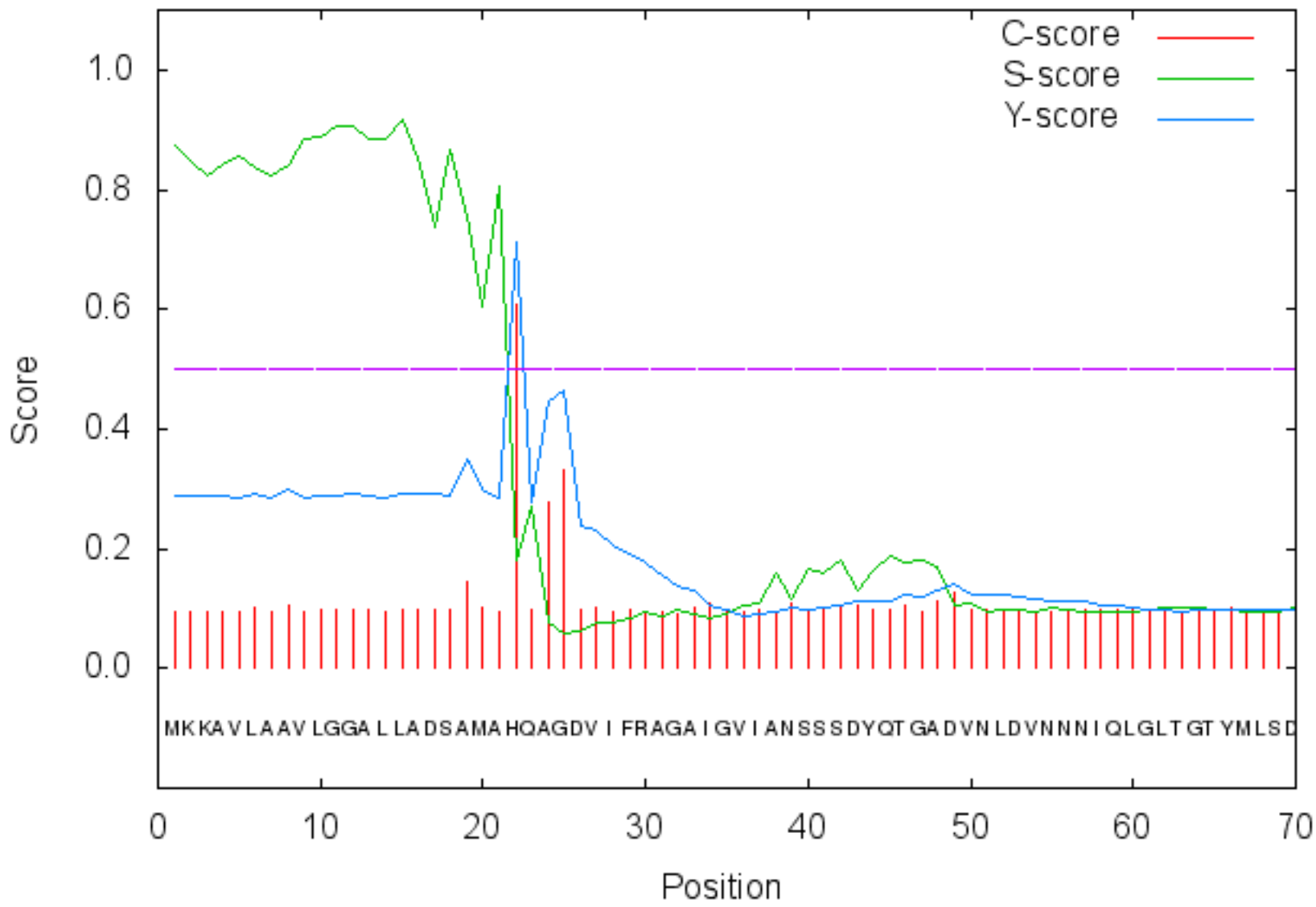


SignalP-4.1 gram- predictions

>ompW

SignalP-4.1 prediction (gram- networks): ompW



# Measure	Position	Value	Cutoff	signal peptide?
max. C	22	0.607		
max. Y	22	0.712		
max. S	15	0.917		
mean S	1-21	0.840		
D	1-21	0.772	0.570	YES

