

garnier

garnier PPF1_PEA.FASTA

功能: 用 GOR 方法预测蛋白质序列 “PPF1_PEA.FASTA” 中二级结构, 结果如下:

```
#####
# Program: garnier
# Rundate: Mon Apr 05 15:32:11 2004
# Report_format: tagseq
# Report_file: ppf1_pea.garnier
#####

#=====
#
# Sequence: PPF1_PEA      from: 1   to: 442
# HitCount: 116
#
```

```

# DCH = 0, DCS = 0
#
# Please cite:
# Garnier, Osguthorpe and Robson (1978) J. Mol. Biol. 120:97-120
#
#=====
      . 10   . 20   . 30   . 40   . 50
      MAKTLISSPSFLGTPLPSLHRTFSPNRTLFTKVQFSFHQLPPIQSVSHS
helix HHH
sheet  EEEE          EE          EEEE E          EEEEE
turns          TTT   T  TT   TTTT   TT TTT   TT
coil        CC  CCCCC   CCC          CCC   C
      . 60   . 70   . 80   . 90   . 100
      VDLSGIFARAEGLLYTLADATVAADAAASTDVAAQKNGWFGFISDGMEF
helix  HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
sheet  E  EE          E          EEE
turns  T          TTTT
coil   CC          C  CCCC
      . 110  . 120  . 130  . 140  . 150
      VLKVLKDGLSSVHPYSYGFAIILLTVIVKAATLPLTKQVESTLAMQNL
helix  HHHHHH          H  HHHH  HHHHHH  HHHHHHH
sheet  EEEEEE  EEEEEE  EE          EEE
turns  TT          TTTT
coil   C          C
      . 160  . 170  . 180  . 190  . 200
      QPKIKAIQERYAGNQERIQLETSRLYTQAGVNPLAGCLPTLATIPVWIGL
helix  HH  H
sheet  EEEEE          EEEE          EE  EE  EEEEEEEEEEEEEEE
turns  T          TTT          TTTTT  TT  TTT
coil   CCCCCC          C  CCCC          C
      . 210  . 220  . 230  . 240  . 250
      YQALSNVANEGLLTEGFLWIPSLGGPTSIAARQSGSGISWLFPFVDGHPL
helix  HHHHHH
sheet  EE          EE  EE          EEEEE          EEEEE
turns          T  TT          TTTT          TTT
coil   CCCCCC          C  CCCC          CC  CCCC
      . 260  . 270  . 280  . 290  . 300
      LGWYDTAAYLVLPVLLIVSQYVSMEIMKPPQTNDPNQKNTLLIFKFLPLM

helix  H
sheet  E EEEEEEEEEEEEEEE EEEEEEE          EEEEEEEEEEE E
turns  TT T          TTT  TTT          T
coil   C          CC  CCC
      . 310  . 320  . 330  . 340  . 350
      IGYFSLSPVPSGLTIYWFTNNVLSTAQQVWLRKLGAKPAVNENAGGIITA
helix  HHH          HH          H
sheet  EEEEEE          EEEEE          EEEEE          EEE          EEEE
turns          TT          TTT          TTT
coil   CCC          CCCCCC          CCCC          C
      . 360  . 370  . 380  . 390  . 400
      GQAKRSASKPEKGGERFRLKEEEKKKLIKALPVEEVQPLASASASNDG
helix  HH          HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
sheet
turns  T          TTT          T
coil   CC CCCCC  C          C          CCCC C
      . 410  . 420  . 430  . 440
      SDVENNKQEVTESNTSKVSQEVQSFSTRERRSKRSKRKPVA
helix  HHHHHHHHHH          HHHH
sheet  EEEEE          EEE          EE
turns          T          TTTTTTT
coil   CCCCC          CCCC  CCC          CC
#-----

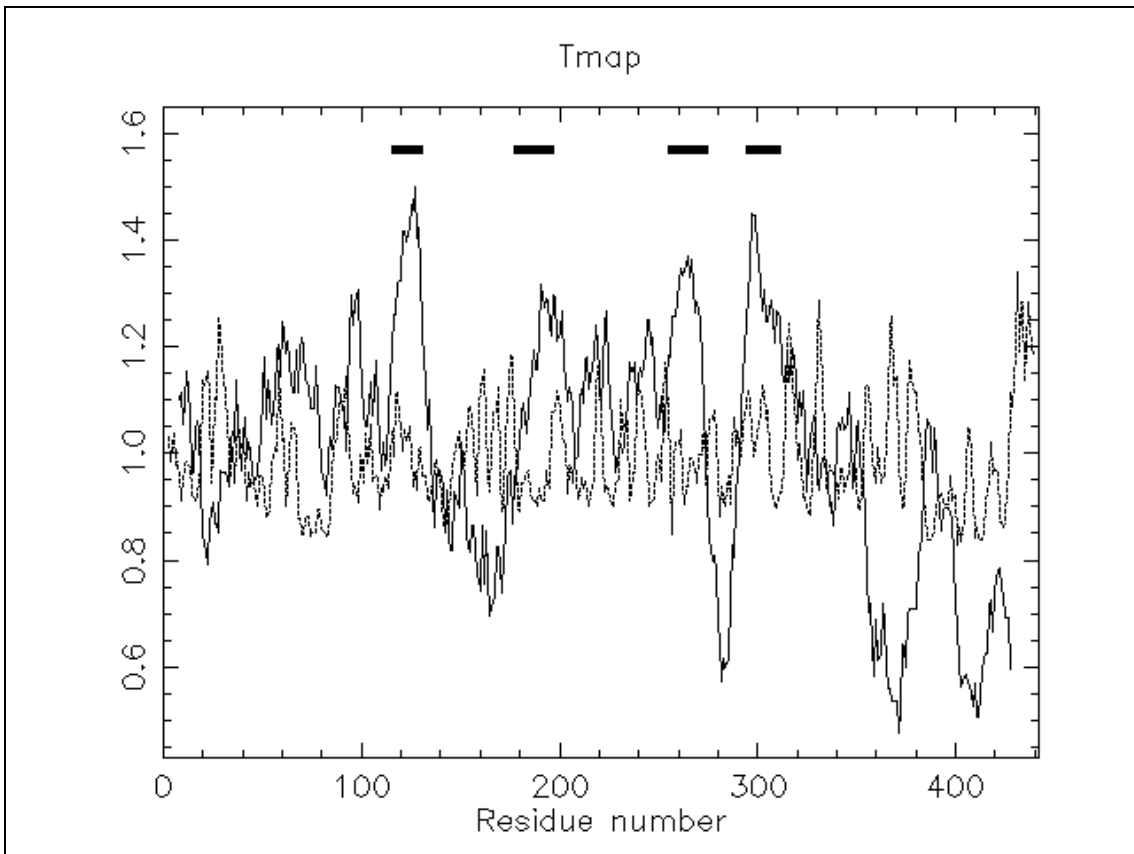
```

```
#  
# Residue totals: H:115 E:147 T: 83 C: 97  
# percent: H: 27.0 E: 34.5 T: 19.5 C: 22.8  
#  
#-----
```

