

Jan Kosinski

List of Publications by Year in descending order

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43
papers

3,378
citations

172207

29
h-index

243296

44
g-index

54
all docs

54
docs citations

54
times ranked

4428
citing authors

#	ARTICLE	IF	CITATIONS
1	In situ structural analysis of the human nuclear pore complex. <i>Nature</i> , 2015, 526, 140-143.	13.7	361
2	Molecular architecture of the inner ring scaffold of the human nuclear pore complex. <i>Science</i> , 2016, 352, 363-365.	6.0	284
3	Systematic analysis of protein turnover in primary cells. <i>Nature Communications</i> , 2018, 9, 689.	5.8	280
4	Molecular structures of unbound and transcribing RNA polymerase III. <i>Nature</i> , 2015, 528, 231-236.	13.7	167
5	Nuclear pores dilate and constrict in cellulose. <i>Science</i> , 2021, 374, eabd9776.	6.0	162
6	Xlink Analyzer: Software for analysis and visualization of cross-linking data in the context of three-dimensional structures. <i>Journal of Structural Biology</i> , 2015, 189, 177-183.	1.3	156
7	A 'Frankenstein's monster' approach to comparative modeling: Merging the finest fragments of Fold-Recognition models and iterative model refinement aided by 3D structure evaluation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 369-379.	1.5	154
8	In-cell architecture of the nuclear pore and snapshots of its turnover. <i>Nature</i> , 2020, 586, 796-800.	13.7	139
9	AI-based structure prediction empowers integrative structural analysis of human nuclear pores. <i>Science</i> , 2022, 376, .	6.0	136
10	Influenza Polymerase Can Adopt an Alternative Configuration Involving a Radical Repacking of PB2 Domains. <i>Molecular Cell</i> , 2016, 61, 125-137.	4.5	123
11	In situ architecture of the algal nuclear pore complex. <i>Nature Communications</i> , 2018, 9, 2361.	5.8	107
12	The PD-(D/E)XK superfamily revisited: identification of new members among proteins involved in DNA metabolism and functional predictions for domains of (hitherto) unknown function. <i>BMC Bioinformatics</i> , 2005, 6, 172.	1.2	84
13	Phylogenetic analysis of haloalkane dehalogenases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 305-316.	1.5	82
14	Architecture of the yeast Elongator complex. <i>EMBO Reports</i> , 2017, 18, 264-279.	2.0	75
15	Frankenstein becomes a cyborg: The automatic recombination and realignment of fold recognition models in CASP6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 106-113.	1.5	66
16	Structure and Evolutionary Origin of Ca ²⁺ -Dependent Herring Type II Antifreeze Protein. <i>PLoS ONE</i> , 2007, 2, e548.	1.1	66
17	REPAIRtoire—a database of DNA repair pathways. <i>Nucleic Acids Research</i> , 2011, 39, D788-D792.	6.5	61
18	Structural insights into transcription initiation by yeast RNA polymerase I. <i>EMBO Journal</i> , 2017, 36, 2698-2709.	3.5	58

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19	The PMS2 Subunit of Human MutL \pm Contains a Metal Ion Binding Domain of the Iron-Dependent Repressor Protein Family. <i>Journal of Molecular Biology</i> , 2008, 382, 610-627.	2.0	55
20	Analysis of the Quaternary Structure of the MutL C-terminal Domain. <i>Journal of Molecular Biology</i> , 2005, 351, 895-909.	2.0	53
21	Identification of Lynch syndrome mutations in the MLH1-PMS2 interface that disturb dimerization and mismatch repair. <i>Human Mutation</i> , 2010, 31, 975-982.	1.1	52
22	Structure of Prototypic Peptide Transporter DtpA from <i>E. coli</i> in Complex with Valganciclovir Provides Insights into Drug Binding of Human PepT1. <i>Journal of the American Chemical Society</i> , 2019, 141, 2404-2412.	6.6	51
23	Automated structure modeling of large protein assemblies using crosslinks as distance restraints. <i>Nature Methods</i> , 2016, 13, 515-520.	9.0	49
24	Novel protein fold discovered in the PabI family of restriction enzymes. <i>Nucleic Acids Research</i> , 2007, 35, 1908-1918.	6.5	47
25	Structure of the mycobacterial ESX-5 type VII secretion system pore complex. <i>Science Advances</i> , 2021, 7, .	4.7	45
26	Molecular basis of tRNA recognition by the Elongator complex. <i>Science Advances</i> , 2019, 5, eaaw2326.	4.7	44
27	Identifying an interaction site between MutH and the C-terminal domain of MutL by crosslinking, affinity purification, chemical coding and mass spectrometry. <i>Nucleic Acids Research</i> , 2006, 34, 3169-3180.	6.5	41
28	Crystal structure of <i>Bacillus subtilis</i> TrmB, the tRNA (m7G46) methyltransferase. <i>Nucleic Acids Research</i> , 2006, 34, 1925-1934.	6.5	36
29	Integrative Structural Biology in the Era of Accurate Structure Prediction. <i>Journal of Molecular Biology</i> , 2021, 433, 167127.	2.0	36
30	Integrative structural modeling of macromolecular complexes using Assemblin. <i>Nature Protocols</i> , 2022, 17, 152-176.	5.5	33
31	A short linear motif in scaffold Nup145C connects Y-complex with pre-assembled outer ring Nup82 complex. <i>Nature Communications</i> , 2017, 8, 1107.	5.8	32
32	Higher-order assemblies of oligomeric cargo receptor complexes form the membrane scaffold of the Cvt vesicle. <i>EMBO Reports</i> , 2016, 17, 1044-1060.	2.0	26
33	Mva1269I: A Monomeric Type IIS Restriction Endonuclease from <i>Micrococcus Varians</i> with Two EcoRI- and FokI-like Catalytic Domains. <i>Journal of Biological Chemistry</i> , 2005, 280, 41584-41594.	1.6	25
34	From the resolution revolution to evolution: structural insights into the evolutionary relationships between vesicle coats and the nuclear pore. <i>Current Opinion in Structural Biology</i> , 2018, 52, 32-40.	2.6	21
35	Structure of the TFIIC subcomplex \bar{I}_{A} provides insights into RNA polymerase III pre-initiation complex formation. <i>Nature Communications</i> , 2020, 11, 4905.	5.8	16
36	Probabilistic cross-link analysis and experiment planning for high-throughput elucidation of protein structure. <i>Protein Science</i> , 2009, 13, 3298-3313.	3.1	15

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37	A model of restriction endonuclease MvaI in complex with DNA: A template for interpretation of experimental data and a guide for specificity engineering. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 324-336.	1.5	13
38	MODexplorer: an integrated tool for exploring protein sequence, structure and function relationships. <i>Bioinformatics</i> , 2013, 29, 953-954.	1.8	13
39	Improving your target-template alignment with MODalign. <i>Bioinformatics</i> , 2012, 28, 1038-1039.	1.8	10
40	Structural role of essential light chains in the apicomplexan glideosome. <i>Communications Biology</i> , 2020, 3, 568.	2.0	10
41	Specialization versus conservation: How Pol I and Pol III use the conserved architecture of the pre-initiation complex for specialized transcription. <i>Transcription</i> , 2016, 7, 127-132.	1.7	9
42	Theoretical model of restriction endonuclease HpaI in complex with DNA, predicted by fold recognition and validated by site-directed mutagenesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 1059-1068.	1.5	8
43	Physiological truncation and domain organization of a novel uracil-DNA-degrading factor. <i>FEBS Journal</i> , 2010, 277, 1245-1259.	2.2	5