Jan Kosinski

List of Publications by Year
in descending order

43 papers	3,378 citations	172386 29 h-index	243529 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. Nature, 2015, 526, 140-143.	13.7	361
2	Molecular architecture of the inner ring scaffold of the human nuclear pore complex. Science, 2016, 352, 363-365.	6.0	284
3	Systematic analysis of protein turnover in primary cells. Nature Communications, 2018, 9, 689.	5.8	280
4	Molecular structures of unbound and transcribing RNA polymerase III. Nature, 2015, 528, 231-236.	13.7	167
5	Nuclear pores dilate and constrict in cellulo. Science, 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. Journal of Structural Biology, 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. Proteins: Structure, Function and Bioinformatics, 2003, 53, 369-379.	1.5	154
8	In-cell architecture of the nuclear pore and snapshots of its turnover. Nature, 2020, 586, 796-800.	13.7	139
9	AI-based structure prediction empowers integrative structural analysis of human nuclear pores. Science, 2022, 376, .	6.0	136
10	Influenza Polymerase Can Adopt an Alternative Configuration Involving a Radical Repacking of PB2 Domains. Molecular Cell, 2016, 61, 125-137.	4.5	123
11	In situ architecture of the algal nuclear pore complex. Nature Communications, 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. BMC Bioinformatics, 2005, 6, 172.	1.2	84
13	Phylogenetic analysis of haloalkane dehalogenases. Proteins: Structure, Function and Bioinformatics, 2007, 67, 305-316.	1.5	82
14	Architecture of the yeast Elongator complex. EMBO Reports, 2017, 18, 264-279.	2.0	75
15	FRankenstein becomes a cyborg: The automatic recombination and realignment of fold recognition models in CASP6. Proteins: Structure, Function and Bioinformatics, 2005, 61, 106-113.	1.5	66
16	Structure and Evolutionary Origin of Ca2+-Dependent Herring Type II Antifreeze Protein. PLoS ONE, 2007, 2, e548.	1.1	66
17	REPAIRtoire--a database of DNA repair pathways. Nucleic Acids Research, 2011, 39, D788-D792.	6.5	61
18	Structural insights into transcription initiation by yeast RNA polymerase I. EMBO Journal, 2017, 36, 2698-2709.	3.5	58

#	ARTICLE	IF	CITATIONS
19	The PMS2 Subunit of Human MutLÎ± Contains a Metal Ion Binding Domain of the Iron-Dependent Repressor Protein Family. Journal of Molecular Biology, 2008, 382, 610-627.	2.0	55
20	Analysis of the Quaternary Structure of the MutL C-terminal Domain. Journal of Molecular Biology, 2005, 351, 895-909.	2.0	53
21	Identification of Lynch syndrome mutations in the MLH1-PMS2 interface that disturb dimerization and mismatch repair. Human Mutation, 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. Journal of the American Chemical Society, 2019, 141, 2404-2412.	6.6	51
23	Automated structure modeling of large protein assemblies using crosslinks as distance restraints. Nature Methods, 2016, 13, 515-520.	9.0	49
24	Novel protein fold discovered in the PabI family of restriction enzymes. Nucleic Acids Research, 2007, 35, 1908-1918.	6.5	47
25	Structure of the mycobacterial ESX-5 type VII secretion system pore complex. Science Advances, 2021, 7, .	4.7	45
26	Molecular basis of tRNA recognition by the Elongator complex. Science Advances, 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. Nucleic Acids Research, 2006, 34, 3169-3180.	6.5	41
28	Crystal structure of Bacillus subtilis TrmB, the tRNA (m7G46) methyltransferase. Nucleic Acids Research, 2006, 34, 1925-1934.	6.5	36
29	Integrative Structural Biology in the Era of Accurate Structure Prediction. Journal of Molecular Biology, 2021, 433, 167127.	2.0	36
30	Integrative structural modeling of macromolecular complexes using Assembline. Nature Protocols, 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. Nature Communications, 2017, 8, 1107.	5.8	32
32	Higherâ€order assemblies of oligomeric cargo receptor complexes form the membrane scaffold of the Cvt vesicle. EMBO Reports, 2016, 17, 1044-1060.	2.0	26
33	Mva1269I: A Monomeric Type IIS Restriction Endonuclease from Micrococcus Varians with Two EcoRI- and FokI-like Catalytic Domains. Journal of Biological Chemistry, 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. Current Opinion in Structural Biology, 2018, 52, 32-40.	2.6	21
35	Structure of the TFIIIC subcomplex Ï„A provides insights into RNA polymerase III pre-initiation complex formation. Nature Communications, 2020, 11, 4905.	5.8	16
36	Probabilistic cross-link analysis and experiment planning for high-throughput elucidation of protein structure. Protein Science, 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. Proteins: Structure, Function and Bioinformatics, 2007, 68, 324-336.	1.5	13
38	MODexplorer: an integrated tool for exploring protein sequence, structure and function relationships. Bioinformatics, 2013, 29, 953-954.	1.8	13
39	Improving your target-template alignment with MODalign. Bioinformatics, 2012, 28, 1038-1039.	1.8	10
40	Structural role of essential light chains in the apicomplexan glideosome. Communications Biology, 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. Transcription, 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. Proteins: Structure, Function and Bioinformatics, 2006, 63, 1059-1068.	1.5	8
43	Physiological truncation and domain organization of a novel uracil€DNA€degrading factor. FEBS Journal, 2010, 277, 1245-1259.	2.2	5