

Srinivas Ramachandran

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

2,173
citations

361413

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302126

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61
all docs

61
docs citations

61
times ranked

3525
citing authors

#	ARTICLE	IF	CITATIONS
1	Managing the Steady State Chromatin Landscape by Nucleosome Dynamics. Annual Review of Biochemistry, 2022, 91, 183-195.	11.1	16
2	A computational pipeline to visualize DNA-protein binding states using dSMF data. STAR Protocols, 2022, 3, 101299.	1.2	0
3	Cooperative binding between distant transcription factors is a hallmark of active enhancers. Molecular Cell, 2021, 81, 1651-1665.e4.	9.7	39
4	JMJD5 couples with CDK9 to release the paused RNA polymerase II. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19888-19895.	7.1	8
5	Phenotypes from cell-free DNA. Open Biology, 2020, 10, 200119.	3.6	9
6	Slow Down to Catch Up. Cell, 2019, 178, 774-776.	28.9	2
7	The CAF-1 complex couples Hippo pathway target gene expression and DNA replication. Molecular Biology of the Cell, 2019, 30, 2929-2942.	2.1	5
8	MINCE-Seq: Mapping In Vivo Nascent Chromatin with EdU and Sequencing. Methods in Molecular Biology, 2018, 1832, 159-168.	0.9	6
9	Pioneers Invade the Nucleosomal Landscape. Molecular Cell, 2018, 71, 193-194.	9.7	3
10	Precise genome-wide mapping of single nucleosomes and linkers in vivo. Genome Biology, 2018, 19, 19.	8.8	128
11	A Structural Model for Vinculin Insertion into PIP2-Containing Membranes and the Effect of Insertion on Vinculin Activation and Localization. Structure, 2017, 25, 264-275.	3.3	23
12	Capitalizing on disaster: Establishing chromatin specificity behind the replication fork. BioEssays, 2017, 39, 1600150.	2.5	15
13	Transcription of Nearly All Yeast RNA Polymerase II-Transcribed Genes Is Dependent on Transcription Factor TFIID. Molecular Cell, 2017, 68, 118-129.e5.	9.7	142
14	Redundant Functions for Nap1 and Chz1 in H2A.Z Deposition. Scientific Reports, 2017, 7, 10791.	3.3	13
15	Transcription and Remodeling Produce Asymmetrically Unwrapped Nucleosomal Intermediates. Molecular Cell, 2017, 68, 1038-1053.e4.	9.7	104
16	Role of PIP2-Dependent Membrane Interactions in Vinculin Activation, Motility and Force Transmission. Biophysical Journal, 2016, 110, 575a.	0.5	0
17	Transcriptional Regulators Compete with Nucleosomes Post-replication. Cell, 2016, 165, 580-592.	28.9	139
18	Nucleosome dynamics during chromatin remodeling in vivo. Nucleus, 2016, 7, 20-26.	2.2	26

#	ARTICLE	IF	CITATIONS
19	Abstract IA09: Nucleosome barriers to transcription. , 2016, , .		0
20	New Models for Regulation of Vinculin by Actin and Phospholipids. Biophysical Journal, 2015, 108, 508a-509a.	0.5	0
21	Non-canonical Bromodomain within DNA-PKcs Promotes DNA Damage Response and Radioresistance through Recognizing an IR-Induced Acetyl-Lysine on H2AX. Chemistry and Biology, 2015, 22, 849-861.	6.0	15
22	Replicating nucleosomes. Science Advances, 2015, 1, .	10.3	67
23	Asymmetric nucleosomes flank promoters in the budding yeast genome. Genome Research, 2015, 25, 381-390.	5.5	96
24	Nucleosomes Are Context-Specific, H2A.Z-Modulated Barriers to RNA Polymerase. Molecular Cell, 2014, 53, 819-830.	9.7	313
25	Computational approaches to understanding protein aggregation in neurodegeneration. Journal of Molecular Cell Biology, 2014, 6, 104-115.	3.3	43
26	Pore Dynamics and Conductance of RyR1 Transmembrane Domain. Biophysical Journal, 2014, 106, 2375-2384.	0.5	20
27	The budding yeast Centromere DNA Element II wraps a stable Cse4 hemisome in either orientation in vivo. ELife, 2014, 3, e01861.	6.0	77
28	Statistical Analysis of SHAPE-Directed RNA Secondary Structure Modeling. Biochemistry, 2013, 52, 596-599.	2.5	14
29	Structural Determinants of Skeletal Muscle Ryanodine Receptor Gating*. Journal of Biological Chemistry, 2013, 288, 6154-6165.	3.4	48
30	Homology Modeling: Generating Structural Models to Understand Protein Function and Mechanism. Biological and Medical Physics Series, 2012, , 97-116.	0.4	9
31	Recognition of Platinumâ€™DNA Adducts by HMGB1a. Biochemistry, 2012, 51, 7608-7617.	2.5	14
32	Discrete Molecular Dynamics: An Efficient And Versatile Simulation Method For Fine Protein Characterization. Journal of Physical Chemistry B, 2012, 116, 8375-8382.	2.6	179
33	ATP hydrolysis at one of the two sites in ABC transporters initiates transport related conformational transitions. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 2954-2964.	2.6	38
34	Flanking Bases Influence the Nature of DNA Distortion by Platinum 1,2-Intrastrand (GG) Cross-Links. PLoS ONE, 2011, 6, e23582.	2.5	19
35	Automated minimization of steric clashes in protein structures. Proteins: Structure, Function and Bioinformatics, 2011, 79, 261-270.	2.6	372
36	Thermodynamic Stability of Histone H3 Is a Necessary but not Sufficient Driving Force for its Evolutionary Conservation. PLoS Computational Biology, 2011, 7, e1001042.	3.2	20

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37	Gaia: automated quality assessment of protein structure models. <i>Bioinformatics</i> , 2011, 27, 2209-2215.	4.1	44
38	Abstract 3504: Debio 0507 primarily forms diaminocyclohexane-d(GpG) and -d(ApG) DNA adducts in HCT116 cells. , 2010, , .		0
39	A Structural Model of the Pore-Forming Region of the Skeletal Muscle Ryanodine Receptor (RyR1). <i>PLoS Computational Biology</i> , 2009, 5, e1000367.	3.2	25
40	Thermodynamics of calmodulin binding to cardiac and skeletal muscle ryanodine receptor ion channels. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 207-211.	2.6	15
41	Solution Structure of the DNA Damage Lesion 8-Oxoguanosine from Ultraviolet Resonance Raman Spectroscopy. <i>Journal of Physical Chemistry A</i> , 2009, 113, 1459-1471.	2.5	37
42	Ryanodine Receptor Pore Structure and Function. <i>Biophysical Journal</i> , 2009, 96, 107a.	0.5	1
43	Structural basis for the sequence-dependent effects of platinumâ€“DNA adducts. <i>Nucleic Acids Research</i> , 2009, 37, 2434-2448.	14.5	27
44	Differences in Conformation and Conformational Dynamics Between Cisplatin and Oxaliplatin DNA Adducts. , 2009, , 157-169.		1
45	Cooperative Binding between Distant Transcription Factors is a Hallmark of Active Enhancers. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0