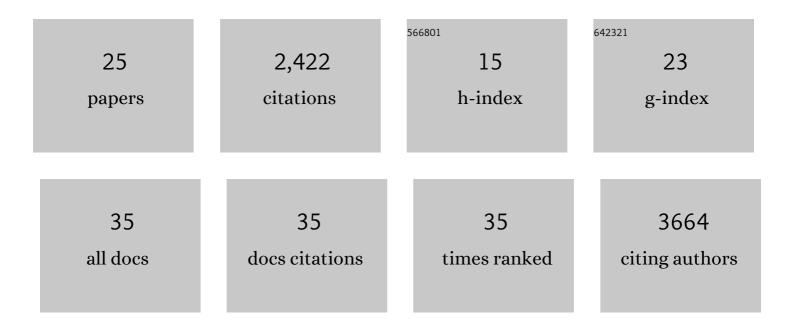
Peter Tessarz

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Histone N-terminal acetyltransferase NAA40 links one-carbon metabolism to chemoresistance. Oncogene, 2022, 41, 571-585.	2.6	8
2	The impact of genomic variation on protein phosphorylation states and regulatory networks. Molecular Systems Biology, 2022, 18, e10712.	3.2	9
3	Metabolism and chromatin: A dynamic duo that regulates development and ageing. BioEssays, 2021, 43, e2000273.	1.2	11
4	Epigenetic alterations in stem cell ageing—a promising target for age-reversing interventions?. Briefings in Functional Genomics, 2021, , .	1.3	1
5	<i>N</i> 1-acetylspermidine is a determinant of hair follicle stem cell fate. Journal of Cell Science, 2021, 134, .	1.2	11
6	Longâ€lived macrophage reprogramming drives spike proteinâ€mediated inflammasome activation in COVIDâ€19. EMBO Molecular Medicine, 2021, 13, e14150.	3.3	98
7	The RNA-binding protein Puf5 contributes to buffering of mRNA upon chromatin-mediated changes in nascent transcription. Journal of Cell Science, 2021, 134, .	1.2	0
8	Nhp2 is a reader of H2AQ105me and part of aÂnetwork integrating metabolism with rRNA synthesis. EMBO Reports, 2021, 22, e52435.	2.0	5
9	Chromatin remodeling due to degradation of citrate carrier impairs osteogenesis of aged mesenchymal stem cells. Nature Aging, 2021, 1, 810-825.	5.3	37
10	NET-prism enables RNA polymerase-dedicated transcriptional interrogation at nucleotide resolution. RNA Biology, 2019, 16, 1156-1165.	1.5	5
11	Ageing and sources of transcriptional heterogeneity. Biological Chemistry, 2019, 400, 867-878.	1.2	26
12	SIRT7-Dependent Deacetylation of Fibrillarin Controls Histone H2A Methylation and rRNA Synthesis during the Cell Cycle. Cell Reports, 2018, 25, 2946-2954.e5.	2.9	60
13	Transcriptional repression by FACT is linked to regulation of chromatin accessibility at the promoter of ES cells. Life Science Alliance, 2018, 1, e201800085.	1.3	30
14	Histone Modifications in Ageing and Lifespan Regulation. Current Molecular Biology Reports, 2016, 2, 26-35.	0.8	30
15	Glutamine methylation in histone H2A is an RNA-polymerase-I-dedicated modification. Nature, 2014, 505, 564-568.	13.7	186
16	Histone core modifications regulating nucleosome structure and dynamics. Nature Reviews Molecular Cell Biology, 2014, 15, 703-708.	16.1	775
17	Cooperative and independent activities of Sgt2 and Get5 in the targeting of tail-anchored proteins. Biological Chemistry, 2011, 392, 601-8.	1.2	28
18	The Yeast AAA ⁺ Chaperone Hsp104 Is Part of a Network That Links the Actin Cytoskeleton with the Inheritance of Damaged Proteins. Molecular and Cellular Biology, 2009, 29, 3738-3745.	1.1	66

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#	Article	IF	CITATIONS
19	Cellular quality control of protein aggregates. FASEB Journal, 2009, 23, 195.2.	0.2	Ο
20	Substrate threading through the central pore of the Hsp104 chaperone as a common mechanism for protein disaggregation and prion propagation. Molecular Microbiology, 2008, 68, 87-97.	1.2	171
21	Common and specific mechanisms of AAA+ proteins involved in protein quality control. Biochemical Society Transactions, 2008, 36, 120-125.	1.6	70
22	Novel insights into the mechanism of chaperone-assisted protein disaggregation. Biological Chemistry, 2005, 386, 739-44.	1.2	92
23	Substrate recognition by the AAA+ chaperone ClpB. Nature Structural and Molecular Biology, 2004, 11, 607-615.	3.6	219
24	Thermotolerance Requires Refolding of Aggregated Proteins by Substrate Translocation through the Central Pore of ClpB. Cell, 2004, 119, 653-665.	13.5	433
25	Inhibition of ubiquitin/proteasome-dependent proteolysis inSaccharomyces cerevisiaeby a Gly-Ala repeat. FEBS Letters, 2003, 555, 397-404.	1.3	39