

Ruth Nussinov

List of Publications by Year in descending order

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Version: 2024-02-01

314
papers

31,524
citations

6592

79
h-index

5806

161
g-index

323
all docs

323
docs citations

323
times ranked

27287
citing authors

#	ARTICLE	IF	CITATIONS
1	Novel MAPK/AKT-impairing germline NRAS variant identified in a melanoma-prone family. <i>Familial Cancer</i> , 2022, 21, 347-355.	0.9	1
2	Mechanism of activation and the rewired network: New drug design concepts. <i>Medicinal Research Reviews</i> , 2022, 42, 770-799.	5.0	15
3	Interpretable artificial intelligence and exascale molecular dynamics simulations to reveal kinetics: Applications to Alzheimer's disease. <i>Current Opinion in Structural Biology</i> , 2022, 72, 103-113.	2.6	13
4	How can same-gene mutations promote both cancer and developmental disorders?. <i>Science Advances</i> , 2022, 8, eabm2059.	4.7	29
5	Allostery, and how to define and measure signal transduction. <i>Biophysical Chemistry</i> , 2022, 283, 106766.	1.5	24
6	Deep learning for drug repurposing: Methods, databases, and applications. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2022, 12, .	6.2	48
7	Artificial intelligence approaches to human-microbiome protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2022, 73, 102328.	2.6	13
8	Allostery: Allosteric Cancer Drivers and Innovative Allosteric Drugs. <i>Journal of Molecular Biology</i> , 2022, 434, 167569.	2.0	26
9	SARS-CoV-2 Interactome 3D: A Web interface for 3D visualization and analysis of SARS-CoV-2-human mimicry and interactions. <i>Bioinformatics</i> , 2022, 38, 1455-1457.	1.8	3
10	The mechanism of activation of MEK1 by B-Raf and KSR1. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 281.	2.4	7
11	Open Structural Data in Precision Medicine. <i>Annual Review of Biomedical Data Science</i> , 2022, 5, 95-117.	2.8	7
12	The structural basis of BCR-ABL recruitment of GRB2 in chronic myelogenous leukemia. <i>Biophysical Journal</i> , 2022, 121, 2251-2265.	0.2	9
13	Neurodevelopmental disorders, immunity, and cancer are connected. <i>iScience</i> , 2022, 25, 104492.	1.9	10
14	PI3K Driver Mutations: A Biophysical Membrane-Centric Perspective. <i>Cancer Research</i> , 2021, 81, 237-247.	0.4	26
15	Phosphorylation and Driver Mutations in PI3K and PTEN Autoinhibition. <i>Molecular Cancer Research</i> , 2021, 19, 543-548.	1.5	23
16	A new precision medicine initiative at the dawn of exascale computing. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 3.	7.1	31
17	The mechanism of activation of monomeric B-Raf V600E. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3349-3363.	1.9	38
18	A network-based deep learning methodology for stratification of tumor mutations. <i>Bioinformatics</i> , 2021, 37, 82-88.	1.8	10

