G
(3)

fi

í

¨ , , ,

„ 4 b , , 4

4

Abbreviations:

ARTICLE HISTORY

I[illegible] 2008 [illegible] A [illegible] F[illegible] [illegible] ([illegible]) [illegible] fl [illegible] ([illegible]). I[illegible] fi

LC3-II.[27]

A fi “ ”

“ 25% .” I GF -A 8/LC3

GF -A 8/LC3 (fi),

fi

I [2]

2 — fl I

fi F fl

fl

fl F

E fl

fl

F

[28-43,44] F

fi

C

A. Methods for monitoring autophagy

1.

A fi E 1950 (

6). I

L

( ),

(B)- (.).[56]

L . / / (A

AL) . ; .

(F . 3A B);[48,53]

-E

AC 2 2, [57,58][59]).

[60]

[48,53] A [54]

[55]

(A)

Conclusion: E E fi E E

2. *A 8/ C3 fi*

A 8/LC3 I

. Western blotting and ubiquitin-like protein conjugation systems

A 8/LC3 E ([137]). I A 8– E. A 8 2 : A 1LC3/LC3 GABA A . LC3A, B, B2 C, GABA A , GABA A L1 GABA A L2/GA E-16.[138] A. A G4B,[139,140] . LC3-I LC3-II, GABA A GABA A – E, . . E- A 8/LC3, D - AGE, A 8/LC3-I (16–18 D) A 8– E/LC3-II (14–16 D). LC3 fi [illegible] ([illegible] 1 [illegible] C1; [illegible] E-64, [illegible] ([illegible] “ [illegible] ” [illegible] “ [illegible] ” [illegible] A, [illegible]),[161,162] [illegible][160], [illegible][158,163,164]). [illegible] fi [illegible] A_1, H_4C [illegible]

[illegible] LC3 [illegible] (Fig. 6);[26,165] [illegible]

[illegible] [187] [illegible] LC3-II [illegible]

D KD
fi -FLAG
-FLAG 2
LC3C,
FLAG-
(. B - L. E . ,
). E
C3C
I
A 8 , . GABA A (
).[141,209] C B I 3L/
I GABA A
LC3 [210,211] F ,
GABA A L1 GABA A ,[138,143]
-GABA A L1
D - AGE
(15%) , . GABA A
GABA A L1 (. B -G ,
; F . 4 143). B GABA A
GABA A L1
, GABA A -I GABA A L1-I

[illegible] (B. L[illegible]). [illegible]

I[illegible], 1 [illegible] 10 μ / [illegible] E-64 [illegible]
[illegible] fi[illegible]
[illegible]

[illegible] fi-

[illegible]

(Fig. 8B,C).[37,257] H [illegible]

H EGF
GF -LC3 GF -LC3 [269]
EGF
A -
A-
GF [263]
D A A ,
GF
5
D - AGE.

[illegible] (, ., H L [illegible]) [illegible] 1 [illegible]
[illegible] GF -LC3 [illegible]
[illegible] H- 5 [illegible]
48 [illegible] GF -LC3 [illegible]

Table 1.

340-342

F / C -GF

fl

343 I

341 fi “ ” (

) “ ”

-fl

LC3- C

LC3-II

A. GF -LC3 fl

(fl). GF - 1 GF - B 1 (B 1

1[364]). GF - 1

fl

(fi H- 5

GF - 1; E.

).[365]

Conclusion: fl

(F . 14).

GF -LC3

/ fl ,

A fl

A K

C1
6,
C1 (
6 6KB1/2
),
6KA/ K. F
C1
fi

LK1

LK1 A K

Conclusion: A A 1/ LK1

. ATG14

A 14 fi 34 I,[545] A G14/A G14L/BA K, fi[546-549] A G14 C- BA GF BEC 1[550] A G14-GF BA -GF fl E , A G14 E[550,551] A , A G14 A

. STX17

[illegible] C3B [illegible] [605] I [illegible] [606] A 5 [illegible] A 7, B 1 [illegible] 3 [illegible] [607] LC3 [illegible] A G5 [illegible] I [illegible]

C.
).[624,629,1704]
A
(, ., LC3 GABA A).
[630]
fl . . I
H3 .
fi
[631]
I A
1 (
)
[632] 1
[322,633] D
[561] 1
1
1
GLI3 . K A
1, [634]
E 300/ 300
A CLEA (
).
fi
[625,635,636]
FEB
CLEA
2
FEB
A 16 I (A)-435738( )9.96315301

8. ***fi*** ***A***

8 8Δ60

fi [677] A fi 60

(8Δ60) E

[261]

(*13*)

().

