots and other entangled structures. <i>Nucleic Acids Research</i> , 2019, 47, D367-D375.	6.5	70
6	Identifying knots in proteins. <i>Biochemical Society Transactions</i> , 2013, 41, 533-537.	1.6	65
7	Knotted a Protein in Explicit Solvent. <i>Journal of Physical Chemistry Letters</i> , 2013, 4, 3570-3573.	2.1	61
8	Hysteresis as a Marker for Complex, Overlapping Landscapes in Proteins. <i>Journal of Physical Chemistry Letters</i> , 2013, 4, 180-188.	2.1	52
9	On folding of entangled proteins: knots, lassos, links and $\langle \text{mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" altimg="si1.svg" \rangle \langle \text{mml:mi} \rangle \langle \text{mml:mi} \rangle \langle \text{mml:math} \rangle$ -curves. <i>Current Opinion in Structural Biology</i> , 2020, 60, 131-141.	2.6	52
10	In Search of Functional Advantages of Knots in Proteins. <i>PLoS ONE</i> , 2016, 11, e0165986.	1.1	51
11	LassoProt: server to analyze biopolymers with lassos. <i>Nucleic Acids Research</i> , 2016, 44, W383-W389.	6.5	50
12	PDBe-KB: collaboratively defining the biological context of structural data. <i>Nucleic Acids Research</i> , 2022, 50, D534-D542.	6.5	46
13	To Tie or Not to Tie? That Is the Question. <i>Polymers</i> , 2017, 9, 454.	2.0	45
14	Pierced Lasso Bundles Are a New Class of Knot-like Motifs. <i>PLoS Computational Biology</i> , 2014, 10, e1003613.	1.5	41
15	LinkProt: a database collecting information about biological links. <i>Nucleic Acids Research</i> , 2017, 45, D243-D249.	6.5	38
16	Connecting Thermal and Mechanical Protein (Un)folding Landscapes. <i>Biophysical Journal</i> , 2014, 107, 2950-2961.	0.2	36
17	Protein Knotting by Active Threading of Nascent Polypeptide Chain Exiting from the Ribosome Exit Channel. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11616-11625.	1.2	36
18	Proteins' Knotty Problems. <i>Journal of Molecular Biology</i> , 2019, 431, 244-257.	2.0	36

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19	Topoly: Python package to analyze topology of polymers. Briefings in Bioinformatics, 2021, 22, .	3.2	32
20	TrmD. The Enzymes, 2017, 41, 89-115.	0.7	24
21	PyLasso: a PyMOL plugin to identify lassos. Bioinformatics, 2017, 33, 3819-3821.	1.8	23
22	The exclusive effects of chaperonin on the behavior of proteins with 52 knot. PLoS Computational Biology, 2018, 14, e1005970.	1.5	23
23	Knotting and unknotting proteins in the chaperonin cage: Effects of the excluded volume. PLoS ONE, 2017, 12, e0176744.	1.1	21
24	Prediction of the optimal set of contacts to fold the smallest knotted protein. Journal of Physics Condensed Matter, 2015, 27, 354109.	0.7	19
25	SARS-CoV-2 Papain-Like Protease Potential Inhibitorsâ€™ In Silico Quantitative Assessment. International Journal of Molecular Sciences, 2021, 22, 3957.	1.8	19
26	Mg ²⁺ -Dependent Methyl Transfer by a Knotted Protein: A Molecular Dynamics Simulation and Quantum Mechanics Study. ACS Catalysis, 2020, 10, 8058-8068.	5.5	15
27	PconsFam: An Interactive Database of Structure Predictions of Pfam Families. Journal of Molecular Biology, 2019, 431, 2442-2448.	2.0	14
28	Restriction of S-adenosylmethionine conformational freedom by knotted protein binding sites. PLoS Computational Biology, 2020, 16, e1007904.	1.5	13
29	GapRepairer: a server to model a structural gap and validate it using topological analysis. Bioinformatics, 2018, 34, 3300-3307.	1.8	10
30	KnotGenome: A server to analyze entanglements of chromosomes. Nucleic Acids Research, 2018, 46, W17-W24.	6.5	10
31	PyLink: a PyMOL plugin to identify links. Bioinformatics, 2019, 35, 3166-3168.	1.8	9
32	Knot_pullâ€™ python package for biopolymer smoothing and knot detection. Bioinformatics, 2020, 36, 953-955.	1.8	8
33	Supercoiling in a Protein Increases its Stability. Physical Review Letters, 2019, 123, 138102.	2.9	8
34	Statistical Properties of Lasso-Shape Polymers and Their Implications for Complex Lasso Proteins Function. Polymers, 2019, 11, 707.	2.0	7
35	Genus for biomolecules. Nucleic Acids Research, 2020, 48, D1129-D1135.	6.5	6
36	GLN: a method to reveal unique properties of lasso type topology in proteins. Scientific Reports, 2020, 10, 15186.	1.6	6

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37	Genus trace reveals the topological complexity and domain structure of biomolecules. Scientific Reports, 2018, 8, 17537.	1.6	5
38	Defining and detecting links in chromosomes. Scientific Reports, 2019, 9, 11753.	1.6	5
39	DCA-MOL: A PyMOL Plugin To Analyze Direct Evolutionary Couplings. Journal of Chemical Information and Modeling, 2019, 59, 625-629.	2.5	5
40	The Folding of Knotted Proteins: Distinguishing the Distinct Behavior of Shallow and Deep Knots. Israel Journal of Chemistry, 2020, 60, 713-724.	1.0	5
41	Slipknotted and unknotted monovalent cation-proton antiporters evolved from a common ancestor. PLoS Computational Biology, 2021, 17, e1009502.	1.5	5
42	Entangled Proteins: Knots, Slipknots, Links, and Lassos. Springer Series in Solid-state Sciences, 2018, , 201-226.	0.3	4
43	Lasso Proteins—Unifying Cysteine Knots and Miniproteins. Polymers, 2021, 13, 3988.	2.0	3
44	The APS-bracket “ A topological tool to classify lasso proteins, RNAs and other tadpole-like structures. Reactive and Functional Polymers, 2018, 132, 19-25.	2.0	2
45	Restriction of S-adenosylmethionine conformational freedom by knotted protein binding sites. , 2020, 16, e1007904.		0
46	Restriction of S-adenosylmethionine conformational freedom by knotted protein binding sites. , 2020, 16, e1007904.		0
47	Restriction of S-adenosylmethionine conformational freedom by knotted protein binding sites. , 2020, 16, e1007904.		0
48	Restriction of S-adenosylmethionine conformational freedom by knotted protein binding sites. , 2020, 16, e1007904.		0
49	Restriction of S-adenosylmethionine conformational freedom by knotted protein binding sites. , 2020, 16, e1007904.		0
50	Restriction of S-adenosylmethionine conformational freedom by knotted protein binding sites. , 2020, 16, e1007904.		0