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19	Active and Inactive Cdc42 Differ in Their Insert Region Conformational Dynamics. <i>Biophysical Journal</i> , 2021, 120, 306-318.	0.2	20
20	Inhibition of Nonfunctional Ras. <i>Cell Chemical Biology</i> , 2021, 28, 121-133.	2.5	23
21	Amyloid Oligomers: A Joint Experimental/Computational Perspective on Alzheimer's Disease, Parkinson's Disease, Type II Diabetes, and Amyotrophic Lateral Sclerosis. <i>Chemical Reviews</i> , 2021, 121, 2545-2647.	23.0	406
22	Trastuzumab Blocks the Receiver Function of HER2 Leading to the Population Shifts of HER2-Containing Homodimers and Heterodimers. <i>Antibodies</i> , 2021, 10, 7.	1.2	10
23	MSA-Regularized Protein Sequence Transformer toward Predicting Genome-Wide Chemical-Protein Interactions: Application to GPCRome Deorphanization. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 1570-1582.	2.5	20
24	Drugging multiple same-allele driver mutations in cancer. <i>Expert Opinion on Drug Discovery</i> , 2021, 16, 1-6.	2.5	10
25	Mechanistic Differences of Activation of Rac1 ^{P29S} and Rac1 ^{A159V} . <i>Journal of Physical Chemistry B</i> , 2021, 125, 3790-3802.	1.2	9
26	The mechanism of full activation of tumor suppressor PTEN at the phosphoinositide-enriched membrane. <i>IScience</i> , 2021, 24, 102438.	1.9	30
27	The structural basis of Akt PH domain interaction with calmodulin. <i>Biophysical Journal</i> , 2021, 120, 1994-2008.	0.2	10
28	Normal Mode Analysis of KRas4B Reveals Partner Specific Dynamics. <i>Journal of Physical Chemistry B</i> , 2021, 125, 5210-5221.	1.2	7
29	Ras isoform-specific expression, chromatin accessibility, and signaling. <i>Biophysical Reviews</i> , 2021, 13, 489-505.	1.5	14
30	B-Raf autoinhibition in the presence and absence of 14-3-3. <i>Structure</i> , 2021, 29, 768-777.e2.	1.6	26
31	Signaling in the crowded cell. <i>Current Opinion in Structural Biology</i> , 2021, 71, 43-50.	2.6	8
32	The dynamic nature of the K-Ras/calmodulin complex can be altered by oncogenic mutations. <i>Current Opinion in Structural Biology</i> , 2021, 71, 164-170.	2.6	8
33	My personal mutanome: a computational genomic medicine platform for searching network perturbing alleles linking genotype to phenotype. <i>Genome Biology</i> , 2021, 22, 53.	3.8	11
34	Editorial overview: Catalysis and regulation: The beating heart of biology. <i>Current Opinion in Structural Biology</i> , 2021, 71, iii-v.	2.6	1
35	The mechanism of Raf activation through dimerization. <i>Chemical Science</i> , 2021, 12, 15609-15619.	3.7	15
36	Anticancer drug resistance: An update and perspective. <i>Drug Resistance Updates</i> , 2021, 59, 100796.	6.5	122

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37	Antigen Binding Reshapes Antibody Energy Landscape and Conformation Dynamics. , 2021, , .		1
38	Computational network biology: Data, models, and applications. Physics Reports, 2020, 846, 1-66.	10.3	126
39	Autoinhibition can identify rare driver mutations and advise pharmacology. FASEB Journal, 2020, 34, 16-29.	0.2	23
40	Structural Features that Distinguish Inactive and Active PI3K Lipid Kinases. Journal of Molecular Biology, 2020, 432, 5849-5859.	2.0	28
41	Medin Oligomer Membrane Pore Formation: A Potential Mechanism of Vascular Dysfunction. Biophysical Journal, 2020, 118, 2769-2782.	0.2	9
42	The Mystery of Rap1 Suppression of Oncogenic Ras. Trends in Cancer, 2020, 6, 369-379.	3.8	23
43	Harnessing endophenotypes and network medicine for Alzheimer's drug repurposing. Medicinal Research Reviews, 2020, 40, 2386-2426.	5.0	61
44	Nucleotide-Specific Autoinhibition of Full-Length K-Ras4B Identified by Extensive Conformational Sampling. Frontiers in Molecular Biosciences, 2020, 7, 145.	1.6	11
45	SOS1 interacts with Grb2 through regions that induce closed nSH3 conformations. Journal of Chemical Physics, 2020, 153, 045106.	1.2	14
46	Computational Investigation of Gantenerumab and Crenezumab Recognition of A β Fibrils in Alzheimer's Disease Brain Tissue. ACS Chemical Neuroscience, 2020, 11, 3233-3244.	1.7	12
47	Artificial intelligence in COVID-19 drug repurposing. The Lancet Digital Health, 2020, 2, e667-e676.	5.9	349
48	Peptide-MHC Binding Reveals Conserved Allosteric Sites in MHC Class I- and Class II-Restricted T Cell Receptors (TCRs). Journal of Molecular Biology, 2020, 432, 166697.	2.0	12
49	PI3K inhibitors: review and new strategies. Chemical Science, 2020, 11, 5855-5865.	3.7	106
50	Are Parallel Proliferation Pathways Redundant?. Trends in Biochemical Sciences, 2020, 45, 554-563.	3.7	21
51	Ras assemblies and signaling at the membrane. Current Opinion in Structural Biology, 2020, 62, 140-148.	2.6	26
52	Individualized genetic network analysis reveals new therapeutic vulnerabilities in 6,700 cancer genomes. PLoS Computational Biology, 2020, 16, e1007701.	1.5	32
53	HMI-PRED: A Web Server for Structural Prediction of Host-Microbe Interactions Based on Interface Mimicry. Journal of Molecular Biology, 2020, 432, 3395-3403.	2.0	34
54	Oncogenic K-Ras4B Dimerization Enhances Downstream Mitogen-activated Protein Kinase Signaling. Journal of Molecular Biology, 2020, 432, 1199-1215.	2.0	16