Cautionary notes:

[3] I [678]

FI C fi GF -) fl
[553,683,689-691] I
2 H 1 ;
2 H 1
fi
(F . 20).[508] I
fi
[692] C

[illegible] J. [illegible]
[illegible] GF -A, 8/LC3 [illegible]
[illegible] GF - 1/ . 1
[illegible] 1-GF . [illegible] GF [illegible]
[illegible] GF [illegible]
[illegible] I, fl [illegible]
[illegible] C [illegible] (L -
C) [illegible]
[illegible] 1, [illegible] 8. [illegible]
D . [illegible]
. 719.

L . [illegible] (L) [illegible] fi [illegible] (20–24) [illegible][720] L [illegible] 1 [illegible] 8 [illegible] J. . A. [illegible] A, [illegible] L , A, 11 [illegible] . 34- [illegible] I. . 3K [illegible] I [illegible] . L

[illegible] (-t [illegible]) [illegible] ([illegible]), [illegible][720] D [illegible] ([illegible]), [illegible] 1-E F , [illegible] AB35-D. . 3 (AB35 [illegible] 2 A- [illegible] D. . 3 [illegible] H-. [illegible] fl [illegible]) [illegible] L , [illegible] F [illegible][720]
L [illegible]

I, [illegible] fi [illegible] 100 [illegible] A [illegible] B [illegible] GF [illegible] *A* [illegible][721] I, [illegible][723] I,

. H , (*A*

),

GF -

fi 0. 6(J-2.59892-1.2007 D)140.2(,)-21.59(02(,)-38( )

(fi

fi

fi fl

IH I J.[758] I

fl

[761,762] E

C (fl

) D A (D A). A

D A

C D2 (ADH

2) D A:

(.)- fi fl

(D. K ,). F LC3

. Zymophagy

fi fi [909]

L [910]

2

“ - fl ”

/

E 1

1-EGF ,

C

1/ (LC3, GF - ( ) F -LC3

fl

, D -B A [930]

F , D -B A
GF -LC3.

(D -B A).

(). A

F -LC3 L G
(. B K.A. H ,),
C -LC3 L B ,[332]
LC3 LA 1 (K. ,)
CD63[331]
I
H-
K [760]

LC3.

Cautionary notes:
(, ., 3- A)
(, ., AB7). D -B A.
(, .,
[931]). I

[illegible][946,947] “B [illegible]” [illegible] “D [illegible]” [illegible]
D [illegible]
[illegible]
[illegible] I [illegible]

/ I LC3 fi

fi

IHC fl

[197,958-964]

IHC

1, B 1,

fl (

1 C3).

B

(, ., [965]).

G 2 (2)

(

),

I G 2

I 1 (1,4,5-

[966] 1) C 2+-

I

fl

fi A1 A

fl

4

[967,968]

« » [967,968]

[950,969] [970]

fl

12

fi [971,972]

I

fi

[153,974-976]

( ) ( )

A.

[illegible]

[illegible][1038,1039] [illegible][217,1040,1041] [illegible]

[illegible] 2 [illegible][1042] H [illegible], [illegible]

[illegible]

[illegible] C A ([illegible]) [illegible]

[illegible] ([illegible]) [illegible]

[illegible] C A. [illegible] H [illegible],

[illegible] fi [illegible] C A [illegible],

[illegible] A [illegible] fi [illegible]

C A ([illegible] H A8 [illegible]),

[illegible] [948] [illegible]

. C [illegible]

[illegible] H A8. D [illegible] fi [illegible]

H A8 [illegible]

. C [illegible]

LA 2A.[1108] D [illegible] fi [illegible] LA 2A [illegible] ([illegible] 1 [illegible] 3

LA 2 [illegible] C A[92,1109]) [illegible]

[illegible] LA 2A, [illegible]

E C I II (, ., 4 G101) - I .
C A. ( ) I
C A,
- I I
- I,
C A. ( ) I
- I.
C A.

