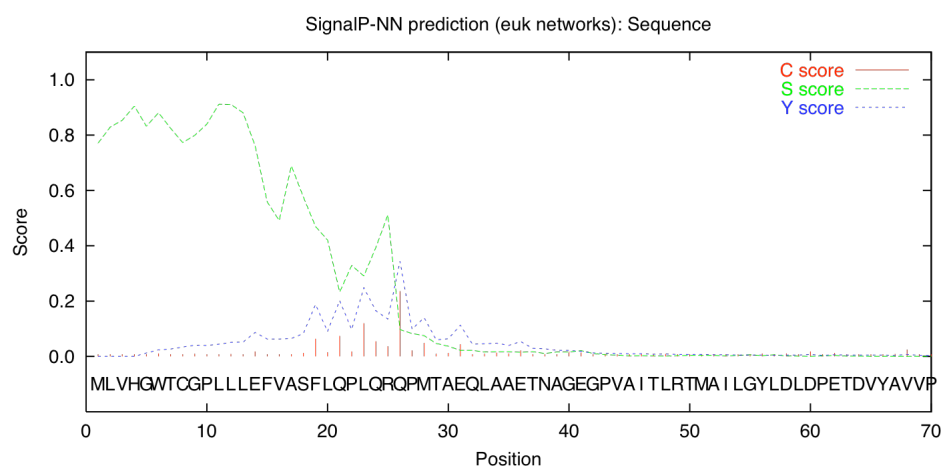
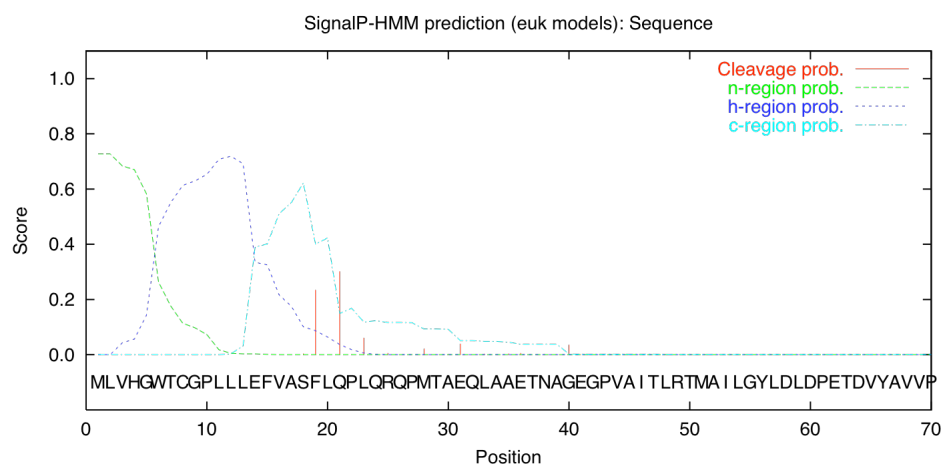


Supporting Information S3a:

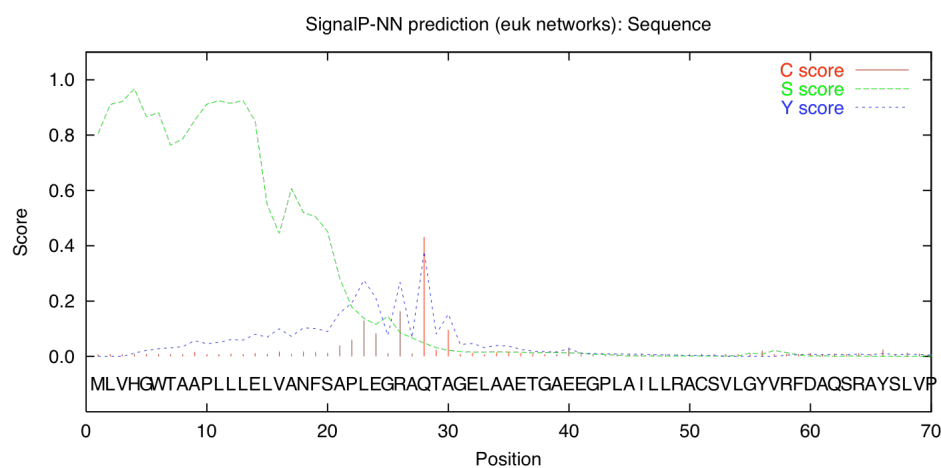


```
>Sequence length = 70
# Measure Position Value Cutoff signal peptide?
max. C 26 0.236 0.32 NO
max. Y 26 0.344 0.33 YES
max. S 11 0.912 0.87 YES
mean S 1-25 0.670 0.48 YES
D 1-25 0.507 0.43 YES
# Most likely cleavage site between pos. 25 and 26: LQR-QP
```

