

Franz Herzog

List of Publications by Year in descending order

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Version: 2024-02-01

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	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
2	False discovery rate estimation for cross-linked peptides identified by mass spectrometry. <i>Nature Methods</i> , 2012, 9, 901-903.	19.0	273
3	Structure of transcribing mammalian RNA polymerase II. <i>Nature</i> , 2016, 529, 551-554.	27.8	174
4	Characterization of a DNA exit gate in the human cohesin ring. <i>Science</i> , 2014, 346, 968-972.	12.6	170
5	Insights from biochemical reconstitution into the architecture of human kinetochores. <i>Nature</i> , 2016, 537, 249-253.	27.8	148
6	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
7	Structure of the MIS12 Complex and Molecular Basis of Its Interaction with CENP-C at Human Kinetochores. <i>Cell</i> , 2016, 167, 1028-1040.e15.	28.9	126
8	<i>xVis</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
9	Molecular Basis of Transcription-Coupled Pre-mRNA Capping. <i>Molecular Cell</i> , 2015, 58, 1079-1089.	9.7	109
10	The pseudo GTPase CENP-M drives human kinetochore assembly. <i>ELife</i> , 2014, 3, e02978.	6.0	107
11	Mec1, INO80, and the PAF1 complex cooperate to limit transcription replication conflicts through RNAPII removal during replication stress. <i>Genes and Development</i> , 2016, 30, 337-354.	5.9	103
12	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	6.5	100
13	A conserved filamentous assembly underlies the structure of the meiotic chromosome axis. <i>ELife</i> , 2019, 8, .	6.0	100
14	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
15	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
16	The <sc>AAA</sc> + <sc>ATP</sc> ase <sc>TRIP</sc> 13 remodels <sc>HORMA</sc> domains through N-terminal engagement and unfolding. <i>EMBO Journal</i> , 2017, 36, 2419-2434.	7.8	69
17	Structure of the RZZ complex and molecular basis of its interaction with Spindly. <i>Journal of Cell Biology</i> , 2017, 216, 961-981.	5.2	65
18	The COMA complex interacts with Cse4 and positions Sli15/Ipl1 at the budding yeast inner kinetochore. <i>ELife</i> , 2019, 8, .	6.0	64

#	ARTICLE	IF	CITATIONS
19	Determination of local chromatin composition by CasID. <i>Nucleus</i> , 2016, 7, 476-484.	2.2	55
20	Architecture and RNA binding of the human negative elongation factor. <i>ELife</i> , 2016, 5, .	6.0	54
21	Structural basis for the disaggregase activity and regulation of Hsp104. <i>ELife</i> , 2016, 5, .	6.0	48
22	Proteasome assembly from 15S precursors involves major conformational changes and recycling of the Pba1 and Pba2 chaperone. <i>Nature Communications</i> , 2015, 6, 6123.	12.8	42
23	Topology and structure of an engineered human cohesin complex bound to Pds5B. <i>Nature Communications</i> , 2016, 7, 12523.	12.8	42
24	Insights from the reconstitution of the divergent outer kinetochore of <i>Drosophila melanogaster</i> . <i>Open Biology</i> , 2016, 6, 150236.	3.6	41
25	Conserved architecture of the core RNA polymerase II initiation complex. <i>Nature Communications</i> , 2014, 5, 4310.	12.8	37
26	A structural inventory of native ribosomal ABCE1 and 43S pre-initiation complexes. <i>EMBO Journal</i> , 2021, 40, e105179.	7.8	35
27	Molecular requirements for the inter-subunit interaction and kinetochore recruitment of SKAP and Astrin. <i>Nature Communications</i> , 2016, 7, 11407.	12.8	31
28	Fuzzy Interactions Form and Shape the Histone Transport Complex. <i>Molecular Cell</i> , 2019, 73, 1191-1203.e6.	9.7	21
29	Autoinhibition of Mif2/CENP-E ensures centromere-dependent kinetochore assembly in budding yeast. <i>EMBO Journal</i> , 2020, 39, e102938.	7.8	21
30	Phosphoregulated Bim1/EB1 interactions trigger Dam1c ring assembly at the budding yeast outer kinetochore. <i>EMBO Journal</i> , 2021, 40, e108004.	7.8	12
31	Structural and functional insights into the fly microRNA biogenesis factor Loquacious. <i>Rna</i> , 2016, 22, 383-396.	3.5	11
32	C-Terminal Motifs of the MTW1 Complex Cooperatively Stabilize Outer Kinetochore Assembly in Budding Yeast. <i>Cell Reports</i> , 2020, 32, 108190.	6.4	5
33	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