

Antonina Andreeva

List of Publications by Year in descending order

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45
papers

3,975
citations

218381

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243296

44
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all docs

48
docs citations

48
times ranked

4954
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular mechanisms underlying the role of the centriolar CEP164-TTBK2 complex in ciliopathies. <i>Structure</i> , 2022, 30, 114-128.e9.	1.6	11
2	Structural validation and assessment of AlphaFold2 predictions for centrosomal and centriolar proteins and their complexes. <i>Communications Biology</i> , 2022, 5, 312.	2.0	30
3	Deaminated purine bypass by DNA polymerase $\hat{\iota}$. <i>Biochemical Journal</i> , 2021, 478, 1309-1313.	1.7	0
4	Substrate recognition determinants of human eIF2 $\hat{\iota}$ phosphatases. <i>Open Biology</i> , 2021, 11, 210205.	1.5	4
5	The SCOP database in 2020: expanded classification of representative family and superfamily domains of known protein structures. <i>Nucleic Acids Research</i> , 2020, 48, D376-D382.	6.5	238
6	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. <i>Nucleic Acids Research</i> , 2020, 48, D314-D319.	6.5	13
7	Mechanism of completion of peptidyltransferase centre assembly in eukaryotes. <i>ELife</i> , 2019, 8, .	2.8	49
8	Direct binding of CEP85 to STIL ensures robust PLK4 activation and efficient centriole assembly. <i>Nature Communications</i> , 2018, 9, 1731.	5.8	32
9	Disease-Associated Mutations in CEP120 Destabilize the Protein and Impair Ciliogenesis. <i>Cell Reports</i> , 2018, 23, 2805-2818.	2.9	16
10	The Ciliopathy-Associated Cep104 Protein Interacts with Tubulin and Nek1 Kinase. <i>Structure</i> , 2017, 25, 146-156.	1.6	36
11	Consequences of point mutations in melanoma-associated antigen 4 (MAGE-A4) protein: Insights from structural and biophysical studies. <i>Scientific Reports</i> , 2016, 6, 25182.	1.6	17
12	Lessons from making the Structural Classification of Proteins (SCOP) and their implications for protein structure modelling. <i>Biochemical Society Transactions</i> , 2016, 44, 937-943.	1.6	6
13	Crystal Structure of a Group I Energy Coupling Factor Vitamin Transporter S Component in Complex with Its Cognate Substrate. <i>Cell Chemical Biology</i> , 2016, 23, 827-836.	2.5	9
14	Genome3D: exploiting structure to help users understand their sequences. <i>Nucleic Acids Research</i> , 2015, 43, D382-D386.	6.5	42
15	Investigating Protein Structure and Evolution with SCOP2. <i>Current Protocols in Bioinformatics</i> , 2015, 49, 1.26.1-1.26.21.	25.8	18
16	SCOP2 prototype: a new approach to protein structure mining. <i>Nucleic Acids Research</i> , 2014, 42, D310-D314.	6.5	260
17	Tracing the Evolution of the p53 Tetramerization Domain. <i>Structure</i> , 2014, 22, 1301-1310.	1.6	27
18	Crystal structures of the CPAP/STIL complex reveal its role in centriole assembly and human microcephaly. <i>ELife</i> , 2013, 2, e01071.	2.8	90

