

Srinivas Chakravarthy

List of Publications by Year in descending order

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45
papers

2,498
citations

377584

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263392

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46
docs citations

46
times ranked

3959
citing authors

#	ARTICLE	IF	CITATIONS
1	Solution structure and dynamics of the mitochondrial-targeted GTPase-activating protein (GAP) VopE by an integrated NMR / SAXS approach. Protein Science, 2022, , .	3.1	2
2	Long promoter sequences form higher-order G-quadruplexes: an integrative structural biology study of <i>c-Myc</i> , <i>k-Ras</i> and <i>c-Kit</i> promoter sequences. Nucleic Acids Research, 2022, 50, 4127-4147.	6.5	23
3	A CRISPR Screen Reveals Resistance Mechanisms to CD3-Bispecific Antibody Therapy. Cancer Immunology Research, 2021, 9, 34-49.	1.6	7
4	An Eight Amino Acid Segment Controls Oligomerization and Preferred Conformation of the two Non-visual Arrestins. Journal of Molecular Biology, 2021, 433, 166790.	2.0	15
5	A multi-step nucleation process determines the kinetics of prion-like domain phase separation. Nature Communications, 2021, 12, 4513.	5.8	73
6	Osmosensing by WNK Kinases. Molecular Biology of the Cell, 2021, 32, 1614-1623.	0.9	16
7	The solution structures of higher-order human telomere G-quadruplex multimers. Nucleic Acids Research, 2021, 49, 1749-1768.	6.5	32
8	Insight into human Miro1/2 domain organization based on the structure of its N-terminal GTPase. Journal of Structural Biology, 2020, 212, 107656.	1.3	17
9	Novel structure of the N-terminal helical domain of BibA, a group B streptococcus immunogenic bacterial adhesin. Acta Crystallographica Section D: Structural Biology, 2020, 76, 759-770.	1.1	8
10	The hTERT core promoter forms three parallel G-quadruplexes. Nucleic Acids Research, 2020, 48, 5720-5734.	6.5	61
11	Frustration and folding of a TIM barrel protein. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16378-16383.	3.3	18
12	Conserved residue His-257 of Vibrio cholerae flavin transferase ApbE plays a critical role in substrate binding and catalysis. Journal of Biological Chemistry, 2019, 294, 13800-13810.	1.6	10
13	Structural Organization and Dynamics of Homodimeric Cytohesin Family Arf GTPase Exchange Factors in Solution and on Membranes. Structure, 2019, 27, 1782-1797.e7.	1.6	14
14	Structural Dynamics Control Allosteric Activation of Cytohesin Family Arf GTPase Exchange Factors. Structure, 2018, 26, 106-117.e6.	1.6	11
15	Direct observation of conformational dynamics of the PH domain in phospholipases C ϵ and ζ may contribute to subfamily-specific roles in regulation. Journal of Biological Chemistry, 2018, 293, 17477-17490.	1.6	16
16	NAD ⁺ promotes assembly of the active tetramer of aldehyde dehydrogenase 7A1. FEBS Letters, 2018, 592, 3229-3238.	1.3	11
17	Redox Modulation of Oligomeric State in Proline Utilization A. Biophysical Journal, 2018, 114, 2833-2843.	0.2	2
18	BECN2 interacts with ATG14 through a metastable coiled-coil to mediate autophagy. Protein Science, 2017, 26, 972-984.	3.1	10

