

Anna R Panchenko

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

3,382
citations

136950

32
h-index

161849

54
g-index

67
all docs

67
docs citations

67
times ranked

4647
citing authors

#	ARTICLE	IF	CITATIONS
1	Deciphering Protein-Protein Interactions. Part I. Experimental Techniques and Databases. PLoS Computational Biology, 2007, 3, e42.	3.2	334
2	Deciphering Protein-Protein Interactions. Part II. Computational Methods to Predict Protein and Domain Interaction Partners. PLoS Computational Biology, 2007, 3, e43.	3.2	305
3	Physicochemical mechanisms of protein regulation by phosphorylation. Frontiers in Genetics, 2014, 5, 270.	2.3	152
4	Coupling between Histone Conformations and DNA Geometry in Nucleosomes on a Microsecond Timescale: Atomistic Insights into Nucleosome Functions. Journal of Molecular Biology, 2016, 428, 221-237.	4.2	131
5	Prediction of functional sites by analysis of sequence and structure conservation. Protein Science, 2004, 13, 884-892.	7.6	128
6	MutaBind estimates and interprets the effects of sequence variants on protein-protein interactions. Nucleic Acids Research, 2016, 44, W494-W501.	14.5	110
7	MutaBind2: Predicting the Impacts of Single and Multiple Mutations on Protein-Protein Interactions. IScience, 2020, 23, 100939.	4.1	109
8	Intrinsic Disorder in Protein Interactions: Insights From a Comprehensive Structural Analysis. PLoS Computational Biology, 2009, 5, e1000316.	3.2	104
9	Predicting the Impact of Missense Mutations on Protein-Protein Binding Affinity. Journal of Chemical Theory and Computation, 2014, 10, 1770-1780.	5.3	102
10	Cancer Missense Mutations Alter Binding Properties of Proteins and Their Interaction Networks. PLoS ONE, 2013, 8, e66273.	2.5	102
11	HistoneDB 2.0: a histone database with variants—an integrated resource to explore histones and their variants. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw014.	3.0	99
12	APOBEC Mutagenesis and Copy-Number Alterations Are Drivers of Proteogenomic Tumor Evolution and Heterogeneity in Metastatic Thoracic Tumors. Cell Reports, 2019, 26, 2651-2666.e6.	6.4	92
13	IBIS (Inferred Biomolecular Interaction Server) reports, predicts and integrates multiple types of conserved interactions for proteins. Nucleic Acids Research, 2012, 40, D834-D840.	14.5	88
14	Clonal Evolution and Heterogeneity of Osimertinib Acquired Resistance Mechanisms in EGFR Mutant Lung Cancer. Cell Reports Medicine, 2020, 1, 100007.	6.5	78
15	Distinct Structures and Dynamics of Chromatosomes with Different Human Linker Histone Isoforms. Molecular Cell, 2021, 81, 166-182.e6.	9.7	74
16	Exploring background mutational processes to decipher cancer genetic heterogeneity. Nucleic Acids Research, 2017, 45, W514-W522.	14.5	65
17	Coevolution in defining the functional specificity. Proteins: Structure, Function and Bioinformatics, 2009, 75, 231-240.	2.6	62
18	Evolution of Protein Binding Modes in Homooligomers. Journal of Molecular Biology, 2010, 395, 860-870.	4.2	61

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19	Finding driver mutations in cancer: Elucidating the role of background mutational processes. PLoS Computational Biology, 2019, 15, e1006981.	3.2	61
20	Finding weak similarities between proteins by sequence profile comparison. Nucleic Acids Research, 2003, 31, 683-689.	14.5	54
21	Threading with explicit models for evolutionary conservation of structure and sequence. , 1999, 37, 133-140.		53
22	Structural and Functional Roles of Coevolved Sites in Proteins. PLoS ONE, 2010, 5, e8591.	2.5	52
23	Nucleosome adaptability conferred by sequence and structural variations in histone H2A-H2B dimers. Current Opinion in Structural Biology, 2015, 32, 48-57.	5.7	52
24	Structural similarity of loops in protein families: toward the understanding of protein evolution. BMC Evolutionary Biology, 2005, 5, 10.	3.2	49
25	Crosstalk between Signaling Pathways Provided by Single and Multiple Protein Phosphorylation Sites. Journal of Molecular Biology, 2015, 427, 511-520.	4.2	47
26	Molecular basis of CENP-C association with the CENP-A nucleosome at yeast centromeres. Genes and Development, 2017, 31, 1958-1972.	5.9	45
27	Evolutionary plasticity of protein families: Coupling between sequence and structure variation. Proteins: Structure, Function and Bioinformatics, 2005, 61, 535-544.	2.6	43
28	Large-scale mapping of human protein interactome using structural complexes. EMBO Reports, 2012, 13, 266-271.	4.5	43
29	Molecular Biology and Evolution of Cancer: From Discovery to Action. Molecular Biology and Evolution, 2020, 37, 320-326.	8.9	43
30	Binding of regulatory proteins to nucleosomes is modulated by dynamic histone tails. Nature Communications, 2021, 12, 5280.	12.8	43
31	MS_HistoneDB, a manually curated resource for proteomic analysis of human and mouse histones. Epigenetics and Chromatin, 2017, 10, 2.	3.9	40
32	Functional States of Homooligomers: Insights from the Evolution of Glycosyltransferases. Journal of Molecular Biology, 2010, 399, 196-206.	4.2	39
33	Balancing Protein Stability and Activity in Cancer: A New Approach for Identifying Driver Mutations Affecting CBL Ubiquitin Ligase Activation. Cancer Research, 2016, 76, 561-571.	0.9	38
34	A comparison of position-specific score matrices based on sequence and structure alignments. Protein Science, 2009, 11, 361-370.	7.6	32
35	Mutational signatures and mutable motifs in cancer genomes. Briefings in Bioinformatics, 2017, 19, 1085-1101.	6.5	32
36	DNA polymerase β mutational signatures are found in a variety of different types of cancer. Cell Cycle, 2018, 17, 348-355.	2.6	32

