Structural basis of protein translocation by the Vps4-Vt

ELife 6, DOI: 10.7554/elife.24487

Citation Report

#	Article	IF	CITATIONS
1	Structure of the mitochondrial inner membrane AAA+ protease YME1 gives insight into substrate processing. Science, 2017, 358, .	12.6	179
2	Structural pathway of regulated substrate transfer and threading through an Hsp100 disaggregase. Science Advances, 2017, 3, e1701726.	10.3	112
3	Dynamic functional assembly of the Torsin AAA+ ATPase and its modulation by LAP1. Molecular Biology of the Cell, 2017, 28, 2765-2772.	2.1	26
4	Katanin spiral and ring structures shed light on power stroke for microtubule severing. Nature Structural and Molecular Biology, 2017, 24, 717-725.	8.2	97
5	Recruitment dynamics of ESCRT-III and Vps4 to endosomes and implications for reverse membrane budding. ELife, 2017, 6, .	6.0	138
6	Cool views of membrane remodeling. Current Opinion in Colloid and Interface Science, 2018, 34, 17-31.	7.4	2
7	Structure and Function of the 26S Proteasome. Annual Review of Biochemistry, 2018, 87, 697-724.	11.1	497
8	A Nonâ€Competitive Inhibitor of VCP/p97 and VPS4 Reveals Conserved Allosteric Circuits in Type I and II AAA ATPases. Angewandte Chemie, 2018, 130, 1592-1596.	2.0	0
9	A Nonâ€Competitive Inhibitor of VCP/p97 and VPS4 Reveals Conserved Allosteric Circuits in Type I and II AAA ATPases. Angewandte Chemie - International Edition, 2018, 57, 1576-1580.	13.8	23
10	Cryo-EM structures of the human INO80 chromatin-remodeling complex. Nature Structural and Molecular Biology, 2018, 25, 37-44.	8.2	46
11	VCP/p97-Mediated Unfolding as a Principle in Protein Homeostasis and Signaling. Molecular Cell, 2018, 69, 182-194.	9.7	288
12	Hinge–Linker Elements in the AAA+ Protein Unfoldase ClpX Mediate Intersubunit Communication, Assembly, and Mechanical Activity. Biochemistry, 2018, 57, 6787-6796.	2.5	18
13	Structural Insights into Mdn1, an Essential AAA Protein Required for Ribosome Biogenesis. Cell, 2018, 175, 822-834.e18.	28.9	42
14	Substrate-engaged 26 <i>S</i> proteasome structures reveal mechanisms for ATP-hydrolysis–driven translocation. Science, 2018, 362, .	12.6	226
15	Reversible inhibition of the ClpP protease via an N-terminal conformational switch. Proceedings of the United States of America, 2018, 115, E6447-E6456.	7.1	56
16	Mechanism for remodelling of the cell cycle checkpoint protein MAD2 by the ATPase TRIP13. Nature, 2018, 559, 274-278.	27.8	109
17	Expanded Coverage of the 26S Proteasome Conformational Landscape Reveals Mechanisms of Peptidase Gating. Cell Reports, 2018, 24, 1301-1315.e5.	6.4	108
18	Dividing the Archaeal Way: The Ancient Cdv Cell-Division Machinery. Frontiers in Microbiology, 2018, 9, 174.	3.5	56

#	Article	IF	CITATIONS
19	Structural basis for disassembly of katanin heterododecamers. Journal of Biological Chemistry, 2018, 293, 10590-10605.	3.4	21
20	Cotranslocational processing of the protein substrate calmodulin by an AAA+ unfoldase occurs via unfolding and refolding intermediates. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4786-E4795.	7.1	12
21	Structures, Functions, and Dynamics of ESCRT-III/Vps4 Membrane Remodeling and Fission Complexes. Annual Review of Cell and Developmental Biology, 2018, 34, 85-109.	9.4	205
22	ESCRT and Membrane Protein Ubiquitination. Progress in Molecular and Subcellular Biology, 2018, 57, 107-135.	1.6	30
23	Mitochondrial AAA proteases: A stairway to degradation. Mitochondrion, 2019, 49, 121-127.	3.4	11
24	Structural Mapping of Missense Mutations in the Pex1/Pex6 Complex. International Journal of Molecular Sciences, 2019, 20, 3756.	4.1	15
25	Unique Structural Features of the Mitochondrial AAA+ Protease AFG3L2 Reveal the Molecular Basis for Activity in Health and Disease. Molecular Cell, 2019, 75, 1073-1085.e6.	9.7	58
26	Structure of the Cdc48 segregase in the act of unfolding an authentic substrate. Science, 2019, 365, 502-505.	12.6	138
27	Structural Insights into AQP2 Targeting to Multivesicular Bodies. International Journal of Molecular Sciences, 2019, 20, 5351.	4.1	10
28	How the 26S Proteasome Degrades Ubiquitinated Proteins in the Cell. Biomolecules, 2019, 9, 395.	4.0	18
29	Structure and mechanism of the ESCRT pathway AAA+ ATPase Vps4. Biochemical Society Transactions, 2019, 47, 37-45.	3.4	25
30	Two-Step Activation Mechanism of the ClpB Disaggregase for Sequential Substrate Threading by the Main ATPase Motor. Cell Reports, 2019, 27, 3433-3446.e4.	6.4	46
31	Mechanisms of Ï $_{f}$ 54-Dependent Transcription Initiation and Regulation. Journal of Molecular Biology, 2019, 431, 3960-3974.	4.2	70
32	Structural features underlying recognition and translocation of extracellular polysaccharides. Interface Focus, 2019, 9, 20180060.	3.0	11
33	A lipid gating mechanism for the channel-forming O antigen ABC transporter. Nature Communications, 2019, 10, 824.	12.8	44
34	The role of VPS4 in ESCRT-III polymer remodeling. Biochemical Society Transactions, 2019, 47, 441-448.	3.4	36
35	AMPK regulates ESCRT-dependent microautophagy of proteasomes concomitant with proteasome storage granule assembly during glucose starvation. PLoS Genetics, 2019, 15, e1008387.	3.5	21
36	Cryo-EM structure of substrate-free E.Âcoli Lon protease provides insights into the dynamics of Lon machinery. Current Research in Structural Biology, 2019, 1, 13-20.	2.2	19

