University of Groningen

Atg21p is essential for macropexophagy and microautophagy in the yeast *Hansenula polymorpha*

Leão-Helder, Adriana N; Krikken, Arjen M; Gellissen, Gerd; van der Klei, Ida J; Veenhuis, Marten; Kiel, Jan A K W

Published in:
FEBS Letters

DOI:
[10.1016/j.febslet.2004.10.055](https://doi.org/10.1016/j.febslet.2004.10.055)

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date:
2004

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):

Leão-Helder, A. N., Krikken, A. M., Gellissen, G., van der Klei, I. J., Veenhuis, M., & Kiel, J. A. K. W. (2004). Atg21p is essential for macropexophagy and microautophagy in the yeast *Hansenula polymorpha*. *FEBS Letters*, 577(3), 491 - 495. <https://doi.org/10.1016/j.febslet.2004.10.055>

Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: <https://www.rug.nl/library/open-access/self-archiving-pure/taverne-amendment>.

Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

Alignment of *H. polymorpha* Atg21p and other members of a WD40 family identified in *H. polymorpha*, *S. cerevisiae* and *P. pastoris*. The Hp-Atg21p primary sequence was aligned with *S. cerevisiae* (Sc) Atg18p (SwissProt P43601), Atg21p (SwissProt Q02887), Ygr233cp (SwissProt P50079), *P. pastoris* (Pp) Atg18p (SwissProt Q8X1F5) and the Atg18p and Ygr223cp homologues encoded by the *H. polymorpha* genome sequence ([27]; Genbank AY756175 and AY756176, respectively). The one-letter code is shown. Gaps were introduced to maximise the similarity. Residues that are similar in all proteins are in black; those that are similar in six of the proteins are shaded dark grey, while those that are similar in four of the proteins are shaded light grey.