

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	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	6.5	46
2	Topoly: Python package to analyze topology of polymers. Briefings in Bioinformatics, 2021, 22, .	3.2	32
3	SARS-CoV-2 Papain-Like Protease Potential Inhibitorsâ€™ In Silico Quantitative Assessment. International Journal of Molecular Sciences, 2021, 22, 3957.	1.8	19
4	Slipknotted and unknotted monovalent cation-proton antiporters evolved from a common ancestor. PLoS Computational Biology, 2021, 17, e1009502.	1.5	5
5	Lasso Proteinsâ€™ Unifying Cysteine Knots and Miniproteins. Polymers, 2021, 13, 3988.	2.0	3
6	Knot_pullâ€™ python package for biopolymer smoothing and knot detection. Bioinformatics, 2020, 36, 953-955.	1.8	8
7	Genus for biomolecules. Nucleic Acids Research, 2020, 48, D1129-D1135.	6.5	6
8	GLN: a method to reveal unique properties of lasso type topology in proteins. Scientific Reports, 2020, 10, 15186.	1.6	6
9	Restriction of S-adenosylmethionine conformational freedom by knotted protein binding sites. PLoS Computational Biology, 2020, 16, e1007904.	1.5	13
10	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
11	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
12	On folding of entangled proteins: knots, lassos, links and \mathbb{R}^3 -curves. Current Opinion in Structural Biology, 2020, 60, 131-141.	2.6	52
13	Restriction of S-adenosylmethionine conformational freedom by knotted protein binding sites. , 2020, 16, e1007904.		0
14	Restriction of S-adenosylmethionine conformational freedom by knotted protein binding sites. , 2020, 16, e1007904.		0
15	Restriction of S-adenosylmethionine conformational freedom by knotted protein binding sites. , 2020, 16, e1007904.		0
16	Restriction of S-adenosylmethionine conformational freedom by knotted protein binding sites. , 2020, 16, e1007904.		0
17	Restriction of S-adenosylmethionine conformational freedom by knotted protein binding sites. , 2020, 16, e1007904.		0
18	Restriction of S-adenosylmethionine conformational freedom by knotted protein binding sites. , 2020, 16, e1007904.		0

#	ARTICLE	IF	CITATIONS
19	Defining and detecting links in chromosomes. <i>Scientific Reports</i> , 2019, 9, 11753.	1.6	5
20	PyLink: a PyMOL plugin to identify links. <i>Bioinformatics</i> , 2019, 35, 3166-3168.	1.8	9
21	Supercoiling in a Protein Increases its Stability. <i>Physical Review Letters</i> , 2019, 123, 138102.	2.9	8
22	Statistical Properties of Lasso-Shape Polymers and Their Implications for Complex Lasso Proteins Function. <i>Polymers</i> , 2019, 11, 707.	2.0	7
23	PconsFam: An Interactive Database of Structure Predictions of Pfam Families. <i>Journal of Molecular Biology</i> , 2019, 431, 2442-2448.	2.0	14
24	DCA-MOL: A PyMOL Plugin To Analyze Direct Evolutionary Couplings. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 625-629.	2.5	5
25	Proteins' Knotty Problems. <i>Journal of Molecular Biology</i> , 2019, 431, 244-257.	2.0	36
26	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
27	GapRepairer: a server to model a structural gap and validate it using topological analysis. <i>Bioinformatics</i> , 2018, 34, 3300-3307.	1.8	10
28	Entangled Proteins: Knots, Slipknots, Links, and Lassos. <i>Springer Series in Solid-state Sciences</i> , 2018, , 201-226.	0.3	4
29	Genus trace reveals the topological complexity and domain structure of biomolecules. <i>Scientific Reports</i> , 2018, 8, 17537.	1.6	5
30	KnotGenome: A server to analyze entanglements of chromosomes. <i>Nucleic Acids Research</i> , 2018, 46, W17-W24.	6.5	10
31	The APS-bracket " A topological tool to classify lasso proteins, RNAs and other tadpole-like structures. <i>Reactive and Functional Polymers</i> , 2018, 132, 19-25.	2.0	2
32	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
33	The exclusive effects of chaperonin on the behavior of proteins with 52 knot. <i>PLoS Computational Biology</i> , 2018, 14, e1005970.	1.5	23
34	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
35	PyLasso: a PyMOL plugin to identify lassos. <i>Bioinformatics</i> , 2017, 33, 3819-3821.	1.8	23
36	TrmD. <i>The Enzymes</i> , 2017, 41, 89-115.	0.7	24

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37	LinkProt: a database collecting information about biological links. <i>Nucleic Acids Research</i> , 2017, 45, D243-D249.	6.5	38
38	To Tie or Not to Tie? That Is the Question. <i>Polymers</i> , 2017, 9, 454.	2.0	45
39	Knotting and unknotting proteins in the chaperonin cage: Effects of the excluded volume. <i>PLoS ONE</i> , 2017, 12, e0176744.	1.1	21
40	Complex lasso: new entangled motifs in proteins. <i>Scientific Reports</i> , 2016, 6, 36895.	1.6	73
41	Methyl transfer by substrate signaling from a knotted protein fold. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 941-948.	3.6	74
42	LassoProt: server to analyze biopolymers with lassos. <i>Nucleic Acids Research</i> , 2016, 44, W383-W389.	6.5	50
43	In Search of Functional Advantages of Knots in Proteins. <i>PLoS ONE</i> , 2016, 11, e0165986.	1.1	51
44	Prediction of the optimal set of contacts to fold the smallest knotted protein. <i>Journal of Physics Condensed Matter</i> , 2015, 27, 354109.	0.7	19
45	KnotProt: a database of proteins with knots and slipknots. <i>Nucleic Acids Research</i> , 2015, 43, D306-D314.	6.5	159
46	Pierced Lasso Bundles Are a New Class of Knot-like Motifs. <i>PLoS Computational Biology</i> , 2014, 10, e1003613.	1.5	41
47	Connecting Thermal and Mechanical Protein (Un)folded Landscapes. <i>Biophysical Journal</i> , 2014, 107, 2950-2961.	0.2	36
48	Identifying knots in proteins. <i>Biochemical Society Transactions</i> , 2013, 41, 533-537.	1.6	65
49	Knotting a Protein in Explicit Solvent. <i>Journal of Physical Chemistry Letters</i> , 2013, 4, 3570-3573.	2.1	61
50	Hysteresis as a Marker for Complex, Overlapping Landscapes in Proteins. <i>Journal of Physical Chemistry Letters</i> , 2013, 4, 180-188.	2.1	52