

Florian Stengel

List of Publications by Year in descending order

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33
papers

2,104
citations

304743

22
h-index

377865

34
g-index

45
all docs

45
docs citations

45
times ranked

3199
citing authors

#	ARTICLE	IF	CITATIONS
1	Crosslinking and Mass Spectrometry: An Integrated Technology to Understand the Structure and Function of Molecular Machines. <i>Trends in Biochemical Sciences</i> , 2016, 41, 20-32.	7.5	330
2	Crucial HSP70 co-chaperone complex unlocks metazoan protein disaggregation. <i>Nature</i> , 2015, 524, 247-251.	27.8	320
3	Quaternary dynamics and plasticity underlie small heat shock protein chaperone function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2007-2012.	7.1	231
4	Molecular Architecture of the 40Sâ€¦eIF1â€¦eIF3 Translation Initiation Complex. <i>Cell</i> , 2014, 158, 1123-1135.	28.9	193
5	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	6.5	100
6	Structural characterization of the interaction of Ubp6 with the 26S proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8626-8631.	7.1	98
7	Mechanisms for restraining cAMP-dependent protein kinase revealed by subunit quantitation and cross-linking approaches. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10414-10419.	7.1	92
8	Early Scanning of Nascent Polypeptides inside the Ribosomal Tunnel by NAC. <i>Molecular Cell</i> , 2019, 75, 996-1006.e8.	9.7	60
9	Molecular Landscape of the Ribosome Pre-initiation Complex during mRNA Scanning: Structural Role for eIF3c and Its Control by eIF5. <i>Cell Reports</i> , 2017, 18, 2651-2663.	6.4	54
10	Structural dynamics of the E6AP/UBE3A-E6-p53 enzyme-substrate complex. <i>Nature Communications</i> , 2018, 9, 4441.	12.8	52
11	Mechanism of completion of peptidyltransferase centre assembly in eukaryotes. <i>ELife</i> , 2019, 8, .	6.0	49
12	HspB8 prevents aberrant phase transitions of FUS by chaperoning its folded RNA-binding domain. <i>ELife</i> , 2021, 10, .	6.0	42
13	Molecular basis of AKAP79 regulation by calmodulin. <i>Nature Communications</i> , 2017, 8, 1681.	12.8	41
14	Identification of Proteins Interacting with Ubiquitin Chains. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 15764-15768.	13.8	40
15	The Evolving Contribution of Mass Spectrometry to Integrative Structural Biology. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 966-974.	2.8	36
16	Proteome-Wide Structural Probing of Low-Abundant Protein Interactions by Cross-Linking Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 4016-4022.	6.5	36
17	Chemical Cross-Linking/Mass Spectrometry Maps the Amyloid Î² Peptide Binding Region on Both Apolipoprotein E Domains. <i>ACS Chemical Biology</i> , 2015, 10, 1010-1016.	3.4	34
18	The ubiquitin-like modifier FAT10 interferes with SUMO activation. <i>Nature Communications</i> , 2019, 10, 4452.	12.8	29

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19	Structural and Biochemical Characterization of the Cop9 Signalosome CSN5/CSN6 Heterodimer. PLoS ONE, 2014, 9, e105688.	2.5	27
20	Lipidated apolipoprotein E4 structure and its receptor binding mechanism determined by a combined cross-linking coupled to mass spectrometry and molecular dynamics approach. PLoS Computational Biology, 2018, 14, e1006165.	3.2	27
21	A comprehensive landscape of 60S ribosome biogenesis factors. Cell Reports, 2022, 38, 110353.	6.4	23
22	Parkin is an E3 ligase for the ubiquitin-like modifier FAT10, which inhibits Parkin activation and mitophagy. Cell Reports, 2021, 34, 108857.	6.4	22
23	Site-specific ubiquitylation acts as a regulator of linker histone H1. Nature Communications, 2021, 12, 3497.	12.8	17
24	The Length of a Ubiquitin Chain: A General Factor for Selective Recognition by Ubiquitin-Binding Proteins. Angewandte Chemie - International Edition, 2020, 59, 12371-12375.	13.8	14
25	Chemical proteomic profiling reveals protein interactors of the alarmones diadenosine triphosphate and tetraphosphate. Nature Communications, 2021, 12, 5808.	12.8	14
26	Identification of Small-Molecule Activators of the Ubiquitin Ligase E6AP/UBE3A and Angelman Syndrome-Derived E6AP/UBE3A Variants. Cell Chemical Biology, 2020, 27, 1510-1520.e6.	5.2	11
27	Identifizierung von Interaktoren von Ubiquitinketten. Angewandte Chemie, 2017, 129, 15972-15976.	2.0	10
28	Pathological polyQ expansion does not alter the conformation of the Huntingtin-HAP40 complex. Structure, 2021, 29, 804-809.e5.	3.3	8
29	Chemical Proteomics of the Tumor Suppressor Fhit Covalently Bound to the Cofactor Ap ³ A Elucidates Its Inhibitory Action on Translation. Journal of the American Chemical Society, 2022, 144, 8613-8623.	13.7	7
30	Interactome of Site-Specifically Acetylated Linker Histone H1. Journal of Proteome Research, 2021, 20, 4443-4451.	3.7	5
31	A ubiquitin variant-based affinity approach selectively identifies substrates of the ubiquitin ligase E6AP in complex with HPV-11 E6 or HPV-16 E6. Journal of Biological Chemistry, 2020, 295, 15070-15082.	3.4	3
32	Structural Probing of Hsp26 Activation and Client Binding by Quantitative Cross-Linking Mass Spectrometry. Analytical Chemistry, 2021, 93, 13226-13234.	6.5	3
33	Die Länge einer Ubiquitinkette: ein genereller Faktor für die selektive Erkennung durch Ubiquitin-Bindende Proteine. Angewandte Chemie, 2020, 132, 12470-12474.	2.0	0