

Stanisław Dunin-Horkawicz

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

3,419
citations

236925

25
h-index

175258

52
g-index

54
all docs

54
docs citations

54
times ranked

5006
citing authors

#	ARTICLE	IF	CITATIONS
1	MODOMICS: a database of RNA modification pathwaysâ€™2013 update. <i>Nucleic Acids Research</i> , 2012, 41, D262-D267.	14.5	933
2	MODOMICS: a database of RNA modification pathways. <i>Nucleic Acids Research</i> , 2006, 34, D145-D149.	14.5	216
3	MODOMICS: a database of RNA modification pathways. 2008 update. <i>Nucleic Acids Research</i> , 2009, 37, D118-D121.	14.5	184
4	<i>RNA-Puzzles</i> Round II: assessment of RNA structure prediction programs applied to three large RNA structures. <i>Rna</i> , 2015, 21, 1066-1084.	3.5	161
5	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. <i>Rna</i> , 2017, 23, 655-672.	3.5	158
6	Structural and evolutionary bioinformatics of the SPOUT superfamily of methyltransferases. <i>BMC Bioinformatics</i> , 2007, 8, 73.	2.6	137
7	The RNase H-like superfamily: new members, comparative structural analysis and evolutionary classification. <i>Nucleic Acids Research</i> , 2014, 42, 4160-4179.	14.5	135
8	DeepCoilâ€™a fast and accurate prediction of coiled-coil domains in protein sequences. <i>Bioinformatics</i> , 2019, 35, 2790-2795.	4.1	131
9	Rational Design of Helical Nanotubes from Self-Assembly of Coiled-Coil Lock Washers. <i>Journal of the American Chemical Society</i> , 2013, 135, 15565-15578.	13.7	112
10	Phylogenomic analysis of the GIY-YIG nuclease superfamily. <i>BMC Genomics</i> , 2006, 7, 98.	2.8	102
11	Mechanism of Regulation of Receptor Histidine Kinases. <i>Structure</i> , 2012, 20, 56-66.	3.3	87
12	The Mechanisms of HAMP-Mediated Signaling in Transmembrane Receptors. <i>Structure</i> , 2011, 19, 378-385.	3.3	86
13	The Structure and Topology of Î±-Helical Coiled Coils. <i>Sub-Cellular Biochemistry</i> , 2017, 82, 95-129.	2.4	80
14	Comprehensive Analysis of HAMP Domains: Implications for Transmembrane Signal Transduction. <i>Journal of Molecular Biology</i> , 2010, 397, 1156-1174.	4.2	79
15	A coiled-coil motif that sequesters ions to the hydrophobic core. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16950-16955.	7.1	77
16	Complete fiber structures of complex trimeric autotransporter adhesins conserved in enterobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20907-20912.	7.1	57
17	Axial helix rotation as a mechanism for signal regulation inferred from the crystallographic analysis of the <i>E. coli</i> serine chemoreceptor. <i>Journal of Structural Biology</i> , 2014, 186, 349-356.	2.8	50
18	The yfhQ gene of <i>Escherichia coli</i> encodes a tRNA:Cm32/Um32 methyltransferase. <i>BMC Molecular Biology</i> , 2006, 7, 23.	3.0	41

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19	A transition from strong right-handed to canonical left-handed supercoiling in a conserved coiled-coil segment of trimeric autotransporter adhesins. <i>Journal of Structural Biology</i> , 2010, 170, 236-245.	2.8	41
20	Computational modeling of RNA 3D structures, with the aid of experimental restraints. <i>RNA Biology</i> , 2014, 11, 522-536.	3.1	39
21	Measuring the conformational space of square four-helical bundles with the program samCC. <i>Journal of Structural Biology</i> , 2010, 170, 226-235.	2.8	36
22	Novel Highly Thermostable Endolysin from <i>Thermus scotoductus</i> MAT2119 Bacteriophage Ph2119 with Amino Acid Sequence Similarity to Eukaryotic Peptidoglycan Recognition Proteins. <i>Applied and Environmental Microbiology</i> , 2014, 80, 886-895.	3.1	35
23	RNArchitecture: a database and a classification system of RNA families, with a focus on structural information. <i>Nucleic Acids Research</i> , 2017, 46, D202-D205.	14.5	31
24	A composite double-/single-stranded RNA-binding region in protein Prp3 supports tri-snRNP stability and splicing. <i>ELife</i> , 2015, 4, e07320.	6.0	29
25	Computational modeling of protein-RNA complex structures. <i>Methods</i> , 2014, 65, 310-319.	3.8	27
26	The Signature of the Five-Stranded vRRM Fold Defined by Functional, Structural and Computational Analysis of the hnRNP L Protein. <i>Journal of Molecular Biology</i> , 2015, 427, 3001-3022.	4.2	25
27	Phylogenomics and sequence-structure-function relationships in the GmrSD family of Type IV restriction enzymes. <i>BMC Bioinformatics</i> , 2015, 16, 336.	2.6	24
28	Prokaryotic Ancestry of Eukaryotic Protein Networks Mediating Innate Immunity and Apoptosis. <i>Journal of Molecular Biology</i> , 2014, 426, 1568-1582.	4.2	23
29	Combining Rosetta with molecular dynamics (MD): A benchmark of the MD-based ensemble protein design. <i>Journal of Structural Biology</i> , 2018, 203, 54-61.	2.8	21
30	S6:S18 ribosomal protein complex interacts with a structural motif present in its own mRNA. <i>Rna</i> , 2013, 19, 1341-1348.	3.5	20
31	Functional and Bioinformatics Analysis of Two <i>Campylobacter jejuni</i> Homologs of the Thiol-Disulfide Oxidoreductase, DsbA. <i>PLoS ONE</i> , 2014, 9, e106247.	2.5	20
32	STAC: A New Domain Associated with Transmembrane Solute Transport and Two-Component Signal Transduction Systems. <i>Journal of Molecular Biology</i> , 2015, 427, 3327-3339.	4.2	17
33	The GD box: A widespread noncontiguous supersecondary structural element. <i>Protein Science</i> , 2009, 18, 1961-1966.	7.6	15
34	A soluble mutant of the transmembrane receptor Af1503 features strong changes in coiled-coil periodicity. <i>Journal of Structural Biology</i> , 2014, 186, 357-366.	2.8	15
35	Designability landscape reveals sequence features that define axial helix rotation in four-helical homo-oligomeric antiparallel coiled-coil structures. <i>Journal of Structural Biology</i> , 2014, 188, 123-133.	2.8	15
36	PiPred: a deep-learning method for prediction of α -helices in protein sequences. <i>Scientific Reports</i> , 2019, 9, 6888.	3.3	15

