

Esben Lorentzen

List of Articles by Year in descending order

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72

PR articles

4,649

PR citations

131940

32

PR h-index

147584

57

g-index

84

documents

5563

doc citations

144620

33

h-index

9844

citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative in silico and biochemical analyses demonstrate direct Arl3-mediated ODA16 release from the intraflagellar transport machinery. <i>Journal of Biological Chemistry</i> , 2025, 301, 108237.	2.2	3
2	Purine nucleosides replace cAMP in allosteric regulation of PKA in trypanosomatid pathogens. <i>ELife</i> , 2024, 12, .	1.6	9
3	Uncovering structural themes across cilia microtubule inner proteins with implications for human cilia function. <i>Nature Communications</i> , 2024, 15, .	13.7	13
4	DLG1 functions upstream of SDCCAG3 and IFT20 to control ciliary targeting of polycystin-2. <i>EMBO Reports</i> , 2024, 25, 3040-3063.	5.2	7
5	Architecture of RabL2-associated complexes at the ciliary base: A structural modeling perspective. <i>BioEssays</i> , 2024, 46, .	2.1	0
6	The IFT81-IFT74 complex acts as an unconventional RabL2 GTPase-activating protein during intraflagellar transport. <i>EMBO Journal</i> , 2023, 42, .	7.3	9
7	Analysis of cortical cell polarity by imaging flow cytometry. <i>Journal of Cellular Biochemistry</i> , 2023, 124, 1685-1694.	3.0	2
8	Structure of the ciliogenesis-associated CPLANE complex. <i>Science Advances</i> , 2022, 8, .	10.9	30
9	Biallelic DAW1 variants cause a motile ciliopathy characterized by laterality defects and subtle ciliary beating abnormalities. <i>Genetics in Medicine</i> , 2022, 24, 2249-2261.	4.2	10
10	A multi-adenylate cyclase regulator at the flagellar tip controls African trypanosome transmission. <i>Nature Communications</i> , 2022, 13, .	13.7	36
11	Biochemically validated structural model of the 15-subunit intraflagellar transport complex IFT. <i>EMBO Journal</i> , 2022, 41, .	7.3	44
12	A Semester-Long Learning Path Teaching Computational Skills via Molecular Graphics in PyMOL. <i>The Biophysicist</i> , 2022, 3, 106-114.	0.3	4
13	The ins and outs of the Arf4-based ciliary membrane-targeting complex. <i>Small GTPases</i> , 2021, 12, 1-12.	2.1	20
14	Nse5/6 inhibits the Smc5/6 ATPase and modulates DNA substrate binding. <i>EMBO Journal</i> , 2021, 40, .	7.3	55
15	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
16	IFT proteins interact with HSET to promote supernumerary centrosome clustering in mitosis. <i>EMBO Reports</i> , 2020, 21, .	5.2	33
17	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.	5.9	16
18	Structural insights into the architecture and assembly of eukaryotic flagella. <i>Microbial Cell</i> , 2020, 7, 289-299.	3.0	17

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19	Akt Regulates a Rab11-Effector Switch Required for Ciliogenesis. <i>Developmental Cell</i> , 2019, 50, 229-246.e7.	7.7	67
20	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	28
21	Nucleoside analogue activators of cyclic AMP-independent protein kinase A of <i>Trypanosoma</i> . <i>Nature Communications</i> , 2019, 10, .	13.7	47
22	Binding of IFT22 to the intraflagellar transport complex is essential for flagellum assembly. <i>EMBO Journal</i> , 2019, 38, .	7.3	49
23	Crystal structure of tetrameric human Rabin8 GEF domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 405-413.	2.6	5
24	Membrane association and remodeling by intraflagellar transport protein IFT172. <i>Nature Communications</i> , 2018, 9, .	13.7	35
25	Trafficking of ciliary membrane proteins by the intraflagellar transport/BBSome machinery. <i>Essays in Biochemistry</i> , 2018, 62, 753-763.	5.2	154
26	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.	2.2	54
27	Intraflagellar transport protein IFT52 recruits IFT46 to the basal body and flagella. <i>Journal of Cell Science</i> , 2017, 130, 1662-1674.	2.4	43
28	IFT proteins spatially control the geometry of cleavage furrow ingression and lumen positioning. <i>Nature Communications</i> , 2017, 8, .	13.7	26
29	The intraflagellar transport machinery in ciliary signaling. <i>Current Opinion in Structural Biology</i> , 2016, 41, 98-108.	6.4	81
30	Intraflagellar transport proteins 172, 80, 57, 54, 38, and 20 form a stable tubulin-binding IFT B2 complex. <i>EMBO Journal</i> , 2016, 35, 773-790.	7.3	192
31	The Intraflagellar Transport Machinery. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a028092.	7.2	353
32	Novel topography of the Rab11-effector interaction network within a ciliary membrane targeting complex. <i>Small GTPases</i> , 2015, 6, 165-173.	2.1	18
33	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.	8.8	46
34	Mutations in TRAF3IP1/IFT54 reveal a new role for IFT proteins in microtubule stabilization. <i>Nature Communications</i> , 2015, 6, .	13.7	98
35	Getting tubulin to the tip of the cilium: One IFT train, many different tubulin cargo-binding sites?. <i>BioEssays</i> , 2014, 36, 463-467.	2.1	43
36	Structural basis for membrane targeting of the BBSome by ARL6. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 1035-1041.	8.8	86