tmap

tmap PPF1_PEA.FASTA graph x11

功能: 预测蛋白质序列“PPF1_PEA.FASTA”中跨膜区, 结果如下:



输出文件 tmap.res

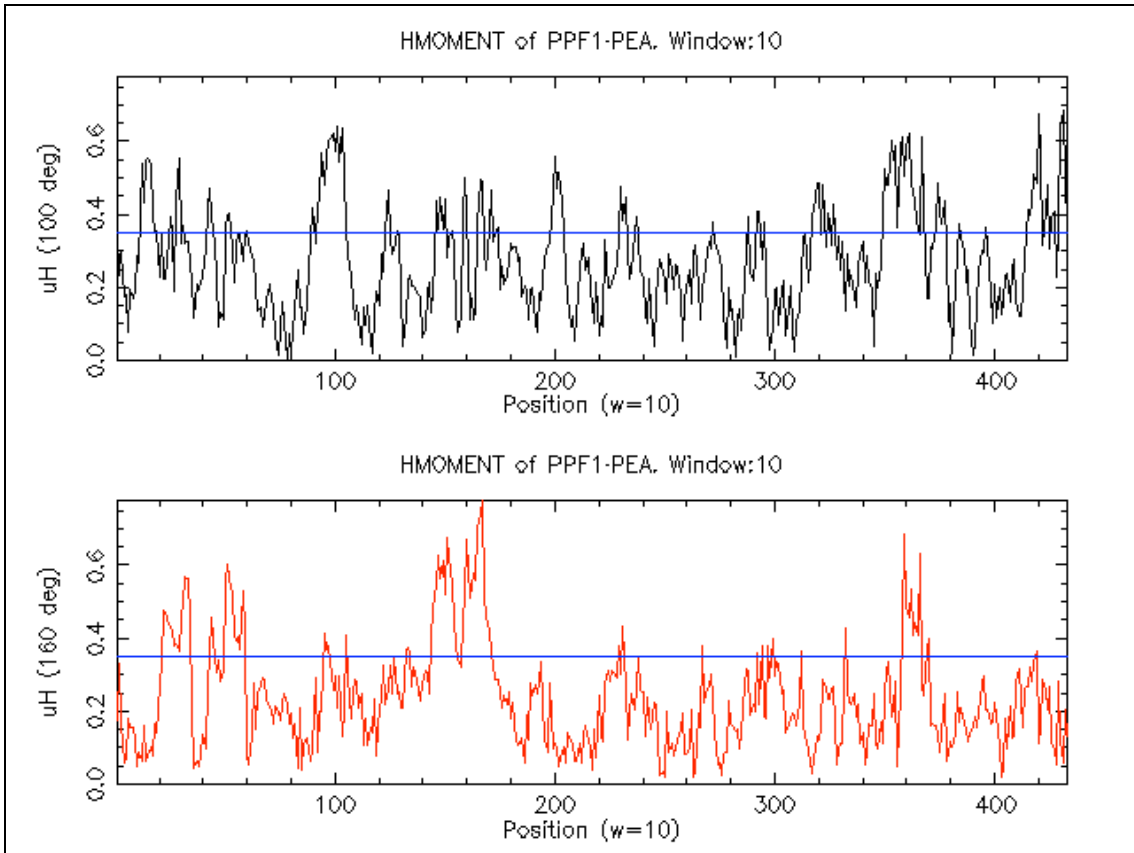
```
PREDICTED TRANSMEMBRANE SEGMENTS FOR PROTEIN PPF1_PEA_1  
TM 1: 111 - 135 (25)  
TM 2: 173 - 201 (29)  
TM 3: 251 - 279 (29)  
TM 4: 290 - 315 (26)
```