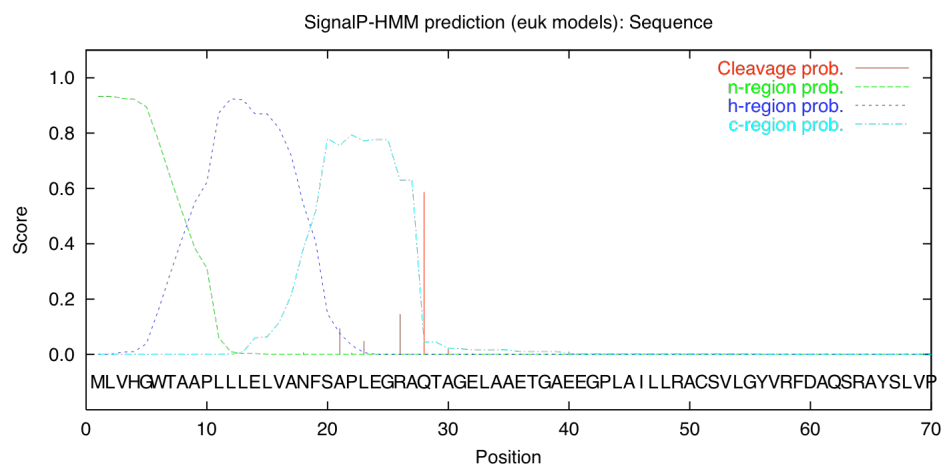


```
>Sequence Prediction: Signal peptide
Signal peptide probability: 0.727
Signal anchor probability: 0.000
Max cleavage site probability: 0.302 between pos. 20 and 21
```

Supporting Information S3b:

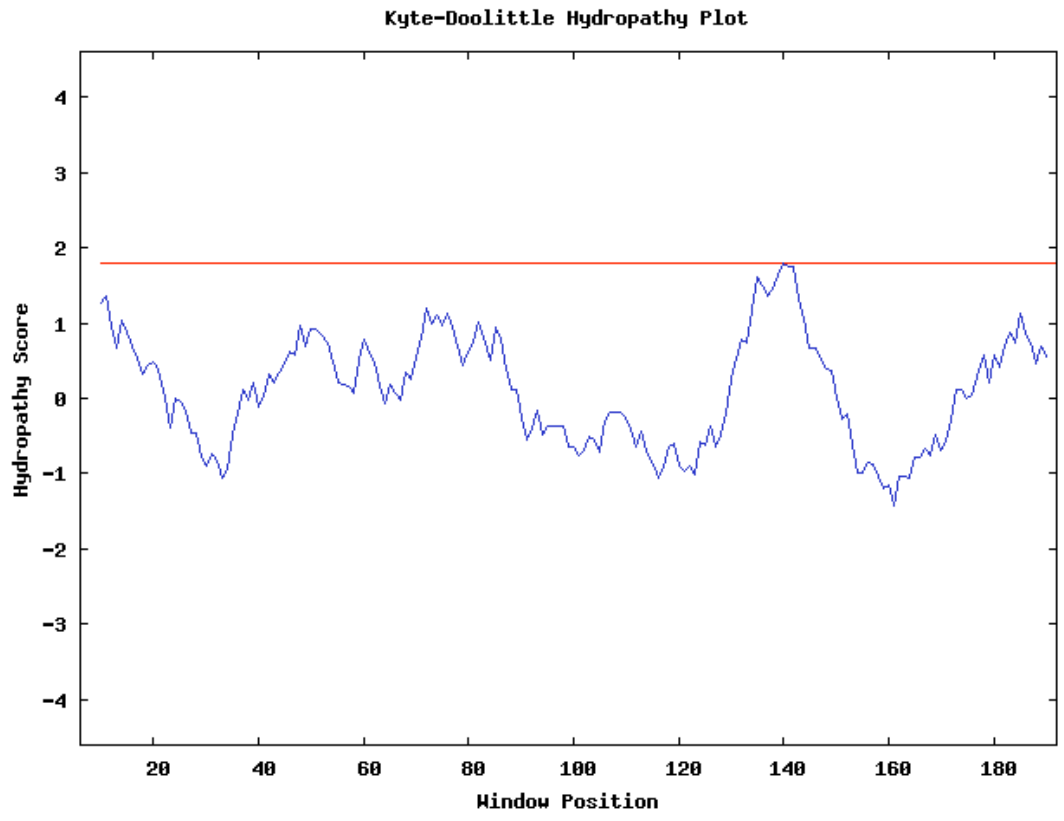
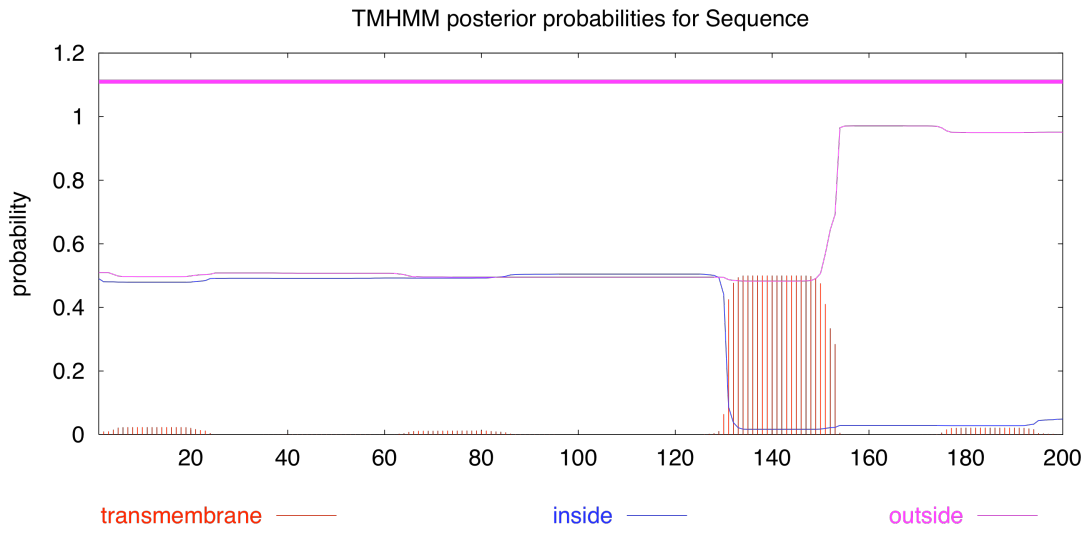


```
>Sequence length = 70
# Measure Position Value Cutoff signal peptide?
max. C 28 0.432 0.32 YES
max. Y 28 0.380 0.33 YES
max. S 4 0.968 0.87 YES
mean S 1-27 0.606 0.48 YES
D 1-27 0.493 0.43 YES
# Most likely cleavage site between pos. 27 and 28: GRA-QT
```



```
>Sequence Prediction: Signal peptide
Signal peptide probability: 0.933
Signal anchor probability: 0.000
Max cleavage site probability: 0.587 between pos. 27 and 28
```

Supporting Information S3c:



Supporting Information S3d:

