

N. crassa* vs. *S. cerevisiae

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N   1  MGNFCSTCFGGRRSDDYDEEDDEAQLFDENNMHYGS-----FDOQHMM 43
      ||...|. | .:..:| | :| | | ..|...| | | :|.:.|.
S   1  MGAVLSCC-----RNHSGEENEA--LLREQQAGYGSQGNANDEYDAEQMR 43

N  44  NQEDPOETEREIAA----LOGVVERTSNNMVDI-----YDMVPHDKPMQD 84
      .:| .|.|:..:| | :.:|. .|:..:| | | .:|. . . . . :| :
S  44  LKE--HEHEQKLLAREQELRDIVANTNDKLIDISMINNSGIVIQGTDLQE 91

N  85  APAPYGFANQRYNALLSKLSTHDDMAAVARVDWGTPEDDSMEMLRKASLP 134
      | .|. . . . . . . | | .|. | . |
S  92  A-----LDKRQQEEG-----GDSREDERSA--- 111

N 135  TIPIKAEGGEALVGNFTDAAAAMR----- 158
      | .: . | . | : . . . : . . . :
S 112  -----GDDNLSGHSVPSSGSAQATTHQTAPRTNTFTLLTSPDSAKISK 154

N 159  ----- 158

S 155  EQLKKLHSNILNEIFSQSQVKNKPGPLTVPF 184
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Identity: 37/230 (16.1%)
Similarity: 61/230 (26.5%)
Gaps: 118/230 (51.3%)
Score: 49.5

N.crassa* vs. *H. sapiens

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N   1  MGNFCSTCFGGRRSDDYDEEDDEAQLFDENN----MHYGSFDQOHMMNOE  46
      ||  |  |  |  :.....|.....:|.:.|.|.:.:  ...|:.....|.:
H   1  MG--C--CYSSENEDSDQDRERKLLDPSSPPTKALNGAEPNYHSL---  43

N  47  DPQETEREIAALQGVVERTSNMVDI----YDMVPHDKPMQDAPAPYGF  91
      |.....|.|.|.:.:.:|.:.:|.:.:  ..|.|.|.:.  |..
H  44  -PSARTDEQALLSSILAKTASNIIDVSAADSQGMEQHE-----YMD  83

N  92  ANQRYN---ALLSKLSTHDDMAAVARVDWGTPEDDSMEMLRKASLPTIP-  137
      .:.:|.:.  |:|.|...||  |  ..|||.:.|
H  84  RARQYSTRLAVLSSSLTH-----W-----KKLPPLPS  110

N 138  IKAEGGEALVGN---FTDAAAAMR-----  158
      :.:.:.:.|.:.  |:|.:.:.|
H 111  LTSQPHQVLASEPIPFSDLQQVSRIAAYAYSALSQIRVDAKEELVVQFGI  160

N 159 - 158

H 161 P 161

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Identity: 34/201 (16.9%)
 Similarity: 61/201 (30.3%)
 Gaps: 83/201 (41.3%)
 Score: 55.5

KEY:

Conserved LAMTOR domains: **blue**
 Potential myristoylation sites: **yellow**
 Potential palmitoylation sites: **green**
 Potential lysosomal/vacuolar localization signals: **underlined bold**
 | Identity
 . : Similarities