hmoment

hmoment PPF1_PEA.FASTA -plot -double -graph png

功能: 以图形方式显示蛋白质序列“PPF1_PEA.FASTA”可能形成 alpha 螺旋和 beta

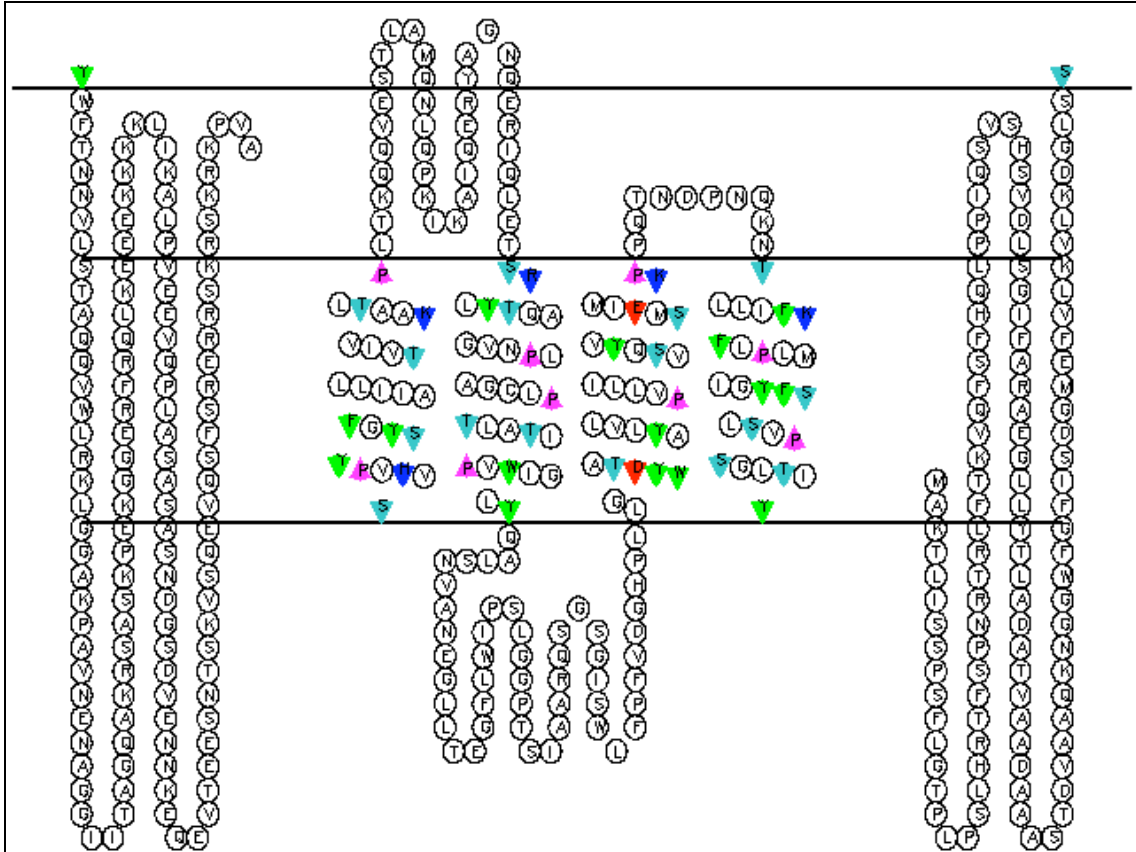
折叠的片段，输出结果如下：



topo

```
topo PPF1_PEA.FASTA -prol=um -cys=cg -gly=sr -acid=dr -basic=db -ohaa=da  
-araa=dg -section "111-135 173-201 251-279 290-315" -nomem -graph png
```

功能：以图形方式显示蛋白质序列“PPF1_PEA.FASTA”跨膜拓扑结构，蓝色表示碱性残基，红色表示酸性残基，绿色表示芳香族残基，粉色表示脯氨酸，浅蓝色表示丝氨酸和苏氨酸，输出结果如下：



pepwheel

```
pepwheel PPF1_PEA.FASTA -sbegin 111 -send 135 -graph x11
```

功能：以图形方式显示蛋白质序列“PPF1_PEA.FASTA”中 111-135 残基的螺旋轮，输出结果如下：