CITATION REPORT

CITATION REPORT

#	Article	IF	CITATIONS
37	Structural basis of nucleosome assembly by the Abo1 AAA+ÂATPase histone chaperone. Nature Communications, 2019, 10, 5764.	12.8	36
38	Cryo-EM structures and dynamics of substrate-engaged human 26S proteasome. Nature, 2019, 565, 49-55.	27.8	264
39	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.	7.5	53
40	Stairway to translocation: AAA+ motor structures reveal the mechanisms of ATPâ€dependent substrate translocation. Protein Science, 2020, 29, 407-419.	7.6	87
41	The molecular principles governing the activity and functional diversity of AAA+ proteins. Nature Reviews Molecular Cell Biology, 2020, 21, 43-58.	37.0	173
42	Kinetic Analysis of AAA+ Translocases by Combined Fluorescence and Anisotropy Methods. Biophysical Journal, 2020, 119, 1335-1350.	0.5	2
43	Structural asymmetry governs the assembly and GTPase activity of McrBC restriction complexes. Nature Communications, 2020, 11, 5907.	12.8	7
44	VPS4A Mutations in Humans Cause Syndromic Congenital Dyserythropoietic Anemia due to Cytokinesis and Trafficking Defects. American Journal of Human Genetics, 2020, 107, 1149-1156.	6.2	20
46	Structure and assembly of ESCRT-III helical Vps24 filaments. Science Advances, 2020, 6, eaba4897.	10.3	32
47	Synthetic Lethal Interaction between the ESCRT Paralog Enzymes VPS4A and VPS4B in Cancers Harboring Loss of Chromosome 18q or 16q. Cell Reports, 2020, 33, 108493.	6.4	28
48	A Structural View on ESCRT-Mediated Abscission. Frontiers in Cell and Developmental Biology, 2020, 8, 586880.	3.7	10
49	The AAA+ ATPase Msp1 is a processive protein translocase with robust unfoldase activity. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14970-14977.	7.1	20
50	Structural basis for distinct operational modes and protease activation in AAA+ protease Lon. Science Advances, 2020, 6, eaba8404.	10.3	55
51	Rearranging AAA+ architecture to accommodate folded substrates. Nature Structural and Molecular Biology, 2020, 27, 225-226.	8.2	1
52	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.	3.4	38
53	Structure of the Bcs1 AAA-ATPase suggests an airlock-like translocation mechanism for folded proteins. Nature Structural and Molecular Biology, 2020, 27, 142-149.	8.2	32
54	AAA+ ATPases in Protein Degradation: Structures, Functions and Mechanisms. Biomolecules, 2020, 10, 629.	4.0	37
55	Cutting, Amplifying, and Aligning Microtubules with Severing Enzymes. Trends in Cell Biology, 2021, 31, 50-61.	7.9	51

