

# Structural basis of protein translocation by the Vps4-Vta1

ELife

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Structure of the mitochondrial inner membrane AAA+ protease YME1 gives insight into substrate processing. <i>Science</i> , 2017, 358, .	6.0	179
2	Structural pathway of regulated substrate transfer and threading through an Hsp100 disaggregase. <i>Science Advances</i> , 2017, 3, e1701726.	4.7	112
3	Dynamic functional assembly of the Torsin AAA+ ATPase and its modulation by LAP1. <i>Molecular Biology of the Cell</i> , 2017, 28, 2765-2772.	0.9	26
4	Katanin spiral and ring structures shed light on power stroke for microtubule severing. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 717-725.	3.6	97
5	Recruitment dynamics of ESCRT-III and Vps4 to endosomes and implications for reverse membrane budding. <i>ELife</i> , 2017, 6, .	2.8	138
6	Cool views of membrane remodeling. <i>Current Opinion in Colloid and Interface Science</i> , 2018, 34, 17-31.	3.4	2
7	Structure and Function of the 26S Proteasome. <i>Annual Review of Biochemistry</i> , 2018, 87, 697-724.	5.0	497
8	A Non-Competitive Inhibitor of VCP/p97 and VPS4 Reveals Conserved Allosteric Circuits in Type I and II AAA ATPases. <i>Angewandte Chemie</i> , 2018, 130, 1592-1596.	1.6	0
9	A Non-Competitive Inhibitor of VCP/p97 and VPS4 Reveals Conserved Allosteric Circuits in Type I and II AAA ATPases. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 1576-1580.	7.2	23
10	Cryo-EM structures of the human INO80 chromatin-remodeling complex. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 37-44.	3.6	46
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14	Substrate-engaged 26 <i>S</i> proteasome structures reveal mechanisms for ATP-hydrolysis-driven translocation. <i>Science</i> , 2018, 362, .	6.0	226
15	Reversible inhibition of the ClpP protease via an N-terminal conformational switch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6447-E6456.	3.3	56
16	Mechanism for remodelling of the cell cycle checkpoint protein MAD2 by the ATPase TRIP13. <i>Nature</i> , 2018, 559, 274-278.	13.7	109
17	Expanded Coverage of the 26S Proteasome Conformational Landscape Reveals Mechanisms of Peptidase Gating. <i>Cell Reports</i> , 2018, 24, 1301-1315.e5.	2.9	108
18	Dividing the Archaeal Way: The Ancient Cdv Cell-Division Machinery. <i>Frontiers in Microbiology</i> , 2018, 9, 174.	1.5	56

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19	Structural basis for disassembly of katanin heterododecamers. <i>Journal of Biological Chemistry</i> , 2018, 293, 10590-10605.	1.6	21
20	Cotranslocational processing of the protein substrate calmodulin by an AAA+ unfoldase occurs via unfolding and refolding intermediates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4786-E4795.	3.3	12
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29	Structure and mechanism of the ESCRT pathway AAA+ ATPase Vps4. <i>Biochemical Society Transactions</i> , 2019, 47, 37-45.	1.6	25
30	Two-Step Activation Mechanism of the ClpB Disaggregase for Sequential Substrate Threading by the Main ATPase Motor. <i>Cell Reports</i> , 2019, 27, 3433-3446.e4.	2.9	46
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39	The regulation of Endosomal Sorting Complex Required for Transport and accessory proteins in multivesicular body sorting and enveloped viral budding - An overview. <i>International Journal of Biological Macromolecules</i> , 2019, 127, 1-11.	3.6	53
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