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55	Target identification among known drugs by deep learning from heterogeneous networks. <i>Chemical Science</i> , 2020, 11, 1775-1797.	3.7	193
56	Network-based prediction of drug-target interactions using an arbitrary-order proximity embedded deep forest. <i>Bioinformatics</i> , 2020, 36, 2805-2812.	1.8	101
57	High-Affinity Interactions of the nSH3/cSH3 Domains of Grb2 with the C-Terminal Proline-Rich Domain of SOS1. <i>Journal of the American Chemical Society</i> , 2020, 142, 3401-3411.	6.6	25
58	The quaternary assembly of KRas4B with Raf-1 at the membrane. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 737-748.	1.9	50
59	Protein ensembles link genotype to phenotype. <i>PLoS Computational Biology</i> , 2019, 15, e1006648.	1.5	58
60	Pathogenic Autoreactive T and B Cells Cross-React with Mimotopes Expressed by a Common Human Gut Commensal to Trigger Autoimmunity. <i>Cell Host and Microbe</i> , 2019, 26, 100-113.e8.	5.1	109
61	The Structural Basis of the Farnesylated and Methylated KRas4B Interaction with Calmodulin. <i>Structure</i> , 2019, 27, 1647-1659.e4.	1.6	30
62	Does Ras Activate Raf and PI3K Allosterically?. <i>Frontiers in Oncology</i> , 2019, 9, 1231.	1.3	41
63	Ca ²⁺ -Dependent Switch of Calmodulin Interaction Mode with Tandem IQ Motifs in the Scaffolding Protein IQGAP1. <i>Biochemistry</i> , 2019, 58, 4903-4911.	1.2	12
64	Head and Neck Cancers Promote an Inflammatory Transcriptome through Coactivation of Classic and Alternative NF- κ B Pathways. <i>Cancer Immunology Research</i> , 2019, 7, 1760-1774.	1.6	17
65	Emerging Allosteric Mechanism of EGFR Activation in Physiological and Pathological Contexts. <i>Biophysical Journal</i> , 2019, 117, 5-13.	0.2	35
66	A Systems Pharmacology Approach Uncovers Wogonoside as an Angiogenesis Inhibitor of Triple-Negative Breast Cancer by Targeting Hedgehog Signaling. <i>Cell Chemical Biology</i> , 2019, 26, 1143-1158.e6.	2.5	53
67	The structural basis for Ras activation of PI3K lipid kinase. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 12021-12028.	1.3	43
68	deepDR: a network-based deep learning approach to <i>in silico</i> drug repositioning. <i>Bioinformatics</i> , 2019, 35, 5191-5198.	1.8	343
69	The mechanism of PI3K activation at the atomic level. <i>Chemical Science</i> , 2019, 10, 3671-3680.	3.7	75
70	Review: Precision medicine and driver mutations: Computational methods, functional assays and conformational principles for interpreting cancer drivers. <i>PLoS Computational Biology</i> , 2019, 15, e1006658.	1.5	83
71	A component overlapping attribute clustering (COAC) algorithm for single-cell RNA sequencing data analysis and potential pathobiological implications. <i>PLoS Computational Biology</i> , 2019, 15, e1006772.	1.5	14
72	Allostery in Its Many Disguises: From Theory to Applications. <i>Structure</i> , 2019, 27, 566-578.	1.6	285