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37	A library of coiled-coil domains: from regular bundles to peculiar twists. <i>Bioinformatics</i> , 2021, 36, 5368-5376.	4.1	15
38	Functional and evolutionary analyses of <i>Helicobacter pylori</i> HP0231 (DsbK) protein with strong oxidative and chaperone activity characterized by a highly diverged dimerization domain. <i>Frontiers in Microbiology</i> , 2015, 6, 1065.	3.5	14
39	Rossmann-toolbox: a deep learning-based protocol for the prediction and design of cofactor specificity in Rossmann fold proteins. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	14
40	Delineation of structural domains and identification of functionally important residues in DNA repair enzyme exonuclease VII. <i>Nucleic Acids Research</i> , 2012, 40, 8163-8174.	14.5	13
41	tRNAmDpred: A computational method for predicting posttranscriptional modifications in tRNAs. <i>Methods</i> , 2016, 107, 34-41.	3.8	12
42	Loss of Conserved Noncoding RNAs in Genomes of Bacterial Endosymbionts. <i>Genome Biology and Evolution</i> , 2016, 8, 426-438.	2.5	11
43	ANO5 mutations in the Polish limb girdle muscular dystrophy patients: Effects on the protein structure. <i>Scientific Reports</i> , 2019, 9, 11533.	3.3	11
44	RRMdb—an evolutionary-oriented database of RNA recognition motif sequences. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	10
45	Genome-wide survey of codons under diversifying selection in a highly recombining bacterial species, <i>Helicobacter pylori</i> . <i>DNA Research</i> , 2016, 23, 135-143.	3.4	8
46	C8J_1298, a bifunctional thiol oxidoreductase of <i>Campylobacter jejuni</i> , affects Dsb (disulfide bond) network functioning. <i>PLoS ONE</i> , 2020, 15, e0230366.	2.5	8
47	Impact of selected amino acids of HP0377 (<i>Helicobacter pylori</i> thiol oxidoreductase) on its functioning as a CcmG (cytochrome c maturation) protein and Dsb (disulfide bond) isomerase. <i>PLoS ONE</i> , 2018, 13, e0195358.	2.5	5
48	Variability of the core geometry in parallel coiled-coil bundles. <i>Journal of Structural Biology</i> , 2018, 204, 117-124.	2.8	5
49	Slipknotted and unknotted monovalent cation-proton antiporters evolved from a common ancestor. <i>PLoS Computational Biology</i> , 2021, 17, e1009502.	3.2	5
50	Interplay between DsbA1, DsbA2 and C8J_1298 Periplasmic Oxidoreductases of <i>Campylobacter jejuni</i> and Their Impact on Bacterial Physiology and Pathogenesis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13451.	4.1	5
51	Siah-1-interacting protein regulates mutated huntingtin protein aggregation in Huntington's disease models. <i>Cell and Bioscience</i> , 2022, 12, 34.	4.8	4
52	localpdb—a Python package to manage protein structures and their annotations. <i>Bioinformatics</i> , 2022, 38, 2633-2635.	4.1	3
53	Two unique membrane-bound AAA proteins from <i>Sulfolobus solfataricus</i> . <i>Biochemical Society Transactions</i> , 2009, 37, 118-122.	3.4	1