

The AAA ATPase Vps4 binds ESCRT-III substrates through dipeptide-binding pockets

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Cool views of membrane remodeling. <i>Current Opinion in Colloid and Interface Science</i> , 2018, 34, 17-31.	3.4	2
2	Structure and Function of the 26S Proteasome. <i>Annual Review of Biochemistry</i> , 2018, 87, 697-724.	5.0	497
3	ESCRT-mediated sorting and intraluminal vesicle concatenation in plants. <i>Biochemical Society Transactions</i> , 2018, 46, 537-545.	1.6	23
4	ATP hydrolysis-coupled peptide translocation mechanism of <i>Mycobacterium tuberculosis</i> ClpB. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9560-E9569.	3.3	72
5	Substrate-engaged 26 <i>S</i> proteasome structures reveal mechanisms for ATP-hydrolysis-driven translocation. <i>Science</i> , 2018, 362, .	6.0	226
6	Microtubule-severing enzymes: From cellular functions to molecular mechanism. <i>Journal of Cell Biology</i> , 2018, 217, 4057-4069.	2.3	135
7	Inside job: how the ESCRTs release HIV-1 from infected cells. <i>Biochemical Society Transactions</i> , 2018, 46, 1029-1036.	1.6	30
8	Structural basis for disassembly of katanin heterododecamers. <i>Journal of Biological Chemistry</i> , 2018, 293, 10590-10605.	1.6	21
9	Structures, Functions, and Dynamics of ESCRT-III/Vps4 Membrane Remodeling and Fission Complexes. <i>Annual Review of Cell and Developmental Biology</i> , 2018, 34, 85-109.	4.0	205
10	A spiral path to unfolding. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 763-765.	3.6	0
11	Sorting out how Msp1 maintains mitochondrial membrane proteostasis. <i>Mitochondrion</i> , 2019, 49, 128-134.	1.6	9
12	An allosteric network in spastin couples multiple activities required for microtubule severing. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 671-678.	3.6	51
13	Structure of the Cdc48 segregase in the act of unfolding an authentic substrate. <i>Science</i> , 2019, 365, 502-505.	6.0	138
14	Substrate processing by the Cdc48 ATPase complex is initiated by ubiquitin unfolding. <i>Science</i> , 2019, 365, .	6.0	233
15	Structure and mechanism of the ESCRT pathway AAA+ ATPase Vps4. <i>Biochemical Society Transactions</i> , 2019, 47, 37-45.	1.6	25
16	Structures and operating principles of the replisome. <i>Science</i> , 2019, 363, .	6.0	119
17	Structural basis for substrate gripping and translocation by the ClpB AAA+ disaggregase. <i>Nature Communications</i> , 2019, 10, 2393.	5.8	88
18	The pre-synaptic fusion machinery. <i>Current Opinion in Structural Biology</i> , 2019, 54, 179-188.	2.6	72

#	ARTICLE	IF	CITATIONS
19	Protein translocation by the SecA ATPase occurs by a powerâ€stroke mechanism. EMBO Journal, 2019, 38, .	3.5	47
20	VPS4 triggers constriction and cleavage of ESCRT-III helical filaments. Science Advances, 2019, 5, eaau7198.	4.7	84
21	Spiraling in Control: Structures and Mechanisms of the Hsp104 Disaggregase. Cold Spring Harbor Perspectives in Biology, 2019, 11, a034033.	2.3	77
22	The role of VPS4 in ESCRT-III polymer remodeling. Biochemical Society Transactions, 2019, 47, 441-448.	1.6	36
23	Cryo-EM structures and dynamics of substrate-engaged human 26S proteasome. Nature, 2019, 565, 49-55.	13.7	264
24	The regulation of Endosomal Sorting Complex Required for Transport and accessory proteins in multivesicular body sorting and enveloped viral budding - An overview. International Journal of Biological Macromolecules, 2019, 127, 1-11.	3.6	53
25	Stairway to translocation: AAA+ motor structures reveal the mechanisms of ATPâ€dependent substrate translocation. Protein Science, 2020, 29, 407-419.	3.1	87
26	Katanin Grips the Î²-Tubulin Tail through an Electropositive Double Spiral to Sever Microtubules. Developmental Cell, 2020, 52, 118-131.e6.	3.1	58
27	HORMA Domain Proteins and a Trip13-like ATPase Regulate Bacterial cGAS-like Enzymes to Mediate Bacteriophage Immunity. Molecular Cell, 2020, 77, 709-722.e7.	4.5	116
28	The molecular principles governing the activity and functional diversity of AAA+ proteins. Nature Reviews Molecular Cell Biology, 2020, 21, 43-58.	16.1	173
29	Modular and coordinated activity of AAA+ active sites in the double-ring ClpA unfoldase of the ClpAP protease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25455-25463.	3.3	11
30	Rubisco activase requires residues in the large subunit N terminus to remodel inhibited plant Rubisco. Journal of Biological Chemistry, 2020, 295, 16427-16435.	1.6	13
31	VPS4A Mutations in Humans Cause Syndromic Congenital Dyserythropoietic Anemia due to Cytokinesis and Trafficking Defects. American Journal of Human Genetics, 2020, 107, 1149-1156.	2.6	20
33	Msp1/ATAD1 in Protein Quality Control and Regulation of Synaptic Activities. Annual Review of Cell and Developmental Biology, 2020, 36, 141-164.	4.0	22
34	Determining the Structural Basis of Cofactor and Substrate Interactions with Cdc48. Microscopy and Microanalysis, 2020, 26, 578-579.	0.2	0
35	Structural basis for distinct operational modes and protease activation in AAA+ protease Lon. Science Advances, 2020, 6, eaba8404.	4.7	55
36	Structures of AAA protein translocase Bcs1 suggest translocation mechanism of a folded protein. Nature Structural and Molecular Biology, 2020, 27, 202-209.	3.6	33
37	Structure of spastin bound to a glutamate-rich peptide implies a hand-over-hand mechanism of substrate translocation. Journal of Biological Chemistry, 2020, 295, 435-443.	1.6	38