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73	Computational Structural Biology: Successes, Future Directions, and Challenges. <i>Molecules</i> , 2019, 24, 637.	1.7	16
74	Why Are Some Driver Mutations Rare?. <i>Trends in Pharmacological Sciences</i> , 2019, 40, 919-929.	4.0	29
75	Oncoviruses Can Drive Cancer by Rewiring Signaling Pathways Through Interface Mimicry. <i>Frontiers in Oncology</i> , 2019, 9, 1236.	1.3	28
76	Antigen binding allosterically promotes Fc receptor recognition. <i>MAbs</i> , 2019, 11, 58-74.	2.6	48
77	Developments in integrative modeling with dynamical interfaces. <i>Current Opinion in Structural Biology</i> , 2019, 56, 11-17.	2.6	14
78	Precision medicine review: rare driver mutations and their biophysical classification. <i>Biophysical Reviews</i> , 2019, 11, 5-19.	1.5	43
79	Personal Mutanomes Meet Modern Oncology Drug Discovery and Precision Health. <i>Pharmacological Reviews</i> , 2019, 71, 1-19.	7.1	47
80	Interface-Based Structural Prediction of Novel Host-Pathogen Interactions. <i>Methods in Molecular Biology</i> , 2019, 1851, 317-335.	0.4	21
81	Oncogenic KRas mobility in the membrane and signaling response. <i>Seminars in Cancer Biology</i> , 2019, 54, 109-113.	4.3	20
82	Is Nanoclustering essential for all oncogenic KRas pathways? Can it explain why wild-type KRas can inhibit its oncogenic variant?. <i>Seminars in Cancer Biology</i> , 2019, 54, 114-120.	4.3	35
83	Dynamic Protein Allosteric Regulation and Disease. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1163, 25-43.	0.8	13
84	Unraveling the molecular mechanism of interactions of the Rho GTPases Cdc42 and Rac1 with the scaffolding protein IQGAP2. <i>Journal of Biological Chemistry</i> , 2018, 293, 3685-3699.	1.6	36
85	Interaction of Calmodulin with the cSH2 Domain of the p85 Regulatory Subunit. <i>Biochemistry</i> , 2018, 57, 1917-1928.	1.2	10
86	Raf-1 Cysteine-Rich Domain Increases the Affinity of K-Ras/Raf at the Membrane, Promoting MAPK Signaling. <i>Structure</i> , 2018, 26, 513-525.e2.	1.6	60
87	Atomistic-level study of the interactions between hIAPP protofibrils and membranes: Influence of pH and lipid composition. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018, 1860, 1818-1825.	1.4	33
88	Oncogenic Ras Isoforms Signaling Specificity at the Membrane. <i>Cancer Research</i> , 2018, 78, 593-602.	0.4	96
89	Structure and energetic basis of overrepresented β light chain in systemic light chain amyloidosis patients. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2294-2303.	1.8	6
90	Calmodulin and IQGAP1 activation of PI3K β and Akt in KRAS, HRAS and NRAS-driven cancers. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2304-2314.	1.8	16

