

Jan Kosinski

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

50
papers

2,257
citations

24
h-index

47
g-index

54
ext. papers

2,894
ext. citations

14.2
avg, IF

4.6
L-index

#	Paper	IF	Citations
50	Nuclear pores dilate and constrict in cellulose. <i>Science</i> , 2021 , 374, eabd9776	33.3	32
49	Integrative structural modeling of macromolecular complexes using Assemblin. <i>Nature Protocols</i> , 2021 ,	18.8	3
48	Structure of the mycobacterial ESX-5 type VII secretion system pore complex. <i>Science Advances</i> , 2021 , 7,	14.3	7
47	Integrative Structural Biology in the Era of Accurate Structure Prediction. <i>Journal of Molecular Biology</i> , 2021 , 433, 167127	6.5	10
46	Structural role of essential light chains in the apicomplexan glideosome. <i>Communications Biology</i> , 2020 , 3, 568	6.7	6
45	Structure of the TFIIC subcomplex α provides insights into RNA polymerase III pre-initiation complex formation. <i>Nature Communications</i> , 2020 , 11, 4905	17.4	7
44	In-cell architecture of the nuclear pore and snapshots of its turnover. <i>Nature</i> , 2020 , 586, 796-800	50.4	71
43	Molecular basis of tRNA recognition by the Elongator complex. <i>Science Advances</i> , 2019 , 5, eaaw2326	14.3	21
42	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	16.4	22
41	Systematic analysis of protein turnover in primary cells. <i>Nature Communications</i> , 2018 , 9, 689	17.4	145
40	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	8.1	14
39	In situ architecture of the algal nuclear pore complex. <i>Nature Communications</i> , 2018 , 9, 2361	17.4	76
38	Architecture of the yeast Elongator complex. <i>EMBO Reports</i> , 2017 , 18, 264-279	6.5	53
37	A short linear motif in scaffold Nup145C connects Y-complex with pre-assembled outer ring Nup82 complex. <i>Nature Communications</i> , 2017 , 8, 1107	17.4	23
36	Structural insights into transcription initiation by yeast RNA polymerase I. <i>EMBO Journal</i> , 2017 , 36, 2698-2709	17.4	45
35	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, 127-32	4.8	6
34	Influenza Polymerase Can Adopt an Alternative Configuration Involving a Radical Repacking of PB2 Domains. <i>Molecular Cell</i> , 2016 , 61, 125-37	17.6	92

33	Higher-order assemblies of oligomeric cargo receptor complexes form the membrane scaffold of the Cvt vesicle. <i>EMBO Reports</i> , 2016 , 17, 1044-60	6.5	20
32	Molecular architecture of the inner ring scaffold of the human nuclear pore complex. <i>Science</i> , 2016 , 352, 363-5	33.3	216
31	Automated structure modeling of large protein assemblies using crosslinks as distance restraints. <i>Nature Methods</i> , 2016 , 13, 515-20	21.6	44
30	In situ structural analysis of the human nuclear pore complex. <i>Nature</i> , 2015 , 526, 140-143	50.4	267
29	Molecular structures of unbound and transcribing RNA polymerase III. <i>Nature</i> , 2015 , 528, 231-6	50.4	127
28	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, 177-83	3.4	104
27	MODexplorer: an integrated tool for exploring protein sequence, structure and function relationships. <i>Bioinformatics</i> , 2013 , 29, 953-4	7.2	13
26	Improving your target-template alignment with MODalign. <i>Bioinformatics</i> , 2012 , 28, 1038-9	7.2	10
25	REPAIRtoire--a database of DNA repair pathways. <i>Nucleic Acids Research</i> , 2011 , 39, D788-92	20.1	44
24	Physiological truncation and domain organization of a novel uracil-DNA-degrading factor. <i>FEBS Journal</i> , 2010 , 277, 1245-59	5.7	5
23	Identification of Lynch syndrome mutations in the MLH1-PMS2 interface that disturb dimerization and mismatch repair. <i>Human Mutation</i> , 2010 , 31, 975-82	4.7	43
22	Template Based Prediction of Three-Dimensional Protein Structures: Fold Recognition and Comparative Modeling 2008 , 87-116		1
21	The PMS2 subunit of human MutLalpha contains a metal ion binding domain of the iron-dependent repressor protein family. <i>Journal of Molecular Biology</i> , 2008 , 382, 610-27	6.5	51
20	Phylogenetic analysis of haloalkane dehalogenases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 67, 305-16	4.2	71
19	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, 324-36	4.2	12
18	Novel protein fold discovered in the PabI family of restriction enzymes. <i>Nucleic Acids Research</i> , 2007 , 35, 1908-18	20.1	45
17	Structure and evolutionary origin of Ca(2+)-dependent herring type II antifreeze protein. <i>PLoS ONE</i> , 2007 , 2, e548	3.7	55
16	Crystal structure of <i>Bacillus subtilis</i> TrmB, the tRNA (m7G46) methyltransferase. <i>Nucleic Acids Research</i> , 2006 , 34, 1925-34	20.1	31

15	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, 3169-80	20.1	40
14	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, 1059-68	4.2	7
13	Analysis of the quaternary structure of the MutL C-terminal domain. <i>Journal of Molecular Biology</i> , 2005 , 351, 895-909	6.5	53
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	3.6	70
11	FRankensteIn becomes a cyborg: the automatic recombination and realignment of fold recognition models in CASP6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61 Suppl 7, 106-13	4.2	63
10	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, 41584-94	5.4	24
9	Probabilistic cross-link analysis and experiment planning for high-throughput elucidation of protein structure. <i>Protein Science</i> , 2004 , 13, 3298-313	6.3	13
8	A "FRankensteIn 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 Suppl 6, 369-79	4.2	146
7	In situ architecture of the algal nuclear pore complex		1
6	Artificial intelligence reveals nuclear pore complexity		7
5	In cell architecture of the nuclear pore complex and snapshots of its turnover		4
4	Nuclear pores constrict upon energy depletion		14
3	Structure of the mycobacterial ESX-5 Type VII Secretion System hexameric pore complex		4
2	Structural role of essential light chains in the apicomplexan glideosome		2
1	Integrative structural modelling of macromolecular complexes using AssemblIne		3