

# Alex Zelter

## List of Publications by Year in descending order

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Version: 2024-02-01

27  
papers

1,167  
citations

471371

17  
h-index

580701

25  
g-index

31  
all docs

31  
docs citations

31  
times ranked

1664  
citing authors

#	ARTICLE	IF	CITATIONS
1	Kojak: Efficient Analysis of Chemically Cross-Linked Protein Complexes. <i>Journal of Proteome Research</i> , 2015, 14, 2190-2198.	1.8	155
2	Phosphoregulation and depolymerization-driven movement of the Dam1 complex do not require ring formation. <i>Nature Cell Biology</i> , 2008, 10, 407-414.	4.6	136
3	Ring closure activates yeast $\hat{1}^3$ TuRC for species-specific microtubule nucleation. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 132-137.	3.6	115
4	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	3.2	100
5	Computationally designed high specificity inhibitors delineate the roles of BCL2 family proteins in cancer. <i>ELife</i> , 2016, 5, .	2.8	65
6	Human Ska complex and Ndc80 complex interact to form a load-bearing assembly that strengthens kinetochoreâ€“microtubule attachments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2740-2745.	3.3	65
7	A Bifunctional Role for the UHRF1âˆ“UBL Domain in the Control of Hemi-methylated DNA-Dependent Histone Ubiquitylation. <i>Molecular Cell</i> , 2018, 72, 753-765.e6.	4.5	58
8	The Ndc80 complex bridges two Dam1 complex rings. <i>ELife</i> , 2017, 6, .	2.8	52
9	The molecular architecture of the Dam1 kinetochore complex is defined by cross-linking based structural modelling. <i>Nature Communications</i> , 2015, 6, 8673.	5.8	51
10	ProXL (Protein Cross-Linking Database): A Platform for Analysis, Visualization, and Sharing of Protein Cross-Linking Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2016, 15, 2863-2870.	1.8	51
11	Regulation of outer kinetochore Ndc80 complex-based microtubule attachments by the central kinetochore Mis12/MIND complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5583-9.	3.3	40
12	Isotope Signatures Allow Identification of Chemically Cross-Linked Peptides by Mass Spectrometry: A Novel Method to Determine Interresidue Distances in Protein Structures through Cross-Linking. <i>Journal of Proteome Research</i> , 2010, 9, 3583-3589.	1.8	32
13	Direct proteinâ€“protein interactions and substrate channeling between cellular retinoic acid binding proteins and <sc>CYP</sc>26B1. <i>FEBS Letters</i> , 2016, 590, 2527-2535.	1.3	31
14	Identification of Wiskott-Aldrich syndrome protein (WASP) binding sites on the branched actin filament nucleator Arp2/3 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1409-E1418.	3.3	30
15	Higher-order oligomerization of Spc110p drives $\hat{1}^3$ -tubulin ring complex assembly. <i>Molecular Biology of the Cell</i> , 2016, 27, 2245-2258.	0.9	29
16	CYP26C1 Is a Hydroxylase of Multiple Active Retinoids and Interacts with Cellular Retinoic Acid Binding Proteins. <i>Molecular Pharmacology</i> , 2018, 93, 489-503.	1.0	27
17	Kinetochore-associated Stu2 promotes chromosome biorientation in vivo. <i>PLoS Genetics</i> , 2019, 15, e1008423.	1.5	26
18	CM1-driven assembly and activation of yeast $\hat{1}^3$ -tubulin small complex underlies microtubule nucleation. <i>ELife</i> , 2021, 10, .	2.8	23

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19	Coupling Unbiased Mutagenesis to High-throughput DNA Sequencing Uncovers Functional Domains in the Ndc80 Kinetochores of <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2013, 195, 159-170.	1.2	21
20	Kinetochores in <i>Saccharomyces cerevisiae</i> Requires a Tightly Folded Conformation of the Ndc80 Complex. <i>Genetics</i> , 2014, 198, 1483-1493.	1.2	17
21	Novel phosphorylation states of the yeast spindle pole body. <i>Biology Open</i> , 2018, 7, .	0.6	12
22	Three interacting regions of the Ndc80 and Dam1 complexes support microtubule tip-coupling under load. <i>Journal of Cell Biology</i> , 2022, 221, .	2.3	11
23	Discovery and Visualization of Uncharacterized Drug-Protein Adducts Using Mass Spectrometry. <i>Analytical Chemistry</i> , 2022, 94, 3501-3509.	3.2	7
24	Cullin-independent recognition of HHARI substrates by a dynamic RBR catalytic domain. <i>Structure</i> , 2022, , .	1.6	6
25	Prox1 (Protein Cross-Linking Database): A Public Server, QC Tools, and Other Major Updates. <i>Journal of Proteome Research</i> , 2019, 18, 759-764.	1.8	4
26	Differential inactivation mechanism and covalent adduct formation of ALDH1A1 and ALDH1A2 by WIN18,446. <i>FASEB Journal</i> , 2018, 32, 833.10.	0.2	0
27	Role of the Spc105 Complex in Organization and Microtubule-Binding Activity of the Budding Yeast Kinetochores. <i>FASEB Journal</i> , 2018, 32, 533.105.	0.2	0