

Nobuo N Noda

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

99 papers	6,582 citations	46 h-index	80 g-index
110 ext. papers	7,832 ext. citations	9.5 avg, IF	6.05 L-index

#	Paper	IF	Citations
99	Phosphorylation by casein kinase 2 enhances the interaction between ER-phagy receptor TEX264 and ATG8 proteins.. <i>EMBO Reports</i> , 2022 , e54801	6.5	3
98	Phase-separated protein droplets of amyotrophic lateral sclerosis-associated p62/SQSTM1 mutants show reduced inner fluidity. <i>Journal of Biological Chemistry</i> , 2021 , 297, 101405	5.4	1
97	Biomolecular condensates in autophagy regulation. <i>Current Opinion in Cell Biology</i> , 2021 , 69, 23-29	9	8
96	Structural and dynamics analysis of intrinsically disordered proteins by high-speed atomic force microscopy. <i>Nature Nanotechnology</i> , 2021 , 16, 181-189	28.7	21
95	p62/SQSTM1-droplet serves as a platform for autophagosome formation and anti-oxidative stress response. <i>Nature Communications</i> , 2021 , 12, 16	17.4	46
94	Structural catalog of core Atg proteins opens new era of autophagy research. <i>Journal of Biochemistry</i> , 2021 , 169, 517-525	3.1	5
93	Membrane perturbation by lipidated Atg8 underlies autophagosome biogenesis. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 583-593	17.6	9
92	Atg2 and Atg9: Intermembrane and interleaflet lipid transporters driving autophagy. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2021 , 1866, 158956	5	7
91	Delineating the lipidated Atg8 structure for unveiling its hidden activity in autophagy. <i>Autophagy</i> , 2021 , 17, 3271-3272	10.2	1
90	A glutamine sensor that directly activates TORC1. <i>Communications Biology</i> , 2021 , 4, 1093	6.7	3
89	Atg12-Interacting Motif Is Crucial for E2-E3 Interaction in Plant Atg8 System. <i>Biological and Pharmaceutical Bulletin</i> , 2021 , 44, 1337-1343	2.3	
88	Super-assembly of ER-phagy receptor Atg40 induces local ER remodeling at contacts with forming autophagosomal membranes. <i>Nature Communications</i> , 2020 , 11, 3306	17.4	26
87	Liquidity Is a Critical Determinant for Selective Autophagy of Protein Condensates. <i>Molecular Cell</i> , 2020 , 77, 1163-1175.e9	17.6	62
86	Phase separation organizes the site of autophagosome formation. <i>Nature</i> , 2020 , 578, 301-305	50.4	138
85	Formation of Autophagy Initiation Complex Mediated by an Intrinsically Disordered Protein. <i>Seibutsu Butsuri</i> , 2020 , 60, 171-173	0	
84	In vitro reconstitution of autophagic processes. <i>Biochemical Society Transactions</i> , 2020 , 48, 2003-2014	5.1	3
83	Liquid-liquid phase separation in autophagy. <i>Journal of Cell Biology</i> , 2020 , 219,	7.3	39

