

Seth M Rubin

List of Publications by Year in descending order

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59
papers

3,904
citations

147801

31
h-index

149698

56
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69
all docs

69
docs citations

69
times ranked

5292
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular mechanisms underlying RB protein function. <i>Nature Reviews Molecular Cell Biology</i> , 2013, 14, 297-306.	37.0	459
2	Structure of the Rb C-Terminal Domain Bound to E2F1-DP1: A Mechanism for Phosphorylation-Induced E2F Release. <i>Cell</i> , 2005, 123, 1093-1106.	28.9	218
3	Deciphering the retinoblastoma protein phosphorylation code. <i>Trends in Biochemical Sciences</i> , 2013, 38, 12-19.	7.5	211
4	Cascades of multisite phosphorylation control Sic1 destruction at the onset of S phase. <i>Nature</i> , 2011, 480, 128-131.	27.8	202
5	Methylation of the Retinoblastoma Tumor Suppressor by SMYD2. <i>Journal of Biological Chemistry</i> , 2010, 285, 37733-37740.	3.4	188
6	Cyclin D-Cdk4,6 Drives Cell-Cycle Progression via the Retinoblastoma Protein's C-Terminal Helix. <i>Molecular Cell</i> , 2019, 74, 758-770.e4.	9.7	162
7	Integrating Old and New Paradigms of G1/S Control. <i>Molecular Cell</i> , 2020, 80, 183-192.	9.7	140
8	Development of a Functionalized Xenon Biosensor. <i>Journal of the American Chemical Society</i> , 2004, 126, 15287-15294.	13.7	132
9	p27 allosterically activates cyclin-dependent kinase 4 and antagonizes palbociclib inhibition. <i>Science</i> , 2019, 366, .	12.6	132
10	An RB-EZH2 Complex Mediates Silencing of Repetitive DNA Sequences. <i>Molecular Cell</i> , 2016, 64, 1074-1087.	9.7	128
11	Phosphorylation-induced Conformational Changes in the Retinoblastoma Protein Inhibit E2F Transactivation Domain Binding. <i>Journal of Biological Chemistry</i> , 2010, 285, 16286-16293.	3.4	122
12	A Cdk7-Cdk4 T-Loop Phosphorylation Cascade Promotes G1 Progression. <i>Molecular Cell</i> , 2013, 50, 250-260.	9.7	115
13	Multisite phosphorylation networks as signal processors for Cdk1. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1415-1424.	8.2	112
14	Structures of inactive retinoblastoma protein reveal multiple mechanisms for cell cycle control. <i>Genes and Development</i> , 2012, 26, 1156-1166.	5.9	111
15	Detection and Characterization of Xenon-binding Sites in Proteins by ¹²⁹ Xe NMR Spectroscopy. <i>Journal of Molecular Biology</i> , 2002, 322, 425-440.	4.2	106
16	An overlapping kinase and phosphatase docking site regulates activity of the retinoblastoma protein. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1051-1057.	8.2	98
17	Structural mechanisms of DREAM complex assembly and regulation. <i>Genes and Development</i> , 2015, 29, 961-974.	5.9	93
18	Rif1 and Rif2 Shape Telomere Function and Architecture through Multivalent Rap1 Interactions. <i>Cell</i> , 2013, 153, 1340-1353.	28.9	92

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19	Cks confers specificity to phosphorylation-dependent CDK signaling pathways. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1407-1414.	8.2	77
20	An N-terminal acidic region of Sgs1 interacts with Rpa70 and recruits Rad53 kinase to stalled forks. <i>EMBO Journal</i> , 2012, 31, 3768-3783.	7.8	74
21	E2F4 regulates transcriptional activation in mouse embryonic stem cells independently of the RB family. <i>Nature Communications</i> , 2019, 10, 2939.	12.8	59
22	Influence of the Substrate on Order and Image Contrast for Physisorbed, Self-Assembled Molecular Monolayers: A STM Studies of Functionalized Hydrocarbons on Graphite and MoS ₂ . <i>Journal of Physical Chemistry B</i> , 1998, 102, 10255-10263.	2.6	55
23	The cell cycle regulatory DREAM complex is disrupted by high expression of oncogenic B-Myb. <i>Oncogene</i> , 2019, 38, 1080-1092.	5.9	54
24	Structural basis for LIN54 recognition of CHR elements in cell cycle-regulated promoters. <i>Nature Communications</i> , 2016, 7, 12301.	12.8	52
25	Characterization of the Effects of Nonspecific Xenon-Protein Interactions on ¹²⁹ Xe Chemical Shifts in Aqueous Solution: Further Development of Xenon as a Biomolecular Probe. <i>Journal of Magnetic Resonance</i> , 2001, 152, 79-86.	2.1	51
26	Structural Basis of BRCC36 Function in DNA Repair and Immune Regulation. <i>Molecular Cell</i> , 2019, 75, 483-497.e9.	9.7	50
27	CDK/cyclin dependencies define extreme cancer cell-cycle heterogeneity and collateral vulnerabilities. <i>Cell Reports</i> , 2022, 38, 110448.	6.4	48
28	Detection of a Conformational Change in Maltose Binding Protein by ¹²⁹ Xe NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2001, 123, 8616-8617.	13.7	47
29	Structural basis of template-boundary definition in <i>Tetrahymena</i> telomerase. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 883-888.	8.2	45
30	Translational and rotational excitation of the CO ₂ (0 ⁰) vibrationless state in the collisional quenching of highly vibrationally excited 2-methylpyrazine: Kinetics and dynamics of large energy transfers. <i>Journal of Chemical Physics</i> , 2000, 113, 4912.	3.0	40
31	Structural basis of divergent cyclin-dependent kinase activation by Spy1/RINGO proteins. <i>EMBO Journal</i> , 2017, 36, 2251-2262.	7.8	40
32	Competition between photochemistry and energy transfer in ultraviolet-excited diazabenzenes. I. Photofragmentation studies of pyrazine at 248 nm and 266 nm. <i>Journal of Chemical Physics</i> , 2000, 112, 5829-5843.	3.0	38
33	Multiple Mechanisms for E2F Binding Inhibition by Phosphorylation of the Retinoblastoma Protein C-Terminal Domain. <i>Journal of Molecular Biology</i> , 2014, 426, 245-255.	4.2	35
34	An order-to-disorder structural switch activates the FoxM1 transcription factor. <i>ELife</i> , 2019, 8, .	6.0	34
35	Distinguishing multiple chemotaxis Y protein conformations with laser-polarized ¹²⁹ Xe NMR. <i>Protein Science</i> , 2005, 14, 848-855.	7.6	33
36	Structural Conservation and E2F Binding Specificity within the Retinoblastoma Pocket Protein Family. <i>Journal of Molecular Biology</i> , 2016, 428, 3960-3971.	4.2	33