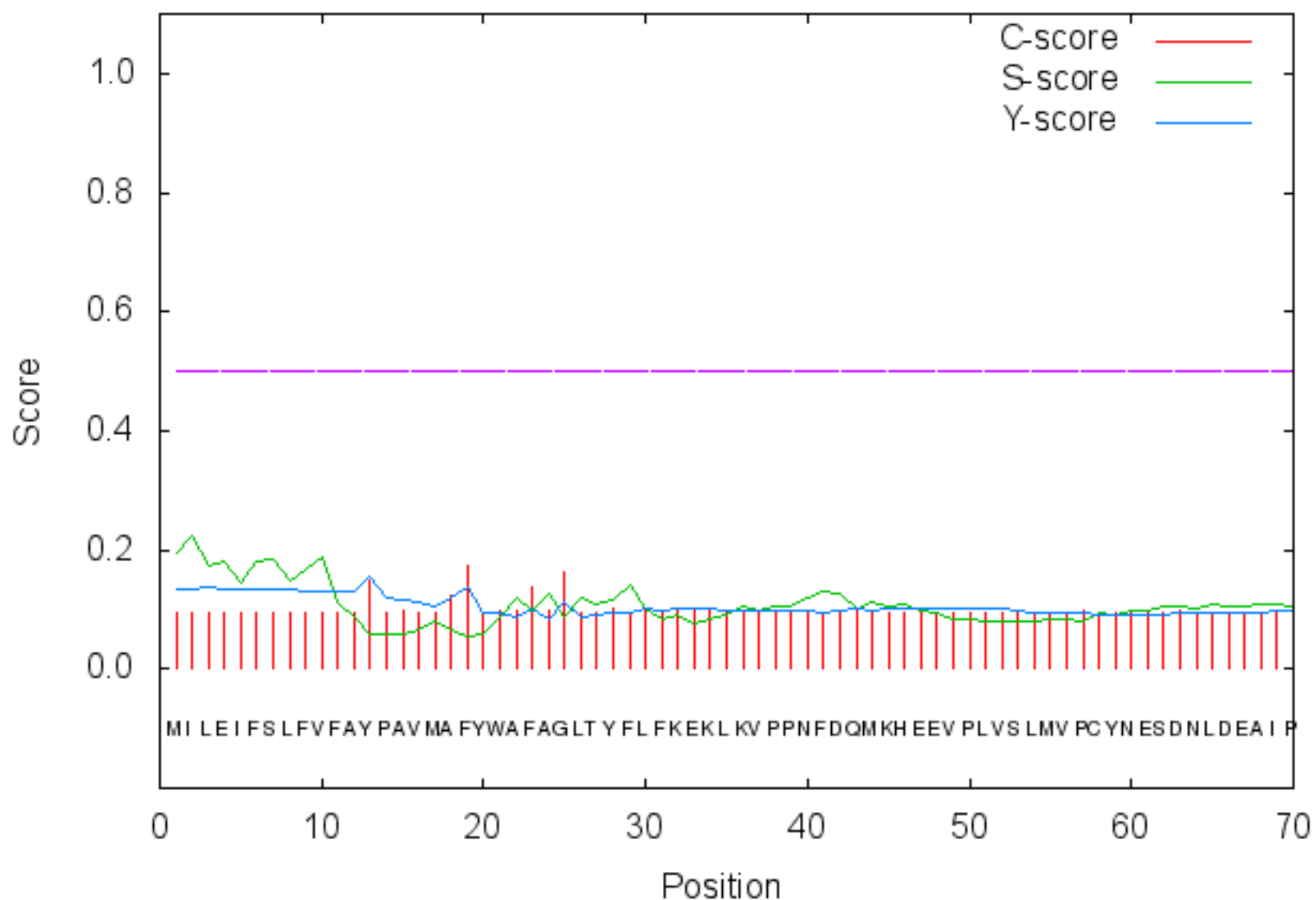
Name=ompW SP='YES' Cleavage site between pos. 21 and 22: AMA-HQ D=0.772 D-cutoff=0.570 Networks=SignalP-noTM

[data](#)

[gnuplot script](#)