82	Human ATG2B possesses a lipid transfer activity which is accelerated by negatively charged lipids and WIPI4. <i>Genes To Cells</i> , 2020 , 25, 65-70	2.3	25
81	Secret of Atg9: lipid scramblase activity drives de novo autophagosome biogenesis. <i>Cell Death and Differentiation</i> , 2020 , 27, 3386-3388	12.7	8
80	Atg9 is a lipid scramblase that mediates autophagosomal membrane expansion. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 1185-1193	17.6	97
79	Atg2: A novel phospholipid transfer protein that mediates de novo autophagosome biogenesis. <i>Protein Science</i> , 2019 , 28, 1005-1012	6.3	28
78	Evolution from covalent conjugation to non-covalent interaction in the ubiquitin-like ATG12 system. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 289-296	17.6	20
77	A C4N4 Diaminopyrimidine Fluorophore. <i>Chemistry - A European Journal</i> , 2019 , 25, 4243-4243	4.8	
76	Atg2 mediates direct lipid transfer between membranes for autophagosome formation. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 281-288	17.6	178
75	A C4N4 Diaminopyrimidine Fluorophore. <i>Chemistry - A European Journal</i> , 2019 , 25, 4299-4304	4.8	1
74	Membrane-binding domains in autophagy. <i>Chemistry and Physics of Lipids</i> , 2019 , 218, 1-9	3.7	8
73	Structural Studies of Selective Autophagy in Yeast. <i>Methods in Molecular Biology</i> , 2019 , 1880, 77-90	1.4	
72	Biophysical characterization of Atg11, a scaffold protein essential for selective autophagy in yeast. <i>FEBS Open Bio</i> , 2018 , 8, 110-116	2.7	14
71	Lipidation-independent vacuolar functions of Atg8 rely on its noncanonical interaction with a vacuole membrane protein. <i>ELife</i> , 2018 , 7,	8.9	20
70	Atg7 Activates an Autophagy-Essential Ubiquitin-like Protein Atg8 through Multi-Step Recognition. <i>Journal of Molecular Biology</i> , 2018 , 430, 249-257	6.5	20
69	Endosomal Rab cycles regulate Parkin-mediated mitophagy. <i>ELife</i> , 2018 , 7,	8.9	78
68	Structural Biology of the Cvt Pathway. <i>Journal of Molecular Biology</i> , 2017 , 429, 531-542	6.5	17
67	Autophagy-regulating protease Atg4: structure, function, regulation and inhibition. <i>Journal of Antibiotics</i> , 2017 ,	3.7	77
66	Structural biology of the core autophagy machinery. <i>Current Opinion in Structural Biology</i> , 2017 , 43, 10-18.	18.1	80
65	Atg101: Not Just an Accessory Subunit in the Autophagy-initiation Complex. <i>Cell Structure and Function</i> , 2016 , 41, 13-20	2.2	14

64	The Intrinsically Disordered Protein Atg13 Mediates Supramolecular Assembly of Autophagy Initiation Complexes. <i>Developmental Cell</i> , 2016 , 38, 86-99	10.2	108
63	Structural basis for the regulation of enzymatic activity of Regnase-1 by domain-domain interactions. <i>Scientific Reports</i> , 2016 , 6, 22324	4.9	31
62	Small differences make a big impact: Structural insights into the differential function of the 2 Atg8 homologs in <i>C. elegans</i> . <i>Autophagy</i> , 2016 , 12, 606-7	10.2	3
61	Structural Basis for Receptor-Mediated Selective Autophagy of Amino-peptidase I Aggregates. <i>Cell Reports</i> , 2016 , 16, 19-27	10.6	19
60	Mechanisms of Autophagy. <i>Annual Review of Biophysics</i> , 2015 , 44, 101-22	21.1	236
59	The Thermotolerant Yeast <i>Kluyveromyces marxianus</i> Is a Useful Organism for Structural and Biochemical Studies of Autophagy. <i>Journal of Biological Chemistry</i> , 2015 , 290, 29506-18	5.4	15
58	Open and closed HORMAS regulate autophagy initiation. <i>Autophagy</i> , 2015 , 11, 2123-2124	10.2	5
57	Structure of the Atg101-Atg13 complex reveals essential roles of Atg101 in autophagy initiation. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 572-80	17.6	71
56	Atg1 family kinases in autophagy initiation. <i>Cellular and Molecular Life Sciences</i> , 2015 , 72, 3083-96	10.3	68
55	Structural Basis of the Differential Function of the Two <i>C. elegans</i> Atg8 Homologs, LGG-1 and LGG-2, in Autophagy. <i>Molecular Cell</i> , 2015 , 60, 914-29	17.6	58
54	Structural basis of starvation-induced assembly of the autophagy initiation complex. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 513-21	17.6	137
53	Architecture of the Atg12-Atg5-Atg16 Complex and its Molecular Role in Autophagy 2014 , 57-65		
52	Selective Autophagy 2014 , 39-48		
51	Proteomic profiling of autophagosome cargo in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2014 , 9, e91651	3.7	13
50	Structure of the Atg12-Atg5 conjugate reveals a platform for stimulating Atg8-PE conjugation. <i>EMBO Reports</i> , 2013 , 14, 206-11	6.5	94
49	Crystallographic and NMR evidence for flexibility in oligosaccharyltransferases and its catalytic significance. <i>Structure</i> , 2013 , 21, 32-41	5.2	22
48	Two-colored fluorescence correlation spectroscopy screening for LC3-P62 interaction inhibitors. <i>Journal of Biomolecular Screening</i> , 2013 , 18, 1103-9		9
47	Atg18 phosphoregulation controls organellar dynamics by modulating its phosphoinositide-binding activity. <i>Journal of Cell Biology</i> , 2013 , 202, 685-98	7.3	36