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38	AAA+ ATPases in Protein Degradation: Structures, Functions and Mechanisms. <i>Biomolecules</i> , 2020, 10, 629.	1.8	37
39	Conformational plasticity of the ClpAP AAA+ protease couples protein unfolding and proteolysis. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 406-416.	3.6	51
40	Structural snapshots of the cellular folded protein translocation machinery Bcs1. <i>FEBS Journal</i> , 2021, 288, 2870-2883.	2.2	1
42	The Cryo-EM Effect: Structural Biology of Neurodegenerative Disease Proteostasis Factors. <i>Journal of Neuro pathology and Experimental Neurology</i> , 2021, 80, 494-513.	0.9	4
43	Design principles of the ESCRT-III Vps24-Vps2 module. <i>ELife</i> , 2021, 10, .	2.8	21
46	Factors underlying asymmetric pore dynamics of disaggregase and microtubule-severing AAA+ machines. <i>Biophysical Journal</i> , 2021, 120, 3437-3454.	0.2	12
48	Molecular basis for ATPase-powered substrate translocation by the Lon AAA+ protease. <i>Journal of Biological Chemistry</i> , 2021, 297, 101239.	1.6	12
49	Structure and Function of the AAA+ ATPase p97, a Key Player in Protein Homeostasis. <i>Sub-Cellular Biochemistry</i> , 2019, 93, 221-272.	1.0	13
50	Structure, Dynamics and Function of the 26S Proteasome. <i>Sub-Cellular Biochemistry</i> , 2021, 96, 1-151.	1.0	64
56	Structural principles of SNARE complex recognition by the AAA+ protein NSF. <i>ELife</i> , 2018, 7, .	2.8	67
57	Structure of Vps4 with circular peptides and implications for translocation of two polypeptide chains by AAA+ ATPases. <i>ELife</i> , 2019, 8, .	2.8	41
58	An ESCRT-LEM protein surveillance system is poised to directly monitor the nuclear envelope and nuclear transport system. <i>ELife</i> , 2019, 8, .	2.8	92
59	Structures of the ATP-fueled ClpXP proteolytic machine bound to protein substrate. <i>ELife</i> , 2020, 9, .	2.8	105
60	Structure of the AAA protein Msp1 reveals mechanism of mislocalized membrane protein extraction. <i>ELife</i> , 2020, 9, .	2.8	38
61	The AAA+ superfamily: a review of the structural and mechanistic principles of these molecular machines. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2022, 57, 156-187.	2.3	54
66	Highly Sensitive and Specific Responses of Oyster Hemocytes to Copper Exposure: Single-Cell Transcriptomic Analysis of Different Cell Populations. <i>Environmental Science & Technology</i> , 2022, 56, 2497-2510.	4.6	24
67	Conserved structural elements specialize ATAD1 as a membrane protein extraction machine. <i>ELife</i> , 2022, 11, .	2.8	6
68	Active conformation of the p97-p47 unfoldase complex. <i>Nature Communications</i> , 2022, 13, 2640.	5.8	18

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69	Proteolytic regulation of mitochondrial oxidative phosphorylation components in plants. <i>Biochemical Society Transactions</i> , 2022, 50, 1119-1132.	1.6	3
70	Insights into the Structure and Function of the Pex1/Pex6 AAA-ATPase in Peroxisome Homeostasis. <i>Cells</i> , 2022, 11, 2067.	1.8	11
71	AAA-ATPase Thorase inhibits mTOR signaling through the disassembly of the mTOR complex 1. <i>Nature Communications</i> , 2022, 13, .	5.8	2
72	Recycling of cell surface membrane proteins from yeast endosomes is regulated by ubiquitinated Ist1. <i>Journal of Cell Biology</i> , 2022, 221, .	2.3	11
74	Modelling membrane reshaping by staged polymerization of ESCRT-III filaments. <i>PLoS Computational Biology</i> , 2022, 18, e1010586.	1.5	6
75	Ubiquitin modulates 26 S proteasome conformational dynamics and promotes substrate degradation. <i>Science Advances</i> , 2022, 8, .	4.7	8
76	Deciphering the mechanism and function of Hsp100 unfoldases from protein structure. <i>Biochemical Society Transactions</i> , 2022, 50, 1725-1736.	1.6	1
77	Structural basis of SecA-mediated protein translocation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	4
78	The <i>S. cerevisiae</i> Yta7 ATPase hexamer contains a unique bromodomain tier that functions in nucleosome disassembly. <i>Journal of Biological Chemistry</i> , 2022, , 102852.	1.6	1