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91	Mutations in LZTR1 drive human disease by dysregulating RAS ubiquitination. <i>Science</i> , 2018, 362, 1177-1182.	6.0	133
92	Autoinhibition in Ras effectors Raf, PI3K, and RASSF5: a comprehensive review underscoring the challenges in pharmacological intervention. <i>Biophysical Reviews</i> , 2018, 10, 1263-1282.	1.5	40
93	Structural disorder in four-repeat Tau fibrils reveals a new mechanism for barriers to cross-seeding of Tau isoforms. <i>Journal of Biological Chemistry</i> , 2018, 293, 17336-17348.	1.6	35
94	Molecular Recognition between A β ² -Specific Single-Domain Antibody and A β ² Misfolded Aggregates. <i>Antibodies</i> , 2018, 7, 25.	1.2	10
95	Allosteric activation of RAF in the MAPK signaling pathway. <i>Current Opinion in Structural Biology</i> , 2018, 53, 100-106.	2.6	23
96	Calmodulin (CaM) Activates PI3K by Targeting the α -CaM-Binding Motifs in Both the nSH2 and cSH2 Domains of p85. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11137-11146.	1.2	15
97	Arl2-Mediated Allosteric Release of Farnesylated KRas4B from Shuttling Factor PDE1. <i>Journal of Physical Chemistry B</i> , 2018, 122, 7503-7513.	1.2	12
98	The distinct structural preferences of tau protein repeat domains. <i>Chemical Communications</i> , 2018, 54, 5700-5703.	2.2	35
99	KRAS Activating Signaling Triggers Arteriovenous Malformations. <i>Trends in Biochemical Sciences</i> , 2018, 43, 481-483.	3.7	17
100	Peptide-MHC (pMHC) binding to a human antiviral T cell receptor induces long-range allosteric communication between pMHC- and CD3-binding sites. <i>Journal of Biological Chemistry</i> , 2018, 293, 15991-16005.	1.6	45
101	Allosteric KRas4B Can Modulate SOS1 Fast and Slow Ras Activation Cycles. <i>Biophysical Journal</i> , 2018, 115, 629-641.	0.2	24
102	Familial Mutations May Switch Conformational Preferences in β -Synuclein Fibrils. <i>ACS Chemical Neuroscience</i> , 2017, 8, 837-849.	1.7	27
103	Calmodulin and PI3K Signaling in KRAS Cancers. <i>Trends in Cancer</i> , 2017, 3, 214-224.	3.8	58
104	A New View of Pathway-Driven Drug Resistance in Tumor Proliferation. <i>Trends in Pharmacological Sciences</i> , 2017, 38, 427-437.	4.0	68
105	The dynamic mechanism of RASSF5 and MST kinase activation by Ras. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 6470-6480.	1.3	22
106	Allostery modulates the beat rate of a cardiac pacemaker. <i>Journal of Biological Chemistry</i> , 2017, 292, 6429-6430.	1.6	5
107	A Protocol for the Design of Protein and Peptide Nanostructure Self-Assemblies Exploiting Synthetic Amino Acids. <i>Methods in Molecular Biology</i> , 2017, 1529, 323-352.	0.4	2
108	Computational Tools for Allosteric Drug Discovery: Site Identification and Focus Library Design. <i>Methods in Molecular Biology</i> , 2017, 1529, 439-446.	0.4	16