A
C A (CA A).[1116]
CA A H A8 LA 2 (
LA 2A).
2 fi -
C A. I
LA 1 LA 2
1 *2*
- fi [1117] I C A, LA 2
[1118,1119] LA 2C, LA 2
A/D A
D A D A
A - [1120-1123]
LA 1 LA 2 fi
C A [1117]
C A
LA 2.[1120,1124,1125]

Conclusion: C A
C A. fl
C A-
fi

19. *C* -

CA A fi
[1116]

L [illegible] , L [illegible] *D.* [illegible] (F [illegible] 26).[279,280] H [illegible] , [illegible] GF -A [illegible] 8/LC3 fl [illegible] E [illegible] , [illegible] LA [illegible] ([illegible]

B [illegible]
[illegible] ([illegible], H_4C [illegible] fi [illegible] A_1)
[illegible] H; [illegible]

K11/LKB1-A K.[935,936,1216] C

C1 (

1).

I / , EGF/

[504,1217-1219] I

1,4,5-

[1220] FDA-

fl [1221,1222] I

/

[956] A

E [297,1175,1223,1224]

C /. - (.),

(AAD)

C

ED-19, - BA A,

[1225] C

- FLI

-B 1 (-BEC 1), [1216,1227]

- BH3D - BH3D,

fi

BCL2-BEC 1 fi ,

[1227]

I I 3K

[1228] [1229] [1230]

fi

I

C1

C1

; , I 3K

[illegible][39-41]

1. C.

C. [illegible]

I

-3, *-4,* *-5,* *-6*

LGG-1-I LGG-1-II -

[563,633,1268,1269] I

LGG-1 ~64-

100- . LGG-1 -

3, *-7,* *-5* *-10* [633,1261]

[563,633]

GF ::LGG-1 *-3*

-7 LGG-1

GF ::LGG-1 -

I -

-34 [1270]

C.

A GL -

(GL-1- GL-3- E A-1)

3. *C*

4. *D*

[illegible] *A* *1*

[illegible] / *A* *8* [illegible] C [1302] [illegible]

A [illegible] *A* [illegible]

[illegible] *A* [illegible]

[illegible] fi [1318] I

A. [illegible]

[illegible] A 8- [illegible] D. 2, [illegible]

[illegible] [276] I *A.* [illegible]

[illegible] “ [illegible] ” GF -A 8 [illegible]

[illegible] GF -A 8 [illegible]

([illegible]), [illegible]

[illegible] GF -A 8- [illegible]

[illegible]

[illegible] I [illegible] „ [illegible]

[illegible] A “ [illegible]

[illegible] “ [illegible] ” A [illegible]

[illegible] “fi ” [illegible] [1319] G [illegible]

[illegible]

[illegible] 7- [illegible] H [illegible] 7 [illegible]

[illegible] fi

[illegible] B/ 5- C E - [illegible]

[illegible] [1319] A [illegible] fi [illegible] / 1 [illegible]

[illegible] *A.* [illegible] ([illegible]

[illegible]). fi [illegible]

[illegible]

9.

C A. C1 H ( ). [1338] I C [1339] F B F ( ) I / I (LC3 fl , E ,) 2 [294] I fl [217,609] CA [1340] I ( ) CA ( ) fi CA ( ) (3- A A 5) fi CA) CA LC3-II CA, 14- D I 1 B 1 LC3-II CA, C LC3-II 1 [1034]

A (.) fi fi F fi [1341,1342] fi [1343] A IHC, fl E LC3 1 [962] D fi fi fi E E fi .8(-311. ,01(9.96980)-528.9(

2

[1344] A

30 ± 20 fl

-80°C.[1061]

A) L . I. fi 6KB EIF4EB 1 - C, H . A A- *1*,[1354,1355] fi A1.[1352,1353]

11.

