Supporting Information

# LC3B binds to the autophagy protease ATG4b with high affinity using a bipartite interface

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**Figure S1**. (a) Representative mass spectra for LC3B constructs. The +178 peak is the a-N-gluconoylated version, a common post translational modification observed with proteins expressed with N-terminal His6 tag in *E. coli*. (b) SDS-PAGE protein gel of LC3B proteins.



**Figure S2**. Evaluation of binding between LC3B truncations and ATG4b by isothermal calorimetry (ITC). Representative data are shown for ATG4b WT binding to LC3B-I and LC3B-115: (a) A 700- $\mu$ M solution of ATG4b was titrated into 68  $\mu$ M LC3B-I; (b) 100  $\mu$ M solution of ATG4b titrated into 10  $\mu$ M LC3B-115. N and K<sub>D</sub> values are the mean and standard deviation for five independent experiments; data are shown for one representative measurement.



**Figure S3**. A Representative mass spectrum for an MS-based assay to evaluate the cleavage of pro-LC3B. The arrows are pointing to the masses corresponding to pro-LC3B (substrate) and LC3B-I (product), respectively.

<b>a</b> sp   Q9Y4P1   ATG4B_HUMAN p62tail	-ERFFDSEDEDFEILSL
b	
sp   Q9Y4P1   ATG4B_HUMAN	N-LSLDSSDVERLER-FF
3RUI_A   PDBID   CHAIN   atg7	SGLSVIKQEVERLGNDVF

Figure S4. Sequence alignment of the C-terminal tail of ATG4b with (a) p62 tail or (b) ATG7.



Figure S5. SDS-PAGE protein gel for all ATG4b constructs.



Figure S6. Representative SPR sensorgrams of ATG4b proteins binding to LC3B-I fit to a 1:1 kinetic binding model.



Figure S7. Representative SPR sensorgrams of ATG4b proteins binding to LC3B-115 fit to a 1:1 kinetic binding model.

	Expected	Observed	in vivo biotinylation (%)	
LC3B-115	18068.5	18068.5	010/	
Biotinylated LC3B-115	18295.5	18294.5	9170	
LC3B-116	18196.6	18196.5	750/	
Biotinylated LC3B-116	18423.6	18423.0	75%	
LC3B-118	18426.8	18426.5	50%	
Biotinylated LC3B-118	18653.8	18625.5	50%	
LC3B-I	18631.0	18631.0	27%	
Biotinylated LC3B-I	18858.0	18858.0		
Pro-LC3B	19189.8	19189.5	64%	
Biotinylated pro-LC3B	19416.0	19416.5		

**Table S1**. Expected masses and observed masses for LC3B constructs.

**Table S2**. Kinetic rate constants for binding of LC3B-I and LC3B-115 to ATG4b truncations.

	LC3B-I		LC3B-115			
	kon (M <sup>-1</sup> S <sup>-1</sup> )	k <sub>off</sub> (S <sup>-1</sup> )	Kinetic K⊳ (µM)	kon (M <sup>-1</sup> S <sup>-1</sup> )	k <sub>off</sub> (S <sup>-1</sup> )	Kinetic $K_D(\mu M)$
ATG4b- WT	$8.6 \times 10^5 \pm 9.7 \times 10^4$	0.046 ± 0.02	0.084 ± 0.047	$5.5 \times 10^6 \pm 8.4 \times 10^5$	0.045 ± 0.007	0.0084 ± 0.0019
ATG4b- 382	No fit	No fit	No fit	$1.9 \times 10^5 \pm 6.5 \times 10^4$	0.82 ± 0.28	$4.4 \pm 0.6$
ATG4b- 366	$1.7 \times 10^4 \pm 1.7 \times 10^4$	0.59 ± 0.22	87 ± 11	$1.4 \times 10^5 \pm 3.8 \times 10^4$	1.3 ± 0.5	9.5 ± 1.4
ATG4b- 354	$3.6 \times 10^3 \pm 9.7 \times 10^4$	0.51 ± 0.27	140 ± 74	$7.5 \times 10^4 \pm 3.8 \times 10^4$	1.1 ± 0.4	15.7 ± 8.4