46	Atg12-Atg5 conjugate enhances E2 activity of Atg3 by rearranging its catalytic site. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 433-9	17.6	102
45	Structural insights into Atg10-mediated formation of the autophagy-essential Atg12-Atg5 conjugate. <i>Structure</i> , 2012 , 20, 1244-54	5.2	52
44	Noncanonical recognition and UBL loading of distinct E2s by autophagy-essential Atg7. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 1250-6	17.6	42
43	Tertiary structure-function analysis reveals the pathogenic signaling potentiation mechanism of <i>Helicobacter pylori</i> oncogenic effector CagA. <i>Cell Host and Microbe</i> , 2012 , 12, 20-33	23.4	112
42	Autophagy-related protein 32 acts as autophagic degron and directly initiates mitophagy. <i>Journal of Biological Chemistry</i> , 2012 , 287, 10631-10638	5.4	104
41	Differential function of the two Atg4 homologues in the aggrephagy pathway in <i>Caenorhabditis elegans</i> . <i>Journal of Biological Chemistry</i> , 2012 , 287, 29457-67	5.4	38
40	Structure of the novel C-terminal domain of vacuolar protein sorting 30/autophagy-related protein 6 and its specific role in autophagy. <i>Journal of Biological Chemistry</i> , 2012 , 287, 16256-66	5.4	54
39	The autophagy-related protein kinase Atg1 interacts with the ubiquitin-like protein Atg8 via the Atg8 family interacting motif to facilitate autophagosome formation. <i>Journal of Biological Chemistry</i> , 2012 , 287, 28503-7	5.4	75
38	Structure-based analyses reveal distinct binding sites for Atg2 and phosphoinositides in Atg18. <i>Journal of Biological Chemistry</i> , 2012 , 287, 31681-90	5.4	93
37	Structural basis of Atg8 activation by a homodimeric E1, Atg7. <i>Molecular Cell</i> , 2011 , 44, 462-75	17.6	122
36	Autoinhibition and phosphorylation-induced activation mechanisms of human cancer and autoimmune disease-related E3 protein Cbl-b. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 20579-84	11.5	68
35	Ser386 phosphorylation of transcription factor IRF-3 induces dimerization and association with CBP/p300 without overall conformational change. <i>Genes To Cells</i> , 2010 , 15, 901-10	2.3	38
34	Autophagy-related protein 8 (Atg8) family interacting motif in Atg3 mediates the Atg3-Atg8 interaction and is crucial for the cytoplasm-to-vacuole targeting pathway. <i>Journal of Biological Chemistry</i> , 2010 , 285, 29599-607	5.4	81
33	Selective transport of alpha-mannosidase by autophagic pathways: structural basis for cargo recognition by Atg19 and Atg34. <i>Journal of Biological Chemistry</i> , 2010 , 285, 30026-33	5.4	40
32	Dimeric coiled-coil structure of <i>Saccharomyces cerevisiae</i> Atg16 and its functional significance in autophagy. <i>Journal of Biological Chemistry</i> , 2010 , 285, 1508-15	5.4	92
31	The NMR structure of the autophagy-related protein Atg8. <i>Journal of Biomolecular NMR</i> , 2010 , 47, 237-43	4.3	42
30	Atg8-family interacting motif crucial for selective autophagy. <i>FEBS Letters</i> , 2010 , 584, 1379-85	3.8	345
29	Structural basis for the antiproliferative activity of the Tob-hCaf1 complex. <i>Journal of Biological Chemistry</i> , 2009 , 284, 13244-55	5.4	69

