ERS1 a seven transmembrane domain protein from *Saccharomyces cerevisiae*

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We have recently reported the cloning and characterisation of the ERD1 (ER Retention Defective) gene product from *S. cerevisiae* (1). It is required for the retention of luminal endoplasmic reticulum proteins and for full glycoprotein processing in the Golgi apparatus.

Here we report the sequence of another yeast membrane protein ERS1 (ERD Suppressor). The gene was isolated from a genomic library in YEp13 (gift from K.Nasmyth) when attempting to clone the ERD1 gene by complementation. It was found, upon subcloning and re-transformation, that ERS1 significantly reduced the erd phenotype (the secretion of endogenous ER proteins and an invertase-HDEL marker construct used in the initial isolation of erd mutants (2)) of multiple erd1 alleles and a strain carrying a disrupted erd1 gene.

Sequence analysis (Fig. 1) predicts a 30 kD protein with seven putative transmembrane domains (overlined in Fig. 1) as indicated by hydropathy analysis (3) as shown in Fig. 2. A gene disruption of ERS1 has been performed; the resulting strain is viable and does not have an erd phenotype.

REFERENCES

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3. Eisenberg *et al.* (1984) *J. Mol. Biol.* **179**, 125–142.

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 M  V  S  L  D  D  I  L  G  I  V  Y  V  T  S  W  S  I  S  M  Y  P  P  I  I  T  N  W  R  H  K  S  A
ATGGTGTCGTTAGACGATATACTAGGTATCGTGTATGTTACGTCATGGTCGATATCGATGTATCCACCGATAATCACCAATTGGCGCCATAAGTCAGCGA 100

 S  A  I  S  M  D  F  V  M  L  N  T  A  G  Y  S  Y  L  V  I  S  I  F  L  Q  L  Y  C  W  K  M  T  G  D
GCGCGATATCGATGGATTTTGTCATGTTAAATACGGCAGGTTACTCTTACCTGGTCATATCCATATTTTTGCAATTGTACTGCTGGAAAATGACGGGTGA 200

 E  S  D  L  G  R  P  K  L  T  Q  F  D  F  W  Y  C  L  H  G  C  L  M  N  V  V  L  L  T  Q  V  V  A
TGAGTCTGACTTGGGCAGGCCCAAGTTGACGCAATTTGATTTCTGGTATTGCCTGCATGGGTGCTTGATGAATGTTGTCTTATTGACCCAGGTGGTAGCT 300

 G  A  R  I  W  R  F  P  G  K  G  H  R  K  M  N  P  W  Y  L  R  I  L  L  A  S  L  A  I  F  S  L  L
GGAGCGAGAATCTGGCGATTTCCAGGTAAAGGTCACCGCAAGATGAATCCATGGTACCTAAGGATTTTACTCGCATCACTGGCCATTTTTTCACTGCTAA 400

 T  V  Q  F  M  Y  S  N  Y  W  Y  D  W  H  N  S  R  T  L  A  Y  C  N  N  L  F  L  L  K  I  S  M  S  L
CCGTACAATTTATGTACTCCAACTACTGGTACGATTGGCATAACTCAAGAACTCTGGCGTATTGCAACAATTTGTTTTTACTCAAAATATCGATGTCACT 500

 I  K  Y  I  P  Q  V  T  H  N  S  T  R  K  S  M  D  C  F  P  I  Q  G  V  F  L  D  V  T  G  G  I  A
AATCAAGTACATCCCACAAGTGACGCATAACTCGACAAGAAAATCTATGGATTGTTTCCCCATTCAGGGTGTGTTTCTAGATGTCACTGGCGGTATCGCC 600

 S  L  L  Q  L  I  W  Q  L  S  N  D  Q  G  F  S  L  D  T  F  V  T  N  F  G  K  V  G  L  S  M  V  T
TCGCTGCTCCAATTGATTTGGCAGTTGTCTAACGATCAAGGTTTCAGTCTGGATACGTTCGTGACAAATTTTGGAAAAGTGGGACTGTCAATGGTAACTT 700

 L  I  F  N  F  I  F  I  M  Q  W  F  V  Y  R  S  R  G  H  D  L  A  S  E  Y  P  L  *
TAATATTCAACTTCATCTTTATCATGCAGTGGTTTGTATATCGATCTCGAGGCCATGATCTGGCGTCAGAGTACCCGCTGTAG
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