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109	Flexible-body motions of calmodulin and the farnesylated hypervariable region yield a high-affinity interaction enabling K-Ras4B membrane extraction. <i>Journal of Biological Chemistry</i> , 2017, 292, 12544-12559.	1.6	40
110	Intrinsic protein disorder in oncogenic KRAS signaling. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 3245-3261.	2.4	45
111	PDE1 Binding to Ras Isoforms Provides a Route to Proper Membrane Localization. <i>Journal of Physical Chemistry B</i> , 2017, 121, 5917-5927.	1.2	26
112	Exploring the Aggregation Mechanism of Intrinsically Disordered Tau Protein. <i>World Scientific Lecture and Course Notes in Chemistry</i> , 2017, , 51-71.	0.2	1
113	Mechanisms of recognition of amyloid- β (A β) monomer, oligomer, and fibril by homologous antibodies. <i>Journal of Biological Chemistry</i> , 2017, 292, 18325-18343.	1.6	53
114	Prediction of Host-Pathogen Interactions for <i>Helicobacter pylori</i> by Interface Mimicry and Implications to Gastric Cancer. <i>Journal of Molecular Biology</i> , 2017, 429, 3925-3941.	2.0	28
115	Phosphorylated Calmodulin Promotes PI3K Activation by Binding to the SH2 Domains. <i>Biophysical Journal</i> , 2017, 113, 1956-1967.	0.2	51
116	Energetic redistribution in allostery to execute protein function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7480-7482.	3.3	41
117	Compilation and Analysis of Enzymes, Engineered Antibodies, and Nanoparticles Designed to Interfere with Amyloid- β Aggregation. <i>Israel Journal of Chemistry</i> , 2017, 57, 622-633.	1.0	2
118	Prediction of Protein Interactions by Structural Matching: Prediction of PPI Networks and the Effects of Mutations on PPIs that Combines Sequence and Structural Information. <i>Methods in Molecular Biology</i> , 2017, 1558, 255-270.	0.4	6
119	How can computation advance microbiome research?. <i>PLoS Computational Biology</i> , 2017, 13, e1005547.	1.5	4
120	Structural host-microbiota interaction networks. <i>PLoS Computational Biology</i> , 2017, 13, e1005579.	1.5	51
121	Network approaches and applications in biology. <i>PLoS Computational Biology</i> , 2017, 13, e1005771.	1.5	40
122	Allostery: An Overview of Its History, Concepts, Methods, and Applications. <i>PLoS Computational Biology</i> , 2016, 12, e1004966.	1.5	194
123	Drugging Ras GTPase: a comprehensive mechanistic and signaling structural view. <i>Chemical Society Reviews</i> , 2016, 45, 4929-4952.	18.7	150
124	Independent and core pathways in oncogenic KRAS signaling. <i>Expert Review of Proteomics</i> , 2016, 13, 711-716.	1.3	16
125	Intracellular and intercellular signaling networks in cancer initiation, development and precision anti-cancer therapy. <i>Seminars in Cell and Developmental Biology</i> , 2016, 58, 55-59.	2.3	17
126	Inhibitors of Ras-SOS Interactions. <i>ChemMedChem</i> , 2016, 11, 814-821.	1.6	62

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127	Insights Into the Allosteric Inhibition of the SUMO E2 Enzyme Ubc9. <i>Angewandte Chemie</i> , 2016, 128, 5797-5801.	1.6	1
128	OUP accepted manuscript. <i>Protein Engineering, Design and Selection</i> , 2016, 30, 67-76.	1.0	8
129	The Structural Basis of Oncogenic Mutations G12, G13 and Q61 in Small GTPase K-Ras4B. <i>Scientific Reports</i> , 2016, 6, 21949.	1.6	149
130	The higher level of complexity of K-Ras4B activation at the membrane. <i>FASEB Journal</i> , 2016, 30, 1643-1655.	0.2	73
131	TRAF3 signaling: Competitive binding and evolvability of adaptive viral molecular mimicry. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2646-2655.	1.1	30
132	How Does Hyperphosphorylation Promote Tau Aggregation and Modulate Filament Structure and Stability?. <i>ACS Chemical Neuroscience</i> , 2016, 7, 565-575.	1.7	27
133	Oncogenic KRAS signaling and YAP1/ β -catenin: Similar cell cycle control in tumor initiation. <i>Seminars in Cell and Developmental Biology</i> , 2016, 58, 79-85.	2.3	54
134	<i>PRISM-EM</i> : template interface-based modelling of multi-protein complexes guided by cryo-electron microscopy density maps. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1137-1148.	1.1	17
135	Conformational dynamics of cancer-associated MyD88-TIR domain mutant L252P (L265P) allosterically tilts the landscape toward homo-dimerization. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 347-354.	1.0	18
136	RASSF5: An MST activator and tumor suppressor in vivo but opposite in vitro. <i>Current Opinion in Structural Biology</i> , 2016, 41, 217-224.	2.6	29
137	Introduction to Protein Ensembles and Allostery. <i>Chemical Reviews</i> , 2016, 116, 6263-6266.	23.0	105
138	Conformational selection in amyloid-based immunotherapy: Survey of crystal structures of antibody-amyloid complexes. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2672-2681.	1.1	23
139	Pathogen mimicry of host protein-protein interfaces modulates immunity. <i>Seminars in Cell and Developmental Biology</i> , 2016, 58, 136-145.	2.3	45
140	Membrane-associated Ras dimers are isoform-specific: K-Ras dimers differ from H-Ras dimers. <i>Biochemical Journal</i> , 2016, 473, 1719-1732.	1.7	92
141	Protein Ensembles: How Does Nature Harness Thermodynamic Fluctuations for Life? The Diverse Functional Roles of Conformational Ensembles in the Cell. <i>Chemical Reviews</i> , 2016, 116, 6516-6551.	23.0	302
142	Ras Conformational Ensembles, Allostery, and Signaling. <i>Chemical Reviews</i> , 2016, 116, 6607-6665.	23.0	290
143	Comparison of the Conformations of <i>KRAS</i> Isoforms, K-Ras4A and K-Ras4B, Points to Similarities and Significant Differences. <i>Journal of Physical Chemistry B</i> , 2016, 120, 667-679.	1.2	45
144	A New View of Ras Isoforms in Cancers. <i>Cancer Research</i> , 2016, 76, 18-23.	0.4	87