>pgac

SignalP-4.1 prediction (gram- networks): pgaC



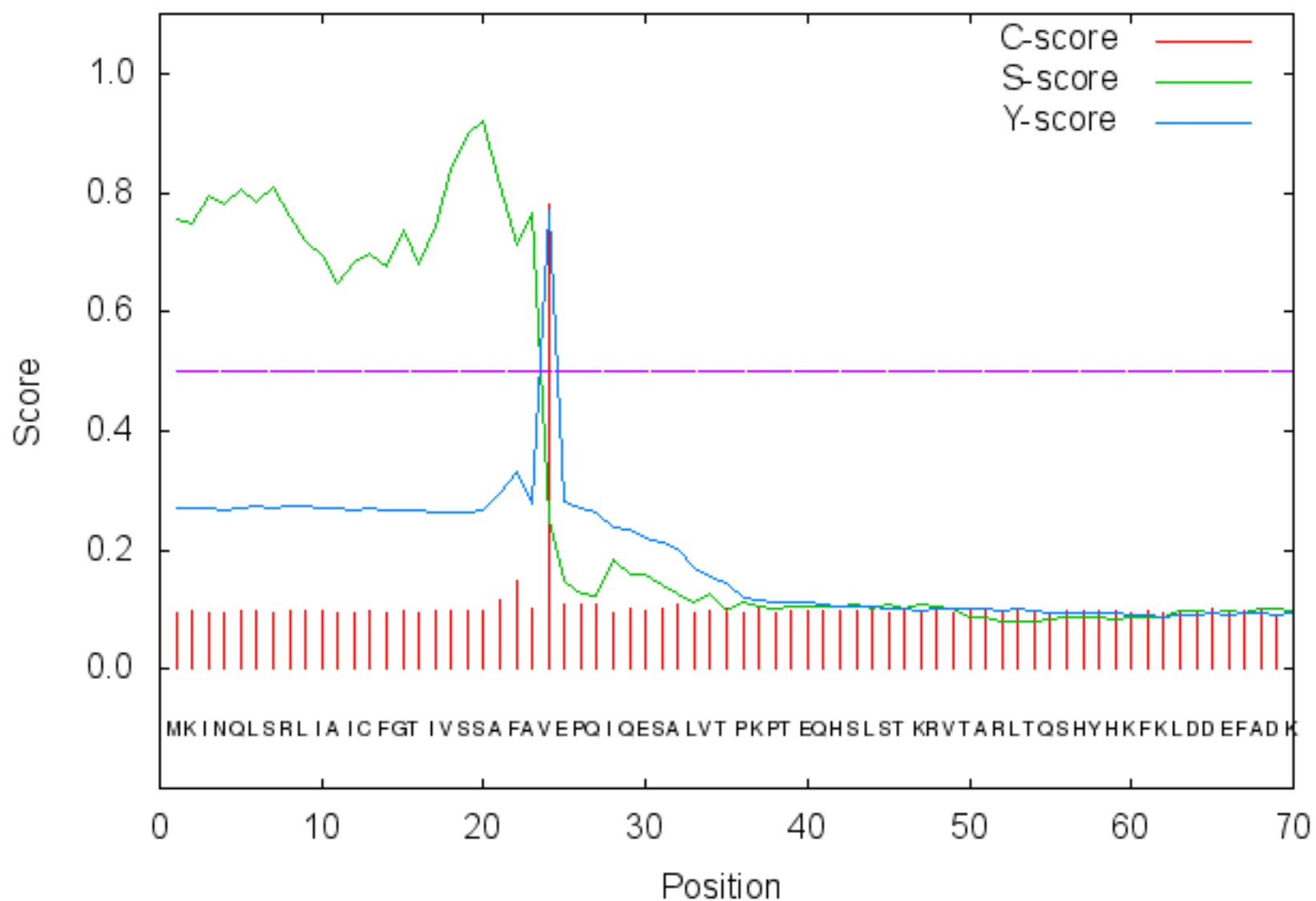
# Measure	Position	Value	Cutoff	signal peptide?
max. C	19	0.175		
max. Y	13	0.157		
max. S	2	0.222		
mean S	1-12	0.165		
D	1-12	0.160	0.510	NO

Name=pgaC SP='NO' D=0.160 D-cutoff=0.510 Networks=SignalP-TM

[data](#)
[gnuplot script](#)