A. (, fl) (.)

GF -A G8 [287,288,1403]
fl A G A G5
A G12.

D
[1404]
D
100,000

D

D
D
[1404,1405] *D.*
D.

A. ( ). I fi [1418] I. fi fi fi fi D A E [1419-1422]

(AK , , A K, F) [628,1423-1425] A G F fl A G8/LC3. [1425] F ( ) A G8/LC3 fi A₁. I A A C A A

20.

[956] LC3 fl F F

E I 3- A A (EL CA 3) [1426] C

21.

I.

[illegible] ABJB000000000). F [illegible]

[illegible]

3. *C3* -

LA , LC3 ( )[181] IF G- G (GB), ; I A G7, A G3, A G12–A G5-A G16L1 , LC3- I fi IF G- F LK1/2 A G14, fi LC3-[1455-1457] *C*[1208,1455] A LA , LC3- GB - fl[1458] GB LC3- C GB

4. *fi*

A G fi F , A G9 I I1, LK1, BEC 1, A G5, A G7 LC3B[1459] *B* I *B.* LK1, A G14 IK3C3/ 34, A G5, A G7, A G4B A G16L1.[1460]

5.

A G[27,75,76,544,572,1449,1461-1465,1466]

E. Interpretation of in silico assays for monitoring autophagy

( )[1467,1468] F ; "BLA "

[illegible] (2)- [illegible] >15 [illegible] [1483] [illegible] (>13) [illegible] [1482] [illegible] ://[illegible]

The Eukaryotic Linear Motif resource (ELM)

[illegible][1484]

[1492] A fi

Conclusions and future perspectives

fi [2] fi [1493,1494]

fl fi fi . A , (4). I fl

fi ﬂ

Acknowledgments

I fi . D.J.K. fi . I : A .. D D

Funding

I H H G 053396 D.J.K. D fi

Disclaimer

ﬂ fi D A F D A D H H

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245. 1 , C 5 - 347(20 09.4H)-49(. 7(093 -282(347(253, 09.4G . - 09.4783 .) 3;)-1347(6(.5(L -4

[illegible] *A* [illegible]. E [illegible] C [illegible] 2006; 5:1328-36; [illegible]://[illegible]/10.1128/EC.00024-06.

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2107. A, E, K, H, D, A, E, B, C, A. L. C2/ HL 1/A. C

A [illegible] 2012; 8:767-79; [illegible]:// [illegible] /10.4161/ [illegible] .19381.

2139. L[illegible] C, F[illegible], K[illegible] B, D[illegible] I, C[illegible] D, [illegible] BH, J[illegible] J[illegible]. A[illegible]-[illegible] B[illegible] 1-[illegible] AG. [illegible]. C[illegible] B[illegible] 2006; 8:688-99; [illegible]:// [illegible] / 10.1038/[illegible]1426.

. E B J 2013; 32:1903-16; :// . /10.1038/
.2013.123.

Aggresome: A [illegible]

ARD1: [illegible] AA10.
Are1: A[illegible]1.
Are2: A[illegible]1.
ARRB1/***β***-arrestin-1 (arrestin, beta 1): [illegible] G- [illegible] A[illegible]B1 [illegible]
AD[illegible]BK/BA[illegible]K ([illegible])- [illegible]

Atg11: A [illegible]

[illegible] C [illegible] A[illegible] 11 [illegible] A[illegible] 19, [illegible] A[illegible] 30 (A[illegible] 30) [illegible] A[illegible] 32 [illegible] fi[illegible] [illegible] I[illegible] A[illegible] 9 [illegible] A[illegible] A[illegible]

LA) [illegible] I [illegible] « [illegible] » [illegible] « [illegible] »[884] [illegible]

Autophagoproteasome (APP): A [illegible] LC3 [illegible][73] [illegible]

Autophagosome (AP): A [illegible] ([illegible], A [illegible]). [illegible]

BCL2 family of proteins: [illegible] 3 [illegible] BCL2 [illegible] BCL2, BCL2L1/B[illegible]-[illegible]L

Cad96Ca/Stit/Stitcher (Cadherin 96Ca): A *D* [illegible] E . C 96C [illegible] A . 1- C1 [illegible] I (I [illegible]). [illegible][1658]

Caf4: A [illegible] fi [illegible] fi fi [illegible][705]

D 1L- fi ;
LC3-II F52
I35 LC3B.[591]

Chaperone-mediated autophagy (CMA): A
KFE
[1675,1676]
LA 2A
H A8.[1677,1678]

CHKB (choline kinase beta): A
C *B*
[1679]

Chloroquine (CQ): C (3-
) H
[1680]

CHMP1A (charged multivesicular body protein 1A): CH 1A CH
CH 1A
A [802]

Chromatophagy: A
/D A [803]

Ciliophagy: D
(
). C

CISD2/NAF-1 (CDGSH iron sulfur domain 2): A
I ;
CI D2 BCL2 E , BCL2
BEC 1, [1681]
CI D2 E ,
C *D2* 2;

fl [1630]

dom (domino): A D I2/ F2 A [1718]

Dopamine: A [1719]

DOR: 53I 2.

DRAM1 (damage-regulated autophagy modulator 1): D A 1, 53 D A [580] D A 1 D A 1 K1 BEC 1.

Draper: A D C CED-1 [1720]

Drs: .

E2F1: A B 3, C3, 1 D A 1 A 5 [614] E2F1 D A

EAT (early autophagy targeting/tethering) domain: C- A 1, [1721] A 13.

EAT-2 (eating abnormal): A -2 [1703,1722,1723]

EDTP: 14.

EEA1 (early endosome antigen 1): A AB5

EEF1A1/EF1A/eF1α (eukaryotic translation elongation factor 1 alpha 1): G- GFA C A. EEF1A1 G- C A [1724]

eF1α: EEF1A1.

EGFR (epidermal growth factor receptor): A. I3K, AK , [523]

EGO complex: I E 1, E 3 G 2 00.

634 1

C .[1788] H 25 A, 36, A, 36 A, 11 .[1789]

HSC70: H A8.

HSP70 (heat shock protein 70): H 70 . H 70 [1794] H A1A.

HSP90: H 90AA1.

HSP90AA1/HSP90/HSPC1 (heat shock protein 90kDa alpha [cytosolic], class A member 1): A BEC 1, [1795] H 90AA1 LA 2A [1796]

HSPA1A (heat shock protein family A [Hsp70] member 1A): H 70 [1790]

HSPA5/GRP78/BiP (heat shock protein 5 family A [Hsp70] member 5): A E [1791]

HSPA8/HSC70 (heat shock protein family A [Hsp70] member 8): H 70 [1792] C A (-H A8) [1793] (KFE -) [1116] KFE - [1115]

HSPC1: H 90AA1.

HTRA2/Omi (HtrA serine peptidase 2): A HA 1, BCL2 [1797] I H A2, H A2 [1798-1800]

Hypersensitive response: A [1092,1096,1801]

IAPP (islet amyloid polypeptide): A 37 89

I / β- IA 2 IA 1- [1802-1804]

iC-MA (immune cell-mediated autophagy): IL2- [1805]

Ice2: A 1.

ICP34.5: A 1 ( ) . EIF2 1-EIF2AK2 [1726] IC 34.5- BEC 1.[892]

IDP (Intrinsically disordered protein): A [1806-1809] ID [1810] [1811-1814] ID [1815,1816]

IDPR (intrinsically disordered protein region): A

Irs4: I 4 4 A A 17.[1827] fi

Isolation membrane:

ITM2A (integral membrane protein 2A): A KA/KA-C EB -A fl.[1828]

ITPR1/2/3 (inositol 1,4,5-trisphosphate receptor, type 1/2/3): A C^{2+}- E / C^{2+} / I 1,4,5- I BCL2- BEC 1. I BEC 1 C^{2+}- A ,[1220,1244,1246] BEC 1- I - C^{2+} (.,) fl.[297]

JNK1: A K8.

Jumpy: 14.