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145	Dimerization of the SP1 Region of HIV-1 Gag Induces a Helical Conformation and Association into Helical Bundles: Implications for Particle Assembly. <i>Journal of Virology</i> , 2016, 90, 1773-1787.	1.5	34
146	Self-aggregation and coaggregation of the p53 core fragment with its aggregation gatekeeper variant. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 8098-8107.	1.3	23
147	The Role of Protein Loops and Linkers in Conformational Dynamics and Allostery. <i>Chemical Reviews</i> , 2016, 116, 6391-6423.	23.0	302
148	K-Ras4B/calmodulin/PI3K: A promising new adenocarcinoma-specific drug target?. <i>Expert Opinion on Therapeutic Targets</i> , 2016, 20, 831-842.	1.5	29
149	Coupling of the non-amyloid-component (NAC) domain and the KTK(E/Q)GV repeats stabilize the β -synuclein fibrils. <i>European Journal of Medicinal Chemistry</i> , 2016, 121, 841-850.	2.6	28
150	Editorial overview: Folding and binding: Dynamic conformational heterogeneity is pivotal to cell life. <i>Current Opinion in Structural Biology</i> , 2016, 36, iv-vi.	2.6	4
151	The disordered hypervariable region and the folded catalytic domain of oncogenic K-Ras4B partner in phospholipid binding. <i>Current Opinion in Structural Biology</i> , 2016, 36, 10-17.	2.6	38
152	Amylin β oligomers at atomic resolution using molecular dynamics simulations: a link between Type 2 diabetes and Alzheimer's disease. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 2330-2338.	1.3	74
153	Principles and Overview of Sampling Methods for Modeling Macromolecular Structure and Dynamics. <i>PLoS Computational Biology</i> , 2016, 12, e1004619.	1.5	188
154	The Structural Basis of ATP as an Allosteric Modulator. <i>Biophysical Journal</i> , 2015, 108, 528a.	0.2	4
155	The Architecture of the TIR Domain Signalosome in the Toll-like Receptor-4 Signaling Pathway. <i>Scientific Reports</i> , 2015, 5, 13128.	1.6	98
156	Mapping the Conformation Space of Wildtype and Mutant H-Ras with a Memetic, Cellular, and Multiscale Evolutionary Algorithm. <i>PLoS Computational Biology</i> , 2015, 11, e1004470.	1.5	47
157	Computational Methods for Exploration and Analysis of Macromolecular Structure and Dynamics. <i>PLoS Computational Biology</i> , 2015, 11, e1004585.	1.5	13
158	Coupling of Zinc-Binding and Secondary Structure in Nonfibrillar A β 240 Peptide Oligomerization. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 1218-1230.	2.5	16
159	GTP Binding and Oncogenic Mutations May Attenuate Hypervariable Region (HVR)-Catalytic Domain Interactions in Small GTPase K-Ras4B, Exposing the Effector Binding Site. <i>Journal of Biological Chemistry</i> , 2015, 290, 28887-28900.	1.6	73
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