#### Table S3. Primers used to make ATG4b constructs.

Primer Name	Primer sequences (5'-3')		
P1	GCTCGGCGCGCCTGCAGGTCGACATGGACGCAGCTACTCTGACCTAC		
P2	GGTTTCTTTACCAGACTCGAGTCAAAGGGACAGGATTTCAAAGTCTTC		
P3	GGTTTCTTTACCAGACTCGAGTCACTGCTCCACCAGCTCAAACATGGG		
P4	GGTTTCTTTACCAGACTCGAGTCAGTCGAAGAATCTTTCCAGTCGCTC		
P5	GGTTTCTTTACCAGACTCGAGTCAGTTCAGGACGTCGGGGCAGGCCAG		

## **Table S4**. Primer combinations for ATG4b pET-15b vector constructs.

No.	Primer combination	Constructs	Notes
1	P1 + P2	ATG4b-WT	Full length
2	P1 + P3	ATG4b-354	C-terminal truncation
3	P1 + P4	ATG4b-382	c-terminal truncation
4	P1 + P5	ATG4b-366	c-terminal truncation

**Table S5**. Primers used to make LC3B constructs.

Primer Name	Primer sequence (5'-3')		
P6	ATGCCGTCGGAGAAGACCTTCAAG		
P7	CACTGACAATTTCATCCCGAACGTC		
P8	CCCGAACGTCTCCTGGGAGGCACAG		
P9	CGTCTCCTGGGAGGCACAGACCATG		
P10	GGAGGCACAGACCATGTACAGGAATC		

Table S6. Primer combinations for LC3B N-His-Avi vector constructs.

No.	Primer combination	Constructs	Notes
1	P6 + P7	Pro-LC3B	Pro-LC3B full length
2	P6 + P8	LC3B-I	LC3B-I full length
3	P6 + P9	LC3B-118	Ubiquitin core + 3 residues
4	P6 + P10	LC3B-115	Ubiquitin core

### 2. Supplementary sequences

LC3B-115: HisTag—TEV cleavage sequence—AviTag—LC3B(1-115) (Vector backbone: pET-15b)

MGSSHHHHHHSSGENLYFQGHMSGLNDIFEAQKIEWHEGGGSMPSEKTFKQRRTFEQRVEDVRLIREQH PTKIPVIIERYKGEKQLPVLDKTKFLVPDHVNMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPIS EVYESEKDEDGFLYMVCAS\*

LC3B-116: HisTag—TEV cleavage sequence—AviTag—LC3B(1-116) (Vector backbone: pET-15b)

MGSSHHHHHHSSGENLYFQGHMSGLNDIFEAQKIEWHEGGGSMPSEKTFKQRRTFEQRVEDVRLIREQH PTKIPVIIERYKGEKQLPVLDKTKFLVPDHVNMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPIS EVYESEKDEDGFLYMVCASQ\*

LC3B-118: HisTag—TEV cleavage sequence—AviTag—LC3B(1-118) (Vector backbone: pET-15b)

MGSSHHHHHHHSSGENLYFQGHMSGLNDIFEAQKIEWHEGGGSMPSEKTFKQRRTFEQRVEDVRLIREQH PTKIPVIIERYKGEKQLPVLDKTKFLVPDHVNMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPIS EVYESEKDEDGFLYMVCASQET\*

**LC3B-I**: HisTag—TEV cleavage sequence—AviTag—LC3B(1-120) (Vector backbone: pET-15b)

MGSSHHHHHHSSGENLYFQGHMSGLNDIFEAQKIEWHEGGGSMPSEKTFKQRRTFEQRVEDVRLIREQH PTKIPVIIERYKGEKQLPVLDKTKFLVPDHVNMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPIS EVYESEKDEDGFLYMVCASQETFG\*

**Pro-LC3B**: HisTag—TEV cleavage sequence—AviTag—LC3B(1-125) (Vector backbone: pET-15b)

MGSSHHHHHHHSSGENLYFQGHMSGLNDIFEAQKIEWHEGGGSMPSEKTFKQRRTFEQRVEDVRLIREQH PTKIPVIIERYKGEKQLPVLDKTKFLVPDHVNMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPIS EVYESEKDEDGFLYMVCASQETFGMKLSV\*