28	Crystallization of <i>Saccharomyces cerevisiae</i> alpha-mannosidase, a cargo protein of the Cvt pathway. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009 , 65, 571-3		4
27	The structure of Atg4B-LC3 complex reveals the mechanism of LC3 processing and delipidation during autophagy. <i>EMBO Journal</i> , 2009 , 28, 1341-50	13	294
26	ATG systems from the protein structural point of view. <i>Chemical Reviews</i> , 2009 , 109, 1587-98	68.1	59
25	Characterization of the Atg17-Atg29-Atg31 complex specifically required for starvation-induced autophagy in <i>Saccharomyces cerevisiae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2009 , 389, 612-5	3.4	87
24	Structural basis of target recognition by Atg8/LC3 during selective autophagy. <i>Genes To Cells</i> , 2008 , 13, 1211-8	2.3	294
23	In vitro reconstitution of plant Atg8 and Atg12 conjugation systems essential for autophagy. <i>Journal of Biological Chemistry</i> , 2008 , 283, 1921-8	5.4	93
22	Crystallization of the Atg12-Atg5 conjugate bound to Atg16 by the free-interface diffusion method. <i>Journal of Synchrotron Radiation</i> , 2008 , 15, 266-8	2.4	7
21	Crystallization of the coiled-coil domain of Atg16 essential for autophagy. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 1046-8		2
20	The Atg12-Atg5 conjugate has a novel E3-like activity for protein lipidation in autophagy. <i>Journal of Biological Chemistry</i> , 2007 , 282, 37298-302	5.4	781
19	Crystallization and preliminary crystallographic analysis of the Tob-hCaf1 complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007 , 63, 1061-3		3
18	Full-length p40phox structure suggests a basis for regulation mechanism of its membrane binding. <i>EMBO Journal</i> , 2007 , 26, 1176-86	13	53
17	The crystal structure of Atg3, an autophagy-related ubiquitin carrier protein (E2) enzyme that mediates Atg8 lipidation. <i>Journal of Biological Chemistry</i> , 2007 , 282, 8036-43	5.4	95
16	Structure of Atg5-Atg16, a complex essential for autophagy. <i>Journal of Biological Chemistry</i> , 2007 , 282, 6763-72	5.4	172
15	Structure of a cell polarity regulator, a complex between atypical PKC and Par6 PB1 domains. <i>Journal of Biological Chemistry</i> , 2005 , 280, 9653-61	5.4	60
14	Structural basis for the specificity and catalysis of human Atg4B responsible for mammalian autophagy. <i>Journal of Biological Chemistry</i> , 2005 , 280, 40058-65	5.4	100
13	Tor2 directly phosphorylates the AGC kinase Ypk2 to regulate actin polarization. <i>Molecular and Cellular Biology</i> , 2005 , 25, 7239-48	4.8	171
12	The crystal structure of plant ATG12 and its biological implication in autophagy. <i>Autophagy</i> , 2005 , 1, 119-26	12.2	94
11	Solution structure of the tandem Src homology 3 domains of p47phox in an autoinhibited form. <i>Journal of Biological Chemistry</i> , 2004 , 279, 29752-60	5.4	44

10	Binding of FAD to cytochrome b558 is facilitated during activation of the phagocyte NADPH oxidase, leading to superoxide production. <i>Journal of Biological Chemistry</i> , 2004 , 279, 26378-86	5.4	26
9	A molecular mechanism for autoinhibition of the tandem SH3 domains of p47phox, the regulatory subunit of the phagocyte NADPH oxidase. <i>Genes To Cells</i> , 2004 , 9, 443-56	2.3	55
8	The crystal structure of microtubule-associated protein light chain 3, a mammalian homologue of <i>Saccharomyces cerevisiae</i> Atg8. <i>Genes To Cells</i> , 2004 , 9, 611-8	2.3	142
7	Structural basis for the specificity, catalysis, and regulation of human uridine-cytidine kinase. <i>Structure</i> , 2004 , 12, 751-64	5.2	57
6	The crystal structure of DJ-1, a protein related to male fertility and Parkinson's disease. <i>Journal of Biological Chemistry</i> , 2003 , 278, 31380-4	5.4	174
5	Crystallization and preliminary X-ray analysis of LC3-I. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 1464-5		9
4	Crystallization and preliminary X-ray analysis of human uridine-cytidine kinase 2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 1477-8		5
3	Crystallization and preliminary crystallographic analysis of the autoinhibited form of the tandem SH3 domain of p47(phox). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 1479-80		11
2	Crystallization and preliminary crystallographic analysis of DJ-1, a protein associated with male fertility and parkinsonism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 1502-3		9
1	X-ray crystal structure of IRF-3 and its functional implications. <i>Nature Structural and Molecular Biology</i> , 2003 , 10, 922-7	17.6	122