

# Esben Lorentzen

## List of Publications by Year in descending order

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Version: 2024-02-01

58  
papers

5,102  
citations

136950

32  
h-index

149698

56  
g-index

70  
all docs

70  
docs citations

70  
times ranked

5176  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of the ciliogenesis-associated CPLANE complex. <i>Science Advances</i> , 2022, 8, eabn0832.	10.3	15
2	The ins and outs of the Arf4-based ciliary membrane-targeting complex. <i>Small GTPases</i> , 2021, 12, 1-12.	1.6	13
3	Nse5/6 inhibits the Smc5/6 ATPase and modulates DNA substrate binding. <i>EMBO Journal</i> , 2021, 40, e107807.	7.8	30
4	Ift88, but not Kif3a, is required for establishment of the periciliary membrane compartment. <i>Biochemical and Biophysical Research Communications</i> , 2021, 584, 19-25.	2.1	1
5	A WDR35-dependent coat protein complex transports ciliary membrane cargo vesicles to cilia. <i>ELife</i> , 2021, 10, .	6.0	29
6	<scp>IFT</scp> proteins interact with <scp>HSET</scp> to promote supernumerary centrosome clustering in mitosis. <i>EMBO Reports</i> , 2020, 21, e49234.	4.5	19
7	Purification and crystal structure of human ODA16 : Implications for ciliary import of outer dynein arms by the intraflagellar transport machinery. <i>Protein Science</i> , 2020, 29, 1502-1510.	7.6	12
8	Moving proteins along in the cilium. <i>ELife</i> , 2020, 9, .	6.0	3
9	Structural insights into the architecture and assembly of eukaryotic flagella. <i>Microbial Cell</i> , 2020, 7, 289-299.	3.2	0
10	Structural insights into the architecture and assembly of eukaryotic flagella. <i>Microbial Cell</i> , 2020, 7, 289-299.	3.2	12
11	Akt Regulates a Rab11-Effector Switch Required for Ciliogenesis. <i>Developmental Cell</i> , 2019, 50, 229-246.e7.	7.0	45
12	Human IFT52 mutations uncover a novel role for the protein in microtubule dynamics and centrosome cohesion. <i>Human Molecular Genetics</i> , 2019, 28, 2720-2737.	2.9	23
13	Nucleoside analogue activators of cyclic AMP-independent protein kinase A of <i>Trypanosoma</i> . <i>Nature Communications</i> , 2019, 10, 1421.	12.8	33
14	Binding of IFT22 to the intraflagellar transport complex is essential for flagellum assembly. <i>EMBO Journal</i> , 2019, 38, .	7.8	38
15	Crystal structure of tetrameric human Rabin8 GEF domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 405-413.	2.6	3
16	Membrane association and remodeling by intraflagellar transport protein IFT172. <i>Nature Communications</i> , 2018, 9, 4684.	12.8	28
17	Crystal structure of intraflagellar transport protein 80 reveals a homo-dimer required for ciliogenesis. <i>ELife</i> , 2018, 7, .	6.0	36
18	Trafficking of ciliary membrane proteins by the intraflagellar transport/BBSome machinery. <i>Essays in Biochemistry</i> , 2018, 62, 753-763.	4.7	120

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19	Structural basis of outer dynein arm intraflagellar transport by the transport adaptor protein ODA16 and the intraflagellar transport protein IFT46. <i>Journal of Biological Chemistry</i> , 2017, 292, 7462-7473.	3.4	48
20	Intraflagellar transport protein IFT52 recruits IFT46 to the basal body and flagella. <i>Journal of Cell Science</i> , 2017, 130, 1662-1674.	2.0	35
21	IFT proteins spatially control the geometry of cleavage furrow ingression and lumen positioning. <i>Nature Communications</i> , 2017, 8, 1928.	12.8	20
22	Systematic proteomic analysis of LRRK2-mediated Rab GTPase phosphorylation establishes a connection to ciliogenesis. <i>ELife</i> , 2017, 6, .	6.0	344
23	Phosphoproteomics reveals that Parkinson's disease kinase LRRK2 regulates a subset of Rab GTPases. <i>ELife</i> , 2016, 5, .	6.0	766
24	Complex Reconstitution from Individual Protein Modules. <i>Advances in Experimental Medicine and Biology</i> , 2016, 896, 305-314.	1.6	3
25	Recombinant Reconstitution and Purification of the IFT-B Core Complex from <i>Chlamydomonas reinhardtii</i> . <i>Methods in Molecular Biology</i> , 2016, 1454, 69-82.	0.9	7
26	The intraflagellar transport machinery in ciliary signaling. <i>Current Opinion in Structural Biology</i> , 2016, 41, 98-108.	5.7	72
27	Intraflagellar transport proteins 172, 80, 57, 54, 38, and 20 form a stable tubulin-binding complex. <i>EMBO Journal</i> , 2016, 35, 773-790.	7.8	162
28	The Intraflagellar Transport Machinery. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a028092.	5.5	289
29	Novel topography of the Rab11-effector interaction network within a ciliary membrane targeting complex. <i>Small GTPases</i> , 2015, 6, 165-173.	1.6	15
30	Structure of Rab11-FIP3-Rabin8 reveals simultaneous binding of FIP3 and Rabin8 effectors to Rab11. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 695-702.	8.2	40
31	<i>IFT81</i> , encoding an IFT-B core protein, as a very rare cause of a ciliopathy phenotype. <i>Journal of Medical Genetics</i> , 2015, 52, 657-665.	3.2	32
32	Mutations in TRAF3IP1/IFT54 reveal a new role for IFT proteins in microtubule stabilization. <i>Nature Communications</i> , 2015, 6, 8666.	12.8	84
33	Getting tubulin to the tip of the cilium: One IFT train, many different tubulin cargo-binding sites?. <i>BioEssays</i> , 2014, 36, 463-467.	2.5	36
34	Structural basis for membrane targeting of the BBSome by ARL6. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 1035-1041.	8.2	77
35	Crystal structures of IFT70/52 and IFT52/46 provide insight into intraflagellar transport B core complex assembly. <i>Journal of Cell Biology</i> , 2014, 207, 269-282.	5.2	115
36	Molecular Basis of Tubulin Transport Within the Cilium by IFT74 and IFT81. <i>Science</i> , 2013, 341, 1009-1012.	12.6	271

