

# 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	DNA methylation cues in nucleosome geometry, stability and unwrapping. <i>Nucleic Acids Research</i> , 2022, 50, 1864-1874.	14.5	25
2	Histone tails as signaling antennas of chromatin. <i>Current Opinion in Structural Biology</i> , 2021, 67, 153-160.	5.7	32
3	Distinct Structures and Dynamics of Chromatosomes with Different Human Linker Histone Isoforms. <i>Molecular Cell</i> , 2021, 81, 166-182.e6.	9.7	74
4	Human Histone Interaction Networks: An Old Concept, New Trends. <i>Journal of Molecular Biology</i> , 2021, 433, 166684.	4.2	4
5	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
6	Diving into Chromatin across Space and Time. <i>Journal of Molecular Biology</i> , 2021, 433, 166884.	4.2	0
7	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
8	Binding of regulatory proteins to nucleosomes is modulated by dynamic histone tails. <i>Nature Communications</i> , 2021, 12, 5280.	12.8	43
9	Molecular Biology and Evolution of Cancer: From Discovery to Action. <i>Molecular Biology and Evolution</i> , 2020, 37, 320-326.	8.9	43
10	Data sets on human histone interaction networks. <i>Data in Brief</i> , 2020, 33, 106555.	1.0	1
11	MutaBind2: Predicting the Impacts of Single and Multiple Mutations on Protein-Protein Interactions. <i>IScience</i> , 2020, 23, 100939.	4.1	109
12	Clonal Evolution and Heterogeneity of Osimertinib Acquired Resistance Mechanisms in EGFR Mutant Lung Cancer. <i>Cell Reports Medicine</i> , 2020, 1, 100007.	6.5	78
13	Editorial overview: Dynamic protein interactions “from complexes to molecular machines. <i>Current Opinion in Structural Biology</i> , 2019, 56, vi-viii.	5.7	1
14	Histone Octamer Structure Is Altered Early in ISW2 ATP-Dependent Nucleosome Remodeling. <i>Cell Reports</i> , 2019, 28, 282-294.e6.	6.4	20
15	Finding driver mutations in cancer: Elucidating the role of background mutational processes. <i>PLoS Computational Biology</i> , 2019, 15, e1006981.	3.2	61
16	Molecular recognition of nucleosomes by binding partners. <i>Current Opinion in Structural Biology</i> , 2019, 56, 164-170.	5.7	21
17	APOBEC Mutagenesis and Copy-Number Alterations Are Drivers of Proteogenomic Tumor Evolution and Heterogeneity in Metastatic Thoracic Tumors. <i>Cell Reports</i> , 2019, 26, 2651-2666.e6.	6.4	92
18	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

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19	DNA polymerase $\beta$ mutational signatures are found in a variety of different types of cancer. <i>Cell Cycle</i> , 2018, 17, 348-355.	2.6	32
20	Computational Approaches to Prioritize Cancer Driver Missense Mutations. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2113.	4.1	20
21	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
22	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
23	Mutational signatures and mutable motifs in cancer genomes. <i>Briefings in Bioinformatics</i> , 2017, 19, 1085-1101.	6.5	32
24	Exploring background mutational processes to decipher cancer genetic heterogeneity. <i>Nucleic Acids Research</i> , 2017, 45, W514-W522.	14.5	65
25	Molecular basis of CENP-C association with the CENP-A nucleosome at yeast centromeres. <i>Genes and Development</i> , 2017, 31, 1958-1972.	5.9	45
26	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
27	MS_HistoneDB, a manually curated resource for proteomic analysis of human and mouse histones. <i>Epigenetics and Chromatin</i> , 2017, 10, 2.	3.9	40
28	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
29	HistoneDB 2.0: a histone database with variants—an integrated resource to explore histones and their variants. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw014.	3.0	99
30	Balancing Protein Stability and Activity in Cancer: A New Approach for Identifying Driver Mutations Affecting CBL Ubiquitin Ligase Activation. <i>Cancer Research</i> , 2016, 76, 561-571.	0.9	38
31	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
32	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
33	Trajectories of microsecond molecular dynamics simulations of nucleosomes and nucleosome core particles. <i>Data in Brief</i> , 2016, 7, 1678-1681.	1.0	3
34	MutaBind estimates and interprets the effects of sequence variants on protein-protein interactions. <i>Nucleic Acids Research</i> , 2016, 44, W494-W501.	14.5	110
35	Coupling between Histone Conformations and DNA Geometry in Nucleosomes on a Microsecond Timescale: Atomistic Insights into Nucleosome Functions. <i>Journal of Molecular Biology</i> , 2016, 428, 221-237.	4.2	131
36	Crosstalk between Signaling Pathways Provided by Single and Multiple Protein Phosphorylation Sites. <i>Journal of Molecular Biology</i> , 2015, 427, 511-520.	4.2	47