JUN/c-Jun/JunB (jun proto-oncogene): A [1829]

KAT5/TIP60 (K[lysine] acetyltransferase 5): I , KA 5 G K3 LK1.[1778]

Kcs1:

Lipoxygenases: [illegible] AL 5 [illegible] AL 15,[528] [illegible] IF G- [illegible]

LIR/LRS (LC3-interacting region): [illegible] L- [illegible] ([illegible] /F/ [illegible] - - - I/L/ [illegible]) [illegible] A 8/LC3/GABA A

NAF-1: CI D2.

NAMPT/visfatin (nicotinamide phosphoribosyltransferase): A 5- -1- (A) A C2- - 6KB1 I 1- [1896]

NAPA/αSNAP (N-ethylmaleimide-sensitive factor attachment protein, alpha): A A E-

Phosphatidylinositol 3,5-bisphosphate (PtdIns[3,5]P_2): [illegible] IKF E ([illegible] F E fi [illegible]) [illegible] I [illegible] [1944] [illegible] A F .[1945] . I (3,5) 2 [illegible] [1946] [illegible]

Phosphoinositide 3-kinase/PI3K: [illegible] I [illegible] 3′ [illegible] I3K [illegible]

Phosphoinositides (PI) or inositol phosphates: [illegible] fi [illegible]

(D , E -10,) (FA : F00610), I 1.[1822] ( )-

Rapamycin: A (, 1) 2

RAPTOR: .

Ras: A .

RB1-E2F1 (Retinoblastoma 1-E2 transcription factor 1): B1 , E2F1 G_1. E2F. I B1 E2F1 ; B1 E2F1 BCL2, [615]

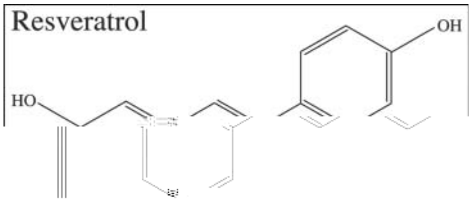
RB1CC1/FIP200 (RB1-inducible coiled-coil 1): A A 17. B1CC1 LK1 .[1533] I , B1CC1

Reactive oxygen species (ROS): C H, $_2^-$. H LC3 A G4,[519] [757]

Ref(2)P: *D* 1.

Residual body: A[2007]

Resveratrol: A I 1 [1510] [2008]



Reticulophagy:

[149]

SNCA/α-synuclein: A CA [2054] C CA CA H GB1 [2055] B. CA, CA. H , CA [1340]

Snx4/Atg24: A I 3 - A 1 A 20.[1600] 4/A 24 I fi [709] , A 24

SNX18: A -BA [2056]

SpeB: A [2057] B [126,2057]

Spautin-1 (specific and potent autophagy inhibitor-1): A 10 13, fi IK3C3/ 34-BEC 1 [2058]

Spermidine

TAK1: [illegible] A 3K7.

TAKA (transport of Atg9 after knocking out [illegible] ***1***) assay: A [illegible] A [illegible] 9-GF [illegible] *A* [illegible] *1.*

( )); G 2 1 [780,2092]

THC (**Δ**9-tetrahydrocannabinol): *C* HC HC

K 53 53- D A F1 70 A fi A 7 A 12.[2117]

TRAF2 (TNF receptor-associated factor 2): A E3 F CCC .[786]

TRAF6 (TNF receptor-associated factor 6, E3 ubiquitin protein ligase): A E3 BEC 1 L 4-[2100]

TRAIL: F F10.

Transgenic: H

Transmitophagy/transcellular mitophagy: A [796]

TRAPPII (transport protein particle II): A 1 31/32 [2118] A II B 3, B 5, 20, 23, 31, 33 65, 120 130.

TRAPPIII (transport protein particle III): A 1. [1321] A III B 3, B 5, 20, 23, 31, 33 85.

TRIB3 (tribbles pseudokinase 3): A (fi) C E IB3 AK C2 AK 1 1/ A 40. C1 [2094] C IB3 1 BA LI fl fi- [2093,2119,2120]

Trichostatin A: A I II HDAC [2121]

TRIM5/TRIM5α (tripartite motif containing 5): A ; I 5 HI -1 [1984]

TRIM20: EF .