**ATG4b-WT**: HisTag—TEV cleavage sequence—AviTag—AT4b(1-393) (Vector backbone: pET-15b)

MGSSHHHHHHSSGENLYFQGHMSGLNDIFEAQKIEWHEGGGSMDAATLTYDTLRFAEFEDFPETSEPVW ILGRKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGCMLRCGQMIFAQALVCRHLGRDW RWTQRKRQPDSYFSVLNAFIDRKDSYYSIHQIAQMGVGEGKSIGQWYGPNTVAQVLKKLAVFDTWSSLA VHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDRHCNGFPAGAEVTNRPSPWRPLVLLIPLRLGLTD INEAYVETLKHCFMMPQSLGVIGGKPNSAHYFIGYVGEELIYLDPHTTQPAVEPTDGCFIPDESFHCQH PPCRMSIAELDPSIAVGFFCKTEDDFNDWCQQVKKLSLLGGALPMFELVEQQPSHLACPDVLNLSLDSS DVERLERFFDSEDEDFEILSL\*

### ATG4b-382: HisTag—TEV cleavage sequence—AviTag—AT4b(1-382) (Vector backbone: pET-15b)

MGSSHHHHHHSSGENLYFQGHMSGLNDIFEAQKIEWHEGGGSMDAATLTYDTLRFAEFEDFPETSEPVW ILGRKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGCMLRCGQMIFAQALVCRHLGRDW RWTQRKRQPDSYFSVLNAFIDRKDSYYSIHQIAQMGVGEGKSIGQWYGPNTVAQVLKKLAVFDTWSSLA VHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDRHCNGFPAGAEVTNRPSPWRPLVLLIPLRLGLTD INEAYVETLKHCFMMPQSLGVIGGKPNSAHYFIGYVGEELIYLDPHTTQPAVEPTDGCFIPDESFHCQH PPCRMSIAELDPSIAVGFFCKTEDDFNDWCQQVKKLSLLGGALPMFELVEQQPSHLACPDVLNLSLDSS DVERLERFFD\*

ATG4b-366: HisTag—TEV cleavage sequence—AviTag—AT4b(1-366) (Vector backbone: pET-15b)

MGSSHHHHHHSSGENLYFQGHMSGLNDIFEAQKIEWHEGGGSMDAATLTYDTLRFAEFEDFPETSEPVW ILGRKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGCMLRCGQMIFAQALVCRHLGRDW RWTQRKRQPDSYFSVLNAFIDRKDSYYSIHQIAQMGVGEGKSIGQWYGPNTVAQVLKKLAVFDTWSSLA VHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDRHCNGFPAGAEVTNRPSPWRPLVLLIPLRLGLTD INEAYVETLKHCFMMPQSLGVIGGKPNSAHYFIGYVGEELIYLDPHTTQPAVEPTDGCFIPDESFHCQH PPCRMSIAELDPSIAVGFFCKTEDDFNDWCQQVKKLSLLGGALPMFELVEQQPSHLACPDVLN\*

ATG4b-354: HisTag—TEV cleavage sequence—AviTag—AT4b(1-354) (Vector backbone: pET-15b)

MGSSHHHHHHSSGENLYFQGHMSGLNDIFEAQKIEWHEGGGSMDAATLTYDTLRFAEFEDFPETSEPVW ILGRKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGCMLRCGQMIFAQALVCRHLGRDW RWTQRKRQPDSYFSVLNAFIDRKDSYYSIHQIAQMGVGEGKSIGQWYGPNTVAQVLKKLAVFDTWSSLA VHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDRHCNGFPAGAEVTNRPSPWRPLVLLIPLRLGLTD INEAYVETLKHCFMMPQSLGVIGGKPNSAHYFIGYVGEELIYLDPHTTQPAVEPTDGCFIPDESFHCQH PPCRMSIAELDPSIAVGFFCKTEDDFNDWCQQVKKLSLLGGALPMFELVEQ\*

# CFP-LC3B-YFP: HisTag-CFP-LC3B-YFP

MHHHHHMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLV TTLTWGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDF KEDGNILGHKLEYNYISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNH YLSTQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYKGSMPSEKTFKQRRTFEQRVEDVRLIREQHP TKIPVIIERYKGEKQLPVLDKTKFLVPDHVNMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPISE VYESEKDEDGFLYMVYASQETFGMKLSVKLMVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDAT YGKLTLKFICTTGKLPVPWPTLVTTFGYGLQCFARYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYK TRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSV QLADHYQQNTPIGDGPVLLPDNHYLSYQSALSKDPNEKRDHMVLLEFVTAAGITLGMDELYK\*