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37	Structural Perspectives on the Evolutionary Expansion of Unique Protein-Protein Binding Sites. <i>Biophysical Journal</i> , 2015, 109, 1295-1306.	0.5	11
38	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
39	Nucleosome adaptability conferred by sequence and structural variations in histone H2Aâ€“H2B dimers. <i>Current Opinion in Structural Biology</i> , 2015, 32, 48-57.	5.7	52
40	Physicochemical mechanisms of protein regulation by phosphorylation. <i>Frontiers in Genetics</i> , 2014, 5, 270.	2.3	152
41	Coverage of protein domain families with structural proteinâ€“protein interactions: Current progress and future trends. <i>Progress in Biophysics and Molecular Biology</i> , 2014, 116, 187-193.	2.9	7
42	Predicting the Impact of Missense Mutations on Proteinâ€“Protein Binding Affinity. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 1770-1780.	5.3	102
43	Computational Largeâ€“Scale Mapping of Proteinâ€“Protein Interactions Using Structural Complexes. <i>Current Protocols in Protein Science</i> , 2013, 73, 3.9.1-3.9.9.	2.8	2
44	Cancer Missense Mutations Alter Binding Properties of Proteins and Their Interaction Networks. <i>PLoS ONE</i> , 2013, 8, e66273.	2.5	102
45	IBIS (Inferred Biomolecular Interaction Server) reports, predicts and integrates multiple types of conserved interactions for proteins. <i>Nucleic Acids Research</i> , 2012, 40, D834-D840.	14.5	88
46	Largeâ€“scale mapping of human protein interactome using structural complexes. <i>EMBO Reports</i> , 2012, 13, 266-271.	4.5	43
47	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
48	Homology Inference of Protein-Protein Interactions via Conserved Binding Sites. <i>PLoS ONE</i> , 2012, 7, e28896.	2.5	15
49	Structural and Functional Roles of Coevolved Sites in Proteins. <i>PLoS ONE</i> , 2010, 5, e8591.	2.5	52
50	Evolution of Protein Binding Modes in Homooligomers. <i>Journal of Molecular Biology</i> , 2010, 395, 860-870.	4.2	61
51	Functional States of Homooligomers: Insights from the Evolution of Glycosyltransferases. <i>Journal of Molecular Biology</i> , 2010, 399, 196-206.	4.2	39
52	Intrinsic Disorder in Protein Interactions: Insights From a Comprehensive Structural Analysis. <i>PLoS Computational Biology</i> , 2009, 5, e1000316.	3.2	104
53	Coevolution in defining the functional specificity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 231-240.	2.6	62
54	Exploring functional roles of multibinding protein interfaces. <i>Protein Science</i> , 2009, 18, 1674-1683.	7.6	28

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55	A comparison of position-specific score matrices based on sequence and structure alignments. <i>Protein Science</i> , 2009, 11, 361-370.	7.6	32
56	Deciphering Protein-Protein Interactions. Part II. Computational Methods to Predict Protein and Domain Interaction Partners. <i>PLoS Computational Biology</i> , 2007, 3, e43.	3.2	305
57	Deciphering Protein-Protein Interactions. Part I. Experimental Techniques and Databases. <i>PLoS Computational Biology</i> , 2007, 3, e42.	3.2	334
58	Structural similarity of loops in protein families: toward the understanding of protein evolution. <i>BMC Evolutionary Biology</i> , 2005, 5, 10.	3.2	49
59	Evolutionary plasticity of protein families: Coupling between sequence and structure variation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 535-544.	2.6	43
60	Prediction of functional sites by analysis of sequence and structure conservation. <i>Protein Science</i> , 2004, 13, 884-892.	7.6	128
61	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
62	Finding weak similarities between proteins by sequence profile comparison. <i>Nucleic Acids Research</i> , 2003, 31, 683-689.	14.5	54
63	Threading with explicit models for evolutionary conservation of structure and sequence. , 1999, 37, 133-140.		53