ARTICLE IF CITATIONS Viral packaging ATPases utilize a glutamate switch to couple ATPase activity and DNA translocation. 7.1 12 Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . Design principles of the ESCRT-III Vps24-Vps2 module. ELife, 2021, 10, . 6.0 EMNUSS: a deep learning framework for secondary structure annotation in cryo-EM maps. Briefings in 6.5 16 Bioinformatics, 2021, 22, . Atomistic basis of force generation, translocation, and coordination in a viral genome packaging 14.5 motor. Nucleic Acids Research, 2021, 49, 6474-6488. A viral genome packaging motor transitions between cyclic and helical symmetry to translocate 10.3 35 dsDNA. Science Advances, 2021, 7, . HIV-1 Hijacking of Host ATPases and GTPases That Control Protein Trafficking. Frontiers in Cell and Developmental Biology, 2021, 9, 622610. 3.7 Mechanistic insight into substrate processing and allosteric inhibition of human p97. Nature 8.2 56 Structural and Molecular Biology, 2021, 28, 614-625. Factors underlying asymmetric pore dynamics of disaggregase and microtubule-severing AAA+ machines. Biophysical Journal, 2021, 120, 3437-3454. Molecular basis for ATPase-powered substrate translocation by the Lon AAA+ protease. Journal of 3.4 12 Biological Chemistry, 2021, 297, 101239. Principles of membrane remodeling by dynamic ESCRT-III polymers. Trends in Cell Biology, 2021, 31, 856-868. Regulation | AAA-ATPases., 2021, , 513-523. 1 Structure, Dynamics and Function of the 26S Proteasome. Sub-Cellular Biochemistry, 2021, 96, 1-151. 2.4 64 Structural insights into ATP hydrolysis by the MoxR ATPase RavA and the Ldcl-RavA cage-like complex. 4.4 26 Communications Biology, 2020, 3, 46. The AAA ATPase Vps4 binds ESCRT-III substrates through a repeating array of dipeptide-binding pockets. 6.0 ELife, 2017, 6, . Structure of Vps4 with circular peptides and implications for translocation of two polypeptide 6.0 41 chains by AAA+ ATPases. ELife, 2019, 8, . An ESCRT-LEM protein surveillance system is poised to directly monitor the nuclear envelope and nuclear transport system. ELife, 2019, 8, . Interactions between a subset of substrate side chains and AAA+ motor pore loops determine grip 6.0 20 during protein unfolding. ELife, 2019, 8, .

CITATION REPORT

#

58

61

63

67

71

73

74

75

82

84

⁸⁵A processive rotary mechanism couples substrate unfolding and proteolysis in the ClpXP degradation
machinery. ELife, 2020, 9, .6.094

#	Article	IF	CITATIONS
86	Structures of the ATP-fueled ClpXP proteolytic machine bound to protein substrate. ELife, 2020, 9, .	6.0	105
87	Structure of the AAA protein Msp1 reveals mechanism of mislocalized membrane protein extraction. ELife, 2020, 9, .	6.0	38
88	The AAA+ superfamily: a review of the structural and mechanistic principles of these molecular machines. Critical Reviews in Biochemistry and Molecular Biology, 2022, 57, 156-187.	5.2	54
97	Preparation of Proteins and Macromolecular Assemblies for Cryo-electron Microscopy. Methods in Molecular Biology, 2020, 2073, 221-246.	0.9	1
100	Fluoxetine targets an allosteric site in the enterovirus 2C AAA+ ATPase and stabilizes a ring-shaped hexameric complex. Science Advances, 2022, 8, eabj7615.	10.3	11
101	An empirical energy landscape reveals mechanism of proteasome in polypeptide translocation. ELife, 2022, 11, .	6.0	5
105	Conserved structural elements specialize ATAD1 as a membrane protein extraction machine. ELife, 2022, 11, .	6.0	6
106	Active conformation of the p97-p47 unfoldase complex. Nature Communications, 2022, 13, 2640.	12.8	18
107	The force required to remove tubulin from the microtubule lattice by pulling on its α-tubulin C-terminal tail. Nature Communications, 2022, 13, .	12.8	11
108	Insights into the Structure and Function of the Pex1/Pex6 AAA-ATPase in Peroxisome Homeostasis. Cells, 2022, 11, 2067.	4.1	11
109	Bro1 family proteins harmonize cargo sorting with vesicle formation. BioEssays, 0, , 2100276.	2.5	2
111	Modelling membrane reshaping by staged polymerization of ESCRT-III filaments. PLoS Computational Biology, 2022, 18, e1010586.	3.2	6
112	Ubiquitin modulates 26 <i>S</i> proteasome conformational dynamics and promotes substrate degradation. Science Advances, 2022, 8, .	10.3	8
113	Mechanisms of DNA opening revealed in AAA+ transcription complex structures. Science Advances, 2022, 8, .	10.3	8
114	The archaeal Cdv cell division system. Trends in Microbiology, 2023, 31, 601-615.	7.7	5
115	The S. cerevisiae Yta7 ATPase hexamer contains a unique bromodomain tier that functions in nucleosome disassembly. Journal of Biological Chemistry, 2022, , 102852.	3.4	1
116	Lysate-to-grid: Rapid Isolation of Native Complexes from Budding Yeast for Cryo-EM Imaging. Bio-protocol, 2023, 13, .	0.4	1
117	Targeting of client proteins to the VCP/p97/Cdc48 unfolding machine. Frontiers in Molecular Biosciences, 0, 10, .	3.5	10

CITATION REPORT

		CITATION REPORT		
#	Article		IF	Citations
118	The role of Vps4 in cancer development. Frontiers in Oncology, 0, 13, .		2.8	0
120	A concerted ATPase cycle of the protein transporter AAA-ATPase Bcs1. Nature Commu 14, .	inications, 2023,	12.8	0
121	Vps60 initiates alternative ESCRT-III filaments. Journal of Cell Biology, 2023, 222, .		5.2	4
123	Roles of ESCRT-III polymers in cell division across the tree of life. Current Opinion in Ce 2023, 85, 102274.	ell Biology,	5.4	2