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37	Histone tails as signaling antennas of chromatin. <i>Current Opinion in Structural Biology</i> , 2021, 67, 153-160.	5.7	32
38	Exploring Protein-Protein Interactions as Drug Targets for Anti-cancer Therapy with In Silico Workflows. <i>Methods in Molecular Biology</i> , 2017, 1647, 221-236.	0.9	31
39	Exploring functional roles of multibinding protein interfaces. <i>Protein Science</i> , 2009, 18, 1674-1683.	7.6	28
40	Analysis of protein homology by assessing the (dis)similarity in protein loop regions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 539-547.	2.6	27
41	Oncogenic potential is related to activating effect of cancer single and double somatic mutations in receptor tyrosine kinases. <i>Human Mutation</i> , 2012, 33, 1566-1575.	2.5	26
42	Activation induced deaminase mutational signature overlaps with CpG methylation sites in follicular lymphoma and other cancers. <i>Scientific Reports</i> , 2016, 6, 38133.	3.3	26
43	DNA methylation cues in nucleosome geometry, stability and unwrapping. <i>Nucleic Acids Research</i> , 2022, 50, 1864-1874.	14.5	25
44	Molecular recognition of nucleosomes by binding partners. <i>Current Opinion in Structural Biology</i> , 2019, 56, 164-170.	5.7	21
45	Computational Approaches to Prioritize Cancer Driver Missense Mutations. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2113.	4.1	20
46	Histone Octamer Structure Is Altered Early in ISW2 ATP-Dependent Nucleosome Remodeling. <i>Cell Reports</i> , 2019, 28, 282-294.e6.	6.4	20
47	Genomic profiling of multiple sequentially acquired tumor metastatic sites from an "exceptional responder" lung adenocarcinoma patient reveals extensive genomic heterogeneity and novel somatic variants driving treatment response. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a001263.	1.2	18
48	Annotating Mutational Effects on Proteins and Protein Interactions: Designing Novel and Revisiting Existing Protocols. <i>Methods in Molecular Biology</i> , 2017, 1550, 235-260.	0.9	18
49	Hydroxyl-radical footprinting combined with molecular modeling identifies unique features of DNA conformation and nucleosome positioning. <i>Nucleic Acids Research</i> , 2017, 45, 9229-9243.	14.5	18
50	Homology Inference of Protein-Protein Interactions via Conserved Binding Sites. <i>PLoS ONE</i> , 2012, 7, e28896.	2.5	15
51	Molecular Mechanisms of Oncogenesis through the Lens of Nucleosomes and Histones. <i>Journal of Physical Chemistry B</i> , 2021, 125, 3963-3976.	2.6	14
52	Structural Perspectives on the Evolutionary Expansion of Unique Protein-Protein Binding Sites. <i>Biophysical Journal</i> , 2015, 109, 1295-1306.	0.5	11
53	Coverage of protein domain families with structural protein-protein interactions: Current progress and future trends. <i>Progress in Biophysics and Molecular Biology</i> , 2014, 116, 187-193.	2.9	7
54	Structural interpretation of DNA-protein hydroxyl-radical footprinting experiments with high resolution using HYDROID. <i>Nature Protocols</i> , 2018, 13, 2535-2556.	12.0	6

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55	Editorial overview: Linking protein sequence and structural changes to function in the era of next-generation sequencing. <i>Current Opinion in Structural Biology</i> , 2015, 32, viii-x.	5.7	5
56	Human Histone Interaction Networks: An Old Concept, New Trends. <i>Journal of Molecular Biology</i> , 2021, 433, 166684.	4.2	4
57	DNA Methylation, Deamination, and Translesion Synthesis Combine to Generate Footprint Mutations in Cancer Driver Genes in B-Cell Derived Lymphomas and Other Cancers. <i>Frontiers in Genetics</i> , 2021, 12, 671866.	2.3	4
58	Trajectories of microsecond molecular dynamics simulations of nucleosomes and nucleosome core particles. <i>Data in Brief</i> , 2016, 7, 1678-1681.	1.0	3
59	Computational Large-Scale Mapping of Protein-Protein Interactions Using Structural Complexes. <i>Current Protocols in Protein Science</i> , 2013, 73, 3.9.1-3.9.9.	2.8	2
60	Editorial overview: Dynamic protein interactions “from complexes to molecular machines. <i>Current Opinion in Structural Biology</i> , 2019, 56, vi-viii.	5.7	1
61	Data sets on human histone interaction networks. <i>Data in Brief</i> , 2020, 33, 106555.	1.0	1
62	Diving into Chromatin across Space and Time. <i>Journal of Molecular Biology</i> , 2021, 433, 166884.	4.2	0
63	Clonal evolution and osimertinib resistance mechanisms identified by whole exome and transcriptome sequencing in EGFR mutant NSCLC.. <i>Journal of Clinical Oncology</i> , 2019, 37, 9049-9049.	1.6	0