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37	Intraflagellar transport complex structure and cargo interactions. <i>Cilia</i> , 2013, 2, 10.	1.8	99
38	Structural Studies of Ciliary Components. <i>Journal of Molecular Biology</i> , 2012, 422, 163-180.	4.2	69
39	Architecture and function of IFT complex proteins in ciliogenesis. <i>Differentiation</i> , 2012, 83, S12-S22.	1.9	169
40	Crystal Structure of a 9-Subunit Archaeal Exosome in Pre-Catalytic States of the Phosphorolytic Reaction. <i>Archaea</i> , 2012, 2012, 1-7.	2.3	19
41	Crystal structure of the intraflagellar transport complex 25/27. <i>EMBO Journal</i> , 2011, 30, 1907-1918.	7.8	108
42	Biochemical Mapping of Interactions within the Intraflagellar Transport (IFT) B Core Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 26344-26352.	3.4	71
43	RNA channelling by the eukaryotic exosome. <i>EMBO Reports</i> , 2010, 11, 936-942.	4.5	68
44	The Yeast Exosome Functions as a Macromolecular Cage to Channel RNA Substrates for Degradation. <i>Cell</i> , 2009, 139, 547-559.	28.9	225
45	Structural organization of the RNA-degrading exosome. <i>Current Opinion in Structural Biology</i> , 2008, 18, 709-713.	5.7	44
46	Structure of the Active Subunit of the Yeast Exosome Core, Rrp44: Diverse Modes of Substrate Recruitment in the RNase II Nuclease Family. <i>Molecular Cell</i> , 2008, 29, 717-728.	9.7	175
47	Chapter 20 Expression, Reconstitution, and Structure of an Archaeal RNA Degrading Exosome. <i>Methods in Enzymology</i> , 2008, 447, 417-435.	1.0	12
48	Molecular mechanisms of mRNA degradation. <i>FASEB Journal</i> , 2008, 22, 247.3.	0.5	0
49	RNA channelling by the archaeal exosome. <i>EMBO Reports</i> , 2007, 8, 470-476.	4.5	108
50	A single subunit, Dis3, is essentially responsible for yeast exosome core activity. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 15-22.	8.2	381
51	The Exosome and the Proteasome: Nano-Compartments for Degradation. <i>Cell</i> , 2006, 125, 651-654.	28.9	69
52	Characterization of native and reconstituted exosome complexes from the hyperthermophilic archaeon <i>Sulfolobus solfataricus</i> . <i>Molecular Microbiology</i> , 2006, 62, 1076-1089.	2.5	51
53	The archaeal exosome core is a hexameric ring structure with three catalytic subunits. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 575-581.	8.2	198
54	RNA polyadenylation in Archaea: not observed in <i>Haloferax</i> while the exosome polynucleotidylates RNA in <i>Sulfolobus</i> . <i>EMBO Reports</i> , 2005, 6, 1188-1193.	4.5	82

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55	Mechanism of the Schiff Base Forming Fructose-1,6-bisphosphate Aldolase: A Structural Analysis of Reaction Intermediates. <i>Biochemistry</i> , 2005, 44, 4222-4229.	2.5	62
56	Structural Basis of 3' End RNA Recognition and Exoribonucleolytic Cleavage by an Exosome RNase PH Core. <i>Molecular Cell</i> , 2005, 20, 473-481.	9.7	104
57	Structural Basis of Allosteric Regulation and Substrate Specificity of the Non-Phosphorylating Glyceraldehyde 3-Phosphate Dehydrogenase from <i>Thermoproteus tenax</i> . <i>Journal of Molecular Biology</i> , 2004, 341, 815-828.	4.2	48
58	Crystal Structure of an Archaeal Class I Aldolase and the Evolution of (β <sub>2</sub> ) <sub>8</sub> Barrel Proteins. <i>Journal of Biological Chemistry</i> , 2003, 278, 47253-47260.	3.4	45