

Franz Herzog

List of Publications by Year in descending order

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33
papers

2,859
citations

236925

25
h-index

395702

33
g-index

40
all docs

40
docs citations

40
times ranked

4169
citing authors

#	ARTICLE	IF	CITATIONS
1	Phospho-regulated Bim1/EB1 interactions trigger Dam1c ring assembly at the budding yeast outer kinetochore. EMBO Journal, 2021, 40, e108004.	7.8	12
2	A structural inventory of native ribosomal ABCE1-43S pre-initiation complexes. EMBO Journal, 2021, 40, e105179.	7.8	35
3	C-Terminal Motifs of the MTW1 Complex Cooperatively Stabilize Outer Kinetochore Assembly in Budding Yeast. Cell Reports, 2020, 32, 108190.	6.4	5
4	Auto-inhibition of Mif2/CENP-C ensures centromere-dependent kinetochore assembly in budding yeast. EMBO Journal, 2020, 39, e102938.	7.8	21
5	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. Analytical Chemistry, 2019, 91, 6953-6961.	6.5	100
6	Fuzzy Interactions Form and Shape the Histone Transport Complex. Molecular Cell, 2019, 73, 1191-1203.e6.	9.7	21
7	A conserved filamentous assembly underlies the structure of the meiotic chromosome axis. ELife, 2019, 8, .	6.0	100
8	The COMA complex interacts with Cse4 and positions Sli15/Ipl1 at the budding yeast inner kinetochore. ELife, 2019, 8, .	6.0	64
9	Structure of the RZZ complex and molecular basis of its interaction with Spindly. Journal of Cell Biology, 2017, 216, 961-981.	5.2	65
10	The AAA + ATPase TRIP13 remodels HORMA domains through N-terminal engagement and unfolding. EMBO Journal, 2017, 36, 2419-2434.	7.8	69
11	Structural basis for the disaggregase activity and regulation of Hsp104. ELife, 2016, 5, .	6.0	48
12	Molecular requirements for the inter-subunit interaction and kinetochore recruitment of SKAP and Astrin. Nature Communications, 2016, 7, 11407.	12.8	31
13	Topology and structure of an engineered human cohesin complex bound to Pds5B. Nature Communications, 2016, 7, 12523.	12.8	42
14	Determination of local chromatin composition by CasID. Nucleus, 2016, 7, 476-484.	2.2	55
15	Insights from biochemical reconstitution into the architecture of human kinetochores. Nature, 2016, 537, 249-253.	27.8	148
16	Structure of the MIS12 Complex and Molecular Basis of Its Interaction with CENP-C at Human Kinetochores. Cell, 2016, 167, 1028-1040.e15.	28.9	126
17	Mec1, INO80, and the PAF1 complex cooperate to limit transcription replication conflicts through RNAPII removal during replication stress. Genes and Development, 2016, 30, 337-354.	5.9	103
18	Structure of transcribing mammalian RNA polymerase II. Nature, 2016, 529, 551-554.	27.8	174

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19	Structural and functional insights into the fly microRNA biogenesis factor Loquacious. <i>Rna</i> , 2016, 22, 383-396.	3.5	11
20	Insights from the reconstitution of the divergent outer kinetochore of <i>Drosophila melanogaster</i> . <i>Open Biology</i> , 2016, 6, 150236.	3.6	41
21	Architecture and RNA binding of the human negative elongation factor. <i>ELife</i> , 2016, 5, .	6.0	54
22	<i>Vis</i> : a web server for the schematic visualization and interpretation of crosslink-derived spatial restraints. <i>Nucleic Acids Research</i> , 2015, 43, W362-W369.	14.5	116
23	Proteasome assembly from 15S precursors involves major conformational changes and recycling of the Pba1–Pba2 chaperone. <i>Nature Communications</i> , 2015, 6, 6123.	12.8	42
24	CENP-C is a blueprint for constitutive centromere-associated network assembly within human kinetochores. <i>Journal of Cell Biology</i> , 2015, 210, 11-22.	5.2	141
25	Molecular Basis of Transcription-Coupled Pre-mRNA Capping. <i>Molecular Cell</i> , 2015, 58, 1079-1089.	9.7	109
26	A cooperative mechanism drives budding yeast kinetochore assembly downstream of CENP-A. <i>Journal of Cell Biology</i> , 2014, 206, 509-524.	5.2	99
27	Conserved architecture of the core RNA polymerase II initiation complex. <i>Nature Communications</i> , 2014, 5, 4310.	12.8	37
28	Characterization of a DNA exit gate in the human cohesin ring. <i>Science</i> , 2014, 346, 968-972.	12.6	170
29	Structure of the VipA/B Type VI Secretion Complex Suggests a Contraction-State-Specific Recycling Mechanism. <i>Cell Reports</i> , 2014, 8, 20-30.	6.4	74
30	Measuring Spatial Restraints on Native Protein Complexes Using Isotope-Tagged Chemical Cross-Linking and Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2014, 1091, 259-273.	0.9	2
31	The pseudo GTPase CENP-M drives human kinetochore assembly. <i>ELife</i> , 2014, 3, e02978.	6.0	107
32	Structural Probing of a Protein Phosphatase 2A Network by Chemical Cross-Linking and Mass Spectrometry. <i>Science</i> , 2012, 337, 1348-1352.	12.6	357
33	False discovery rate estimation for cross-linked peptides identified by mass spectrometry. <i>Nature Methods</i> , 2012, 9, 901-903.	19.0	273