Alexander Buchberger

List of Publications by Year
in descending order

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40 papers	4,490 citations	185998 28 h-index	288905 40 g-index
42 all docs	42 docs citations	42 times ranked	4033 citing authors

#	Article	IF	Citations
1	Unfolding by Cdc48/p97: different strokes for different folks. Trends in Cell Biology, 2022, , .	3.6	6
2	Role of the Ubiquitin System in Stress Granule Metabolism. International Journal of Molecular Sciences, 2022, 23, 3624.	1.8	12
3	USP28 enables oncogenic transformation of respiratory cells, and its inhibition potentiates molecular therapy targeting mutant EGFR, BRAF and PI3K. Molecular Oncology, 2022, 16, 3082-3106.	2.1	4
4	Comparative profiling of stress granule clearance reveals differential contributions of the ubiquitin system. Life Science Alliance, 2021, 4, e202000927.	1.3	25
5	ZFAND1 Recruits p97 and the 26S Proteasome to Promote the Clearance of Arsenite-Induced Stress Granules. Molecular Cell, 2018, 70, 906-919.e7.	4.5	123
6	Control of p97 function by cofactor binding. FEBS Letters, 2015, 589, 2578-2589.	1.3	181
7	Suppression of <scp>LUBAC</scp>â€mediated linear ubiquitination by a specific interaction between <scp>LUBAC</scp> and the deubiquitinases <scp>CYLD</scp> and <scp>OTULIN</scp>. Genes To Cells, 2014, 19, 254-272.	0.5	107
8	ERQC Autophagy: Yet Another Way to Die. Molecular Cell, 2014, 54, 3-4.	4.5	15
9	Roles of Cdc48 in Regulated Protein Degradation in Yeast. Sub-Cellular Biochemistry, 2013, 66, 195-222.	1.0	30
10	The Budding Yeast Cdc48Shp1 Complex Promotes Cell Cycle Progression by Positive Regulation of Protein Phosphatase 1 (Glc7). PLoS ONE, 2013, 8, e56486.	1.1	19
11	Hierarchical Binding of Cofactors to the AAA ATPase p97. Structure, 2011, 19, 833-843.	1.6	91
12	Cdc48: a power machine in protein degradation. Trends in Biochemical Sciences, 2011, 36, 515-523.	3.7	207
13	Cellular Functions of Ufd2 and Ufd3 in Proteasomal Protein Degradation Depend on Cdc48 Binding. Molecular and Cellular Biology, 2011, 31, 1528-1539.	1.1	45
14	The General Definition of the p97/Valosin-containing Protein (VCP)-interacting Motif (VIM) Delineates a New Family of p97 Cofactors. Journal of Biological Chemistry, 2011, 286, 38670-38678.	1.6	58
15	Imbalances in p97 coâ€factor interactions in human proteinopathy. EMBO Reports, 2010, 11, 479-485.	2.0	95
16	Control of Ubiquitin Conjugation by Cdc48 and Its Cofactors. Sub-Cellular Biochemistry, 2010, 54, 17-30.	1.0	18
17	Protein Quality Control in the Cytosol and the Endoplasmic Reticulum: Brothers in Arms. Molecular Cell, 2010, 40, 238-252.	4.5	441
18	VHL Mutations Linked to Type 2C von Hippel-Lindau Disease Cause Extensive Structural Perturbations in pVHL. Journal of Biological Chemistry, 2009, 284, 10514-10522.	1.6	20

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19	UBXD1 binds p97 through two independent binding sites. Biochemical and Biophysical Research Communications, 2009, 380, 303-307.	1.0	37
20	UBX domain proteins: major regulators of the AAA ATPase Cdc48/p97. Cellular and Molecular Life Sciences, 2008, 65, 2360-2371.	2.4	249
21	A yeast two-hybrid system reconstituting substrate recognition of the von Hippel-Lindau tumor suppressor protein. Nucleic Acids Research, 2007, 35, e142-e142.	6.5	12
22	Renal cell carcinoma risk in type 2 von Hippelâ€“Lindau disease correlates with defects in pVHL stability and HIF-1Î± interactions. Oncogene, 2006, 25, 370-377.	2.6	67
23	The PUB Domain Functions as a p97 Binding Module in Human Peptide N-Glycanase. Journal of Biological Chemistry, 2006, 281, 25502-25508.	1.6	84
24	Membrane-bound Ubx2 recruits Cdc48 to ubiquitin ligases and their substrates to ensure efficient ER-associated protein degradation. Nature Cell Biology, 2005, 7, 999-1006.	4.6	268
25	Shp1 and Ubx2 are adaptors of Cdc48 involved in ubiquitinâ€dependent protein degradation. EMBO Reports, 2004, 5, 818-824.	2.0	156
26	Protein Turnover: A CHIP Programmed for Proteolysis. Current Biology, 2002, 12, R26-R28.	1.8	67
27	From UBA to UBX: new words in the ubiquitin vocabulary. Trends in Cell Biology, 2002, 12, 216-221.	3.6	156
28	The UBX domain: a widespread ubiquitin-like module. Journal of Molecular Biology, 2001, 307, 17-24.	2.0	130
29	Comparative Sequence Analysis of the VHL Tumor Suppressor Gene. Genomics, 2000, 65, 253-265.	1.3	54
30	Biophysical Characterization of Elongin C from Saccharomyces cerevisiae. Biochemistry, 2000, 39, 12512-12512.	1.2	2
31	Biophysical Characterization of Elongin C from Saccharomyces cerevisiae. Biochemistry, 2000, 39, 11137-11146.	1.2	10
32	Functional Defects of the DnaK756 Mutant Chaperone ofEscherichia coli Indicate Distinct Roles for Amino- and Carboxyl-terminal Residues in Substrate and Co-chaperone Interaction and Interdomain Communication. Journal of Biological Chemistry, 1999, 274, 38017-38026.	1.6	25
33	Mutations in the DnaK chaperone affecting interaction with the DnaJ cochaperone. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 15229-15234.	3.3	170
34	GrpE Accelerates Nucleotide Exchange of the Molecular Chaperone DnaK with an Associative Displacement Mechanismâ€. Biochemistry, 1997, 36, 3417-3422.	1.2	175
35	Interaction of Hsp70 chaperones with substrates. Nature Structural and Molecular Biology, 1997, 4, 342-349.	3.6	334
36	Substrate Shuttling Between the DnaK and GroEL Systems Indicates a Chaperone Network Promoting Protein Folding. Journal of Molecular Biology, 1996, 261, 328-333.	2.0	140

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37	Nucleotide-induced Conformational Changes in the ATPase and Substrate Binding Domains of the DnaK Chaperone Provide Evidence for Interdomain Communication. Journal of Biological Chemistry, 1995, 270, 16903-16910.	1.6	233
38	The Role of ATP in the Functional Cycle of the DnaK Chaperone System. Journal of Molecular Biology, 1995, 249, 126-137.	2.0	383
39	The chaperone function of DnaK requires the coupling of ATPase activity with substrate binding through residue E171.. EMBO Journal, 1994, 13, 1687-1695.	3.5	114
40	A conserved loop in the ATPase domain of the DnaK chaperone is essential for stable binding of GrpE. Nature Structural and Molecular Biology, 1994, 1, 95-101.	3.6	124