TRIM21: A I 21 I F3 I [1869]

TRIM28 (tripartite motif containing 28): I 28 E3 KAA1, [1854] AGEA3.

TRIM50 (tripartite motif containing 50): I 50 E3- [2122] 1 HDAC6- [2123,2124]

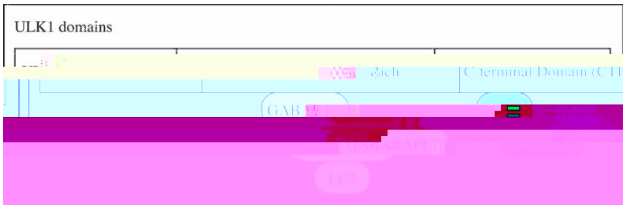
TRIM63/MURF-1 (tripartite motif containing 63, E3 ubiquitin protein ligase): fi E3 [2125,2126] H3GLB1 CH A1 [2036]

TRPC4 (transient receptor potential cation channel, subfamily C, member 4): A

Ubp3: A B 5 [847] C 3-B 5 [2131]

UBQLN/Ubiquilins: [2132]

ULK family (unc-51 like autophagy activating kinase): LK A 1. I 5 LK1, LK2, LK3, LK4, K36/ LK5. LK1 LK2 LK3 [535,2133,2134] A 1. F fi F . 2 . 2135.



Ume6: A 3L 1. *A 8* [1233] 3 3/ I 3.

UNC-51: *C.* A 1/ LK1/ LK2 A 1.

UPR (unfolded protein response): A E fl

USP8 (ubiquitin specific peptidase 8): A K6- A K2 A K2

1233C 57.5( )0( )-330.8(( )-10 6-371.7(J/F401 .87832680 D() /F191 .57470 D (6-323.8( )-9.1(

VAMP7 (vesicle-associated membrane protein 7): A 7 A E A G16L1 7 (7), 8 I1B, [2150] A 7 [2149]

VAMP8 (vesicle-associated membrane protein 8): A A E I1B, [2151]

VCP/p97 (valosin-containing protein): A II AAA$^+$- A ; C fi [2152,2153] C 48.

Verteporfin: A FDA- ; [2154]

VHL (von Hippel-Lindau tumor suppressor, E3 ubiquitin protein ligase): HL α HIF1 HIF1A 2 [2155] EGL

VirG: A ; G A G5, I B, [2156] III

VMP1 (vacuole membrane protein 1): A [632,2157] 1 I 3 , [2158] A G12–A G5-A G16L1 , LC3.[2159]

Vps1: A G fi- I A 11 A 36 [1716] D 1.

Vps11: A

E-354 C1 C2, fl [341] K -0063794.

XBP1 (X-box binding protein 1): A E B 1 H 1.[2174]

Xenophagy: C - (, ., , /) - [2175]

Xestospongin B: A I BEC 1 - [2176]

Yeh1: A 1.

Ykt6: A A E G (C [2177]); [2023] 6

Ymr1: A I 3 - fi [2178,2179]

Ypk1: A C2 - [2105] C2 1 3/ -C 1/ - G 2, - G 2.

Ypt1: A G [1321] 1 A 8 A AB1, - [2180,2181] A III.

Ypt7: A AB7, -

YWHAZ/14-3-3/(tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta): A 14-3-3 IK3C3 C2- [2182]

ZFPM1/FOG1 (zinc finger protein, FOG family member 1): A GA A1, - [641] GA A1.

ZFYVE1/DFCP1 (zinc finger, FYVE domain containing 1): A I 3 - - [583] K F E1 -

ZFYVE26/spastizin/SPG15 (zinc finger, FYVE domain containing 26): A - BEC 1- AG- BC [2183]

ZIPK: .

ZKSCAN3/ZNF306 (zinc finger with KRAB and SCAN domains 3): A fi K - CA

- K CA 3 60 - / - *A 1 C3B* *2,* 1 K CA 3 [643]

Zoledronic acid: A -