Srinivas Ramachandran

List of Publications by Year
in descending order

45 papers	2,173 citations	361045 20 h-index	301761 39 g-index
61 all docs	61 docs citations	61 times ranked	3525 citing authors

#	Article	IF	Citations
1	Automated minimization of steric clashes in protein structures. Proteins: Structure, Function and Bioinformatics, 2011, 79, 261-270.	1.5	372
2	Nucleosomes Are Context-Specific, H2A.Z-Modulated Barriers to RNA Polymerase. Molecular Cell, 2014, 53, 819-830.	4.5	313
3	Discrete Molecular Dynamics: An Efficient And Versatile Simulation Method For Fine Protein Characterization. Journal of Physical Chemistry B, 2012, 116, 8375-8382.	1.2	179
4	Transcription of Nearly All Yeast RNA Polymerase II-Transcribed Genes Is Dependent on Transcription Factor TFIID. Molecular Cell, 2017, 68, 118-129.e5.	4.5	142
5	Transcriptional Regulators Compete with Nucleosomes Post-replication. Cell, 2016, 165, 580-592.	13.5	139
6	Precise genome-wide mapping of single nucleosomes and linkers in vivo. Genome Biology, 2018, 19, 19.	3.8	128
7	Transcription and Remodeling Produce Asymmetrically Unwrapped Nucleosomal Intermediates. Molecular Cell, 2017, 68, 1038-1053.e4.	4.5	104
8	Asymmetric nucleosomes flank promoters in the budding yeast genome. Genome Research, 2015, 25, 381-390.	2.4	96
9	The budding yeast Centromere DNA Element II wraps a stable Cse4 hemisome in either orientation in vivo. ELife, 2014, 3, e01861.	2.8	77
10	Replicating nucleosomes. Science Advances, 2015, 1, .	4.7	67
11	Structural Determinants of Skeletal Muscle Ryanodine Receptor Gating*. Journal of Biological Chemistry, 2013, 288, 6154-6165.	1.6	48
12	Gaia: automated quality assessment of protein structure models. Bioinformatics, 2011, 27, 2209-2215.	1.8	44
13	Computational approaches to understanding protein aggregation in neurodegeneration. Journal of Molecular Cell Biology, 2014, 6, 104-115.	1.5	43
14	Cooperative binding between distant transcription factors is a hallmark of active enhancers. Molecular Cell, 2021, 81, 1651-1665.e4.	4.5	39
15	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.	1.4	38
16	Solution Structure of the DNA Damage Lesion 8-Oxoguanosine from Ultraviolet Resonance Raman Spectroscopy. Journal of Physical Chemistry A, 2009, 113, 1459-1471.	1.1	37
17	Structural basis for the sequence-dependent effects of platinumâ€"DNA adducts. Nucleic Acids Research, 2009, 37, 2434-2448.	6.5	27
18	Nucleosome dynamics during chromatin remodelingin vivo. Nucleus, 2016, 7, 20-26.	0.6	26

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19	A Structural Model of the Pore-Forming Region of the Skeletal Muscle Ryanodine Receptor (RyR1). PLoS Computational Biology, 2009, 5, e1000367.	1.5	25
20	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.	1.6	23
21	Thermodynamic Stability of Histone H3 Is a Necessary but not Sufficient Driving Force for its Evolutionary Conservation. PLoS Computational Biology, 2011, 7, e1001042.	1.5	20
22	Pore Dynamics and Conductance of RyR1 Transmembrane Domain. Biophysical Journal, 2014, 106, 2375-2384.	0.2	20
23	Flanking Bases Influence the Nature of DNA Distortion by Platinum 1,2-Intrastrand (GG) Cross-Links. PLoS ONE, 2011, 6, e23582.	1.1	19
24	Managing the Steady State Chromatin Landscape by Nucleosome Dynamics. Annual Review of Biochemistry, 2022, 91, 183-195.	5.0	16
25	Thermodynamics of calmodulin binding to cardiac and skeletal muscle ryanodine receptor ion channels. Proteins: Structure, Function and Bioinformatics, 2009, 74, 207-211.	1.5	15
26	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.	6.2	15
27	Capitalizing on disaster: Establishing chromatin specificity behind the replication fork. BioEssays, 2017, 39, 1600150.	1.2	15
28	Recognition of Platinum–DNA Adducts by HMGB1a. Biochemistry, 2012, 51, 7608-7617.	1.2	14
29	Statistical Analysis of SHAPE-Directed RNA Secondary Structure Modeling. Biochemistry, 2013, 52, 596-599.	1.2	14
30	Redundant Functions for Nap1 and Chz1 in H2A.Z Deposition. Scientific Reports, 2017, 7, 10791.	1.6	13
31	Homology Modeling: Generating Structural Models to Understand Protein Function and Mechanism. Biological and Medical Physics Series, 2012, , 97-116.	0.3	9
32	Phenotypes from cell-free DNA. Open Biology, 2020, 10, 200119.	1.5	9
33	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.	3.3	8
34	MINCE-Seq: Mapping In Vivo Nascent Chromatin with EdU and Sequencing. Methods in Molecular Biology, 2018, 1832, 159-168.	0.4	6
35	The CAF-1 complex couples Hippo pathway target gene expression and DNA replication. Molecular Biology of the Cell, 2019, 30, 2929-2942.	0.9	5
36	Pioneers Invade the Nucleosomal Landscape. Molecular Cell, 2018, 71, 193-194.	4.5	3

#	Article	IF	Citations
37	Slow Down to Catch Up. Cell, 2019, 178, 774-776.	13.5	2
38	Ryanodine Receptor Pore Structure and Function. Biophysical Journal, 2009, 96, 107a.	0.2	1
39	Differences in Conformation and Conformational Dynamics Between Cisplatin and Oxaliplatin DNA Adducts. , 2009, , 157-169.		1
40	New Models for Regulation of Vinculin by Actin and Phospholipids. Biophysical Journal, 2015, 108, 508a-509a.	0.2	0
41	Role of PIP2-Dependent Membrane Interactions in Vinculin Activation, Motility and Force Transmission. Biophysical Journal, 2016, 110, 575a.	0.2	0
42	Abstract 3504: Debio 0507 primarily forms diaminocyclohexane-d(GpG) and -d(ApG) DNA adducts in HCT116 cells. , 2010, , .		0
43	Abstract IA09: Nucleosome barriers to transcription. , 2016, , .		0
44	Cooperative Binding between Distant Transcription Factors is a Hallmark of Active Enhancers. SSRN Electronic Journal, 0, , .	0.4	0
45	A computational pipeline to visualize DNA-protein binding states using dSMF data. STAR Protocols, 2022, 3, 101299.	0.5	0