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19	Structural Basis for the Lesion-scanning Mechanism of the MutY DNA Glycosylase. <i>Journal of Biological Chemistry</i> , 2017, 292, 5007-5017.	1.6	19
20	The POTRA domains of Toc75 exhibit chaperone-like function to facilitate import into chloroplasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4868-E4876.	3.3	40
21	The Chd1 Chromatin Remodeler Shifts Nucleosomal DNA Bidirectionally as a Monomer. <i>Molecular Cell</i> , 2017, 68, 76-88.e6.	4.5	50
22	<i>Bacillus anthracis</i> Prolyl 4-Hydroxylase Interacts with and Modifies Elongation Factor Tu. <i>Biochemistry</i> , 2017, 56, 5771-5785.	1.2	9
23	Structural insights into the interaction of the conserved mammalian proteins GAPR-1 and Beclin 1, a key autophagy protein. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 775-792.	1.1	14
24	Structural transitions in conserved, ordered Beclin 1 domains essential to regulating autophagy. <i>Journal of Biological Chemistry</i> , 2017, 292, 16235-16248.	1.6	10
25	Characterization of Monoclonal Antibody-Protein Antigen Complexes Using Small-Angle Scattering and Molecular Modeling. <i>Antibodies</i> , 2017, 6, 25.	1.2	9
26	Kinetic characterization of <i>Vibrio cholerae</i> ApbE: Substrate specificity and regulatory mechanisms. <i>PLoS ONE</i> , 2017, 12, e0186805.	1.1	14
27	Enzymatic hydrolysis by transition-metal-dependent nucleophilic aromatic substitution. <i>Nature Chemical Biology</i> , 2016, 12, 1031-1036.	3.9	12
28	Succinyl-5-aminoimidazole-4-carboxamide-1-ribose 5-phosphate (SAICAR) Activates Pyruvate Kinase Isoform M2 (PKM2) in Its Dimeric Form. <i>Biochemistry</i> , 2016, 55, 4731-4736.	1.2	24
29	Identification of BECN1 and ATG14 Coiled-Coil Interface Residues That Are Important for Starvation-Induced Autophagy. <i>Biochemistry</i> , 2016, 55, 4239-4253.	1.2	25
30	Conformational Flexibility Enables the Function of a BECN1 Region Essential for Starvation-Mediated Autophagy. <i>Biochemistry</i> , 2016, 55, 1945-1958.	1.2	28
31	Methods for analysis of size-exclusion chromatography-small-angle X-ray scattering and reconstruction of protein scattering. <i>Journal of Applied Crystallography</i> , 2015, 48, 1102-1113.	1.9	46
32	Modulation of frustration in folding by sequence permutation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10562-10567.	3.3	24
33	Microsecond Barrier-Limited Chain Collapse Observed by Time-Resolved FRET and SAXS. <i>Journal of Molecular Biology</i> , 2014, 426, 1980-1994.	2.0	43
34	Structural coupling of the EF hand and C-terminal GTPase domains in the mitochondrial protein Miro. <i>EMBO Reports</i> , 2013, 14, 968-974.	2.0	71
35	Decoupling nucleosome recognition from DNA binding dramatically alters the properties of the Chd1 chromatin remodeler. <i>Nucleic Acids Research</i> , 2013, 41, 1637-1648.	6.5	36
36	Sub-millisecond time-resolved SAXS using a continuous-flow mixer and X-ray microbeam. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 820-825.	1.0	61

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37	The basic linker of macroH2A stabilizes DNA at the entry/exit site of the nucleosome. <i>Nucleic Acids Research</i> , 2012, 40, 8285-8295.	6.5	34
38	Substrate-Specific Kinetics of Dicer-Catalyzed RNA Processing. <i>Journal of Molecular Biology</i> , 2010, 404, 392-402.	2.0	126
39	Structure of the <i>Drosophila</i> nucleosome core particle highlights evolutionary constraints on the H2A-H2B histone dimer. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1-7.	1.5	55
40	The Histone Variant Macro-H2A Preferentially Forms "Hybrid Nucleosomes". <i>Journal of Biological Chemistry</i> , 2006, 281, 25522-25531.	1.6	63
41	Structural Characterization of the Histone Variant macroH2A. <i>Molecular and Cellular Biology</i> , 2005, 25, 7616-7624.	1.1	149
42	Structure and dynamic properties of nucleosome core particles. <i>FEBS Letters</i> , 2005, 579, 895-898.	1.3	68
43	Structural determinants for generating centromeric chromatin. <i>Nature</i> , 2004, 430, 578-582.	13.7	364
44	Structure and dynamics of nucleosomal DNA. <i>Biopolymers</i> , 2003, 68, 547-556.	1.2	48
45	Reconstitution of Nucleosome Core Particles from Recombinant Histones and DNA. <i>Methods in Enzymology</i> , 2003, 375, 23-44.	0.4	709