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37	Crystal structure of a <i>Chlamydomonas reinhardtii</i> flagellar RabGAP TBC-domain at 1.8 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2282-2287.	2.6	5
38	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.	5.4	128
39	Intraflagellar transport complex structure and cargo interactions. <i>Cilia</i> , 2013, 2, .	5.0	105
40	Crystal structure of the invertebrate bifunctional purine biosynthesis enzyme PAICS at 2.8 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1473-1478.	2.6	6
41	Atomic resolution structure of human $\hat{\alpha}$ -tubulin acetyltransferase bound to acetyl-CoA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19649-19654.	7.5	46
42	Structural Studies of Ciliary Components. <i>Journal of Molecular Biology</i> , 2012, 422, 163-180.	4.1	72
43	Architecture and function of IFT complex proteins in ciliogenesis. <i>Differentiation</i> , 2012, 83, S12-S22.	2.4	184
44	Crystal structure of the intraflagellar transport complex 25/27. <i>EMBO Journal</i> , 2011, 30, 1907-1918.	7.3	111
45	Biochemical Mapping of Interactions within the Intraflagellar Transport (IFT) B Core Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 26344-26352.	2.2	78
46	RNA channelling by the eukaryotic exosome. <i>EMBO Reports</i> , 2010, 11, 936-942.	5.2	70
47	The Yeast Exosome Functions as a Macromolecular Cage to Channel RNA Substrates for Degradation. <i>Cell</i> , 2009, 139, 547-559.	33.7	233
48	Crystal structure and stereochemical studies of KD(P)G aldolase from <i>Thermoproteus tenax</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 35-43.	2.6	14
49	Structural organization of the RNA-degrading exosome. <i>Current Opinion in Structural Biology</i> , 2008, 18, 709-713.	6.4	44
50	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.	13.3	179
51	Chapter 20 Expression, Reconstitution, and Structure of an Archaeal RNA Degrading Exosome. <i>Methods in Enzymology</i> , 2008, , 417-435.	2.1	12
52	RNA channelling by the archaeal exosome. <i>EMBO Reports</i> , 2007, 8, 470-476.	5.2	114
53	The Exosome and the Proteasome: Nano-Compartments for Degradation. <i>Cell</i> , 2006, 125, 651-654.	33.7	72
54	The Crystal Structure of the Exon Junction Complex Reveals How It Maintains a Stable Grip on mRNA. <i>Cell</i> , 2006, 126, 713-725.	33.7	390

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55	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	52
56	A single subunit, Dis3, is essentially responsible for yeast exosome core activity. <i>Nature Structural and Molecular Biology</i> , 2006, 14, 15-22.	8.8	401
57	The archaeal exosome core is a hexameric ring structure with three catalytic subunits. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 575-581.	8.8	205
58	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.	5.2	85
59	Mechanism of the Schiff Base Forming Fructose-1,6-bisphosphate Aldolase: A Structural Analysis of Reaction Intermediates. <i>Biochemistry</i> , 2005, 44, 4222-4229.	2.4	68
60	Structural Basis of 3' End RNA Recognition and Exoribonucleolytic Cleavage by an Exosome RNase PH Core. <i>Molecular Cell</i> , 2005, 20, 473-481.	13.3	106
61	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.	4.1	52
62	Structure and Function of a Regulated Archaeal Triosephosphate Isomerase Adapted to High Temperature. <i>Journal of Molecular Biology</i> , 2004, 342, 861-875.	4.1	33
63	Evolutionary markers in the (β/α) ₈ -barrel fold. <i>Current Opinion in Chemical Biology</i> , 2003, 7, 694-701.	5.8	35
64	Crystal Structure of an Archaeal Class I Aldolase and the Evolution of (β/α) ₈ Barrel Proteins. <i>Journal of Biological Chemistry</i> , 2003, 278, 47253-47260.	2.2	49
65	Phosphoproteomics reveals that Parkinson's disease kinase LRRK2 regulates a subset of Rab GTPases. <i>ELife</i> , 0, 5, .	1.6	978
66	Systematic proteomic analysis of LRRK2-mediated Rab GTPase phosphorylation establishes a connection to ciliogenesis. <i>ELife</i> , 0, 6, .	1.6	441
67	Crystal structure of intraflagellar transport protein 80 reveals a homo-dimer required for ciliogenesis. <i>ELife</i> , 0, 7, .	1.6	38
68	Moving proteins along in the cilium. <i>ELife</i> , 0, 9, .	1.6	3
69	A WDR35-dependent coat protein complex transports ciliary membrane cargo vesicles to cilia. <i>ELife</i> , 0, 10, .	1.6	41
70	Purine nucleosides replace cAMP in allosteric regulation of PKA in trypanosomatid pathogens. <i>ELife</i> , 0, 12, .	1.6	0
71	Myristoylated Neuronal Calcium Sensor-1 captures the preciliary vesicle at distal appendages. <i>ELife</i> , 0, 14, .	1.6	2
72	Intraflagellar transport: How kinesin motors hook onto their trains. <i>Current Biology</i> , 0, 35, R928-R931.	3.6	0