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37	Conservation and divergence of C-terminal domain structure in the retinoblastoma protein family. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4942-4947.	7.1	33
38	Applications of laser-polarized ¹²⁹ Xe to biomolecular assays. Magnetic Resonance Imaging, 2003, 21, 1235-1239.	1.8	30
39	Structural mechanism of Myb-MuvB assembly. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10016-10021.	7.1	30
40	Design of a Conformation-Sensitive Xenon-Binding Cavity in the Ribose-Binding Protein. Angewandte Chemie - International Edition, 2004, 43, 6320-6322.	13.8	19
41	Crystal structure of the unliganded retinoblastoma protein pocket domain. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2010-2014.	2.6	16
42	Solution structure of a putative ribosome binding protein from Mycoplasma pneumoniae and comparison to a distant homolog. Journal of Structural and Functional Genomics, 2003, 4, 235-243.	1.2	13
43	The MuvB complex binds and stabilizes nucleosomes downstream of the transcription start site of cell-cycle dependent genes. Nature Communications, 2022, 13, 526.	12.8	12
44	A tyrosine phosphoregulatory system controls exopolysaccharide biosynthesis and biofilm formation in Vibrio cholerae. PLoS Pathogens, 2020, 16, e1008745.	4.7	10
45	Cyclin F drives proliferation through SCF-dependent degradation of the retinoblastoma-like tumor suppressor p130/RBL2. ELife, 2021, 10, .	6.0	9
46	A long lost key opens an ancient lock: <i>Drosophila</i> Myb causes a synthetic multivulval phenotype in nematodes. Biology Open, 2020, 9, .	1.2	8
47	Manipulating the tumour-suppressor protein Rb in lung cancer reveals possible drug targets. Nature, 2019, 569, 343-344.	27.8	7
48	E2F4's cytoplasmic role in multiciliogenesis is mediated via an N-terminal domain that binds two components of the centriole replication machinery, Deup1 and SAS6. Molecular Biology of the Cell, 2021, 32, ar1.	2.1	6
49	Structural basis for tunable affinity and specificity of LxCxE-dependent protein interactions with the retinoblastoma protein family. Structure, 2022, 30, 1340-1353.e3.	3.3	6
50	Structure and function of MuvB complexes. Oncogene, 2022, 41, 2909-2919.	5.9	5
51	The Structure of a Monomeric Mutant Cks Protein Reveals Multiple Functions for a Conserved Hinge-Region Proline. Journal of Molecular Biology, 2011, 411, 520-528.	4.2	3
52	A Strategy for Direct Chemical Activation of the Retinoblastoma Protein. ACS Chemical Biology, 2016, 11, 1192-1197.	3.4	2
53	An Overlapping Kinase and Phosphatase Docking Site Regulates Activity of the Retinoblastoma Protein. Biophysical Journal, 2010, 98, 248a.	0.5	1
54	Defining a new vision for the retinoblastoma gene: report from the 3rd International Rb Meeting. Cell Division, 2013, 8, 13.	2.4	1

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55	Heavy metal in cancer: The cell cycle jams with arsenic. <i>Cell Cycle</i> , 2017, 16, 1641-1642.	2.6	1
56	E2F1 regulation by the APC/C. <i>Cell Cycle</i> , 2010, 9, 4052-4051.	2.6	0
57	Molecular Mechanisms for Phosphorylation Driven Dissociation of Rb-E2F Complexes. <i>Biophysical Journal</i> , 2010, 98, 235a.	0.5	0
58	Molecular mimicry: HUWE1 binds an atypical site in MIZ1 by adopting a typical BTB fold. <i>Structure</i> , 2021, 29, 1217-1218.	3.3	0
59	E2F1 regulation by the APC/C. <i>Cell Cycle</i> , 2010, 9, 4044.	2.6	0