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19	Genome3D: a UK collaborative project to annotate genomic sequences with predicted 3D structures based on SCOP and CATH domains. <i>Nucleic Acids Research</i> , 2012, 41, D499-D507.	6.5	53
20	A bimodular mechanism of calcium control in eukaryotes. <i>Nature</i> , 2012, 491, 468-472.	13.7	110
21	Classification of Proteins: Available Structural Space for Molecular Modeling. <i>Methods in Molecular Biology</i> , 2011, 857, 1-31.	0.4	7
22	Structures of SAS-6 Suggest Its Organization in Centrioles. <i>Science</i> , 2011, 331, 1196-1199.	6.0	284
23	Structural classification of proteins and structural genomics: new insights into protein folding and evolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1190-1197.	0.7	35
24	The structural basis for catalysis and substrate specificity of a rhomboid protease. <i>EMBO Journal</i> , 2010, 29, 3797-3809.	3.5	97
25	Mapping the physical and functional interactions between the tumor suppressors p53 and BRCA2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8587-8592.	3.3	44
26	Biophysical characterizations of human mitochondrial transcription factor A and its binding to tumor suppressor p53. <i>Nucleic Acids Research</i> , 2009, 37, 6765-6783.	6.5	95
27	Interaction between the Transactivation Domain of p53 and PC4 Exemplifies Acidic Activation Domains as Single-stranded DNA Mimics. <i>Journal of Biological Chemistry</i> , 2009, 284, 21728-21737.	1.6	40
28	Solution Structure of the U11-48K CHHC Zinc-Finger Domain that Specifically Binds the 5' Splice Site of U12-Type Introns. <i>Structure</i> , 2009, 17, 294-302.	1.6	25
29	Adaptive Evolution of p53 Thermodynamic Stability. <i>Journal of Molecular Biology</i> , 2009, 393, 161-175.	2.0	28
30	A fortuitous insight into a common mode of RNA recognition by the dsRNA-specific zinc fingers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, E128-9.	3.3	4
31	A novel CHHC Zn-finger domain found in spliceosomal proteins and tRNA modifying enzymes. <i>Bioinformatics</i> , 2008, 24, 2277-2280.	1.8	23
32	SISYPHUS structural alignments for proteins with non-trivial relationships. <i>Nucleic Acids Research</i> , 2007, 35, D253-D259.	6.5	74
33	Data growth and its impact on the SCOP database: new developments. <i>Nucleic Acids Research</i> , 2007, 36, D419-D425.	6.5	854
34	Solution Structure of ASPP2 N-terminal Domain (N-ASPP2) Reveals a Ubiquitin-like Fold. <i>Journal of Molecular Biology</i> , 2007, 371, 948-958.	2.0	22
35	Solution structure of the C4 zinc finger domain of HDM2. <i>Protein Science</i> , 2006, 15, 384-389.	3.1	36
36	Evolution of protein fold in the presence of functional constraints. <i>Current Opinion in Structural Biology</i> , 2006, 16, 399-408.	2.6	104

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37	Core domain interactions in full-length p53 in solution. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2115-2119.	3.3	91
38	Revised structure of the AbrB N-terminal domain unifies a diverse superfamily of putative DNA-binding proteins. FEBS Letters, 2005, 579, 5669-5674.	1.3	45
39	SCOP database in 2004: refinements integrate structure and sequence family data. Nucleic Acids Research, 2004, 32, 226D-229.	6.5	815
40	Insight into the secondary structure of chloramphenicol acetyltransferase type I " computer analysis and FT-IR spectroscopic characterization of the protein structure. Journal of Molecular Structure, 2001, 565-566, 177-182.	1.8	11
41	Assessment of the CASP4 fold recognition category. Proteins: Structure, Function and Bioinformatics, 2001, 45, 55-67.	1.5	61
42	Crystallization of type I chloramphenicol acetyltransferase: an approach based on the concept of ionic strength reducers. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 101-103.	2.5	1
43	Structure-based evaluation of sequence comparison and fold recognition alignment accuracy 1 Edited by B. Honig. Journal of Molecular Biology, 2000, 297, 1003-1013.	2.0	81
44	Second Derivative Spectrophotometric Determination of the Degradation Products of Diclofenac Sodium in Gel-Ointment. Analytical Letters, 1998, 31, 117-129.	1.0	9
45	Spectrophotometric Determination of Diclofenac Sodium in Gel-Ointment. Analytical Letters, 1997, 30, 2235-2249.	1.0	26