>prc

SignalP-4.1 prediction (gram- networks): prc



# Measure	Position	Value	Cutoff	signal peptide?
max. C	24	0.779		
max. Y	24	0.771		

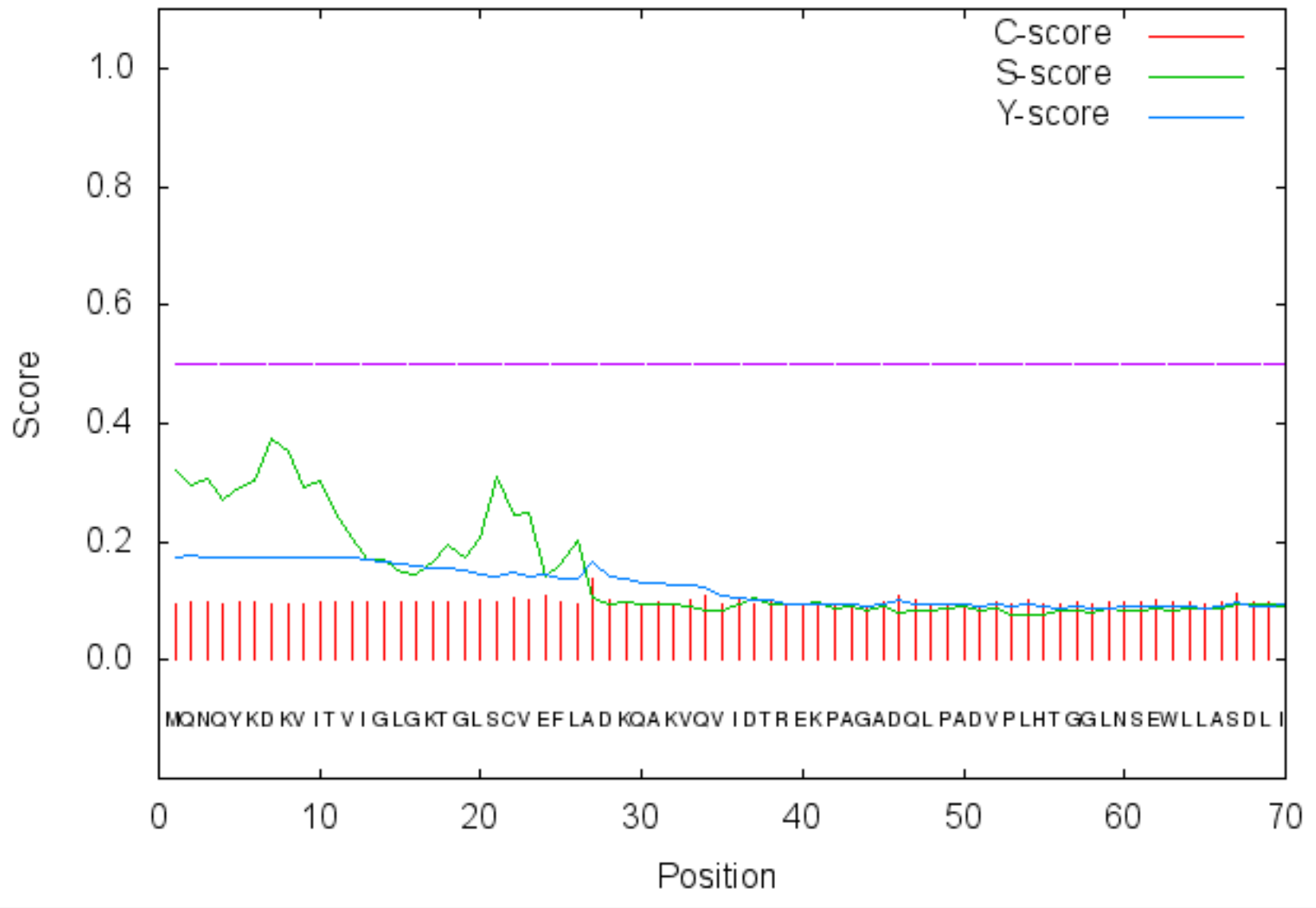
```

max. S    20    0.919
mean S    1-23   0.759
D         1-23   0.766   0.570   YES
Name=prc   SP='YES' Cleavage site between pos. 23 and 24: AFA-VE D=0.766 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script

```

>murD

SignalP-4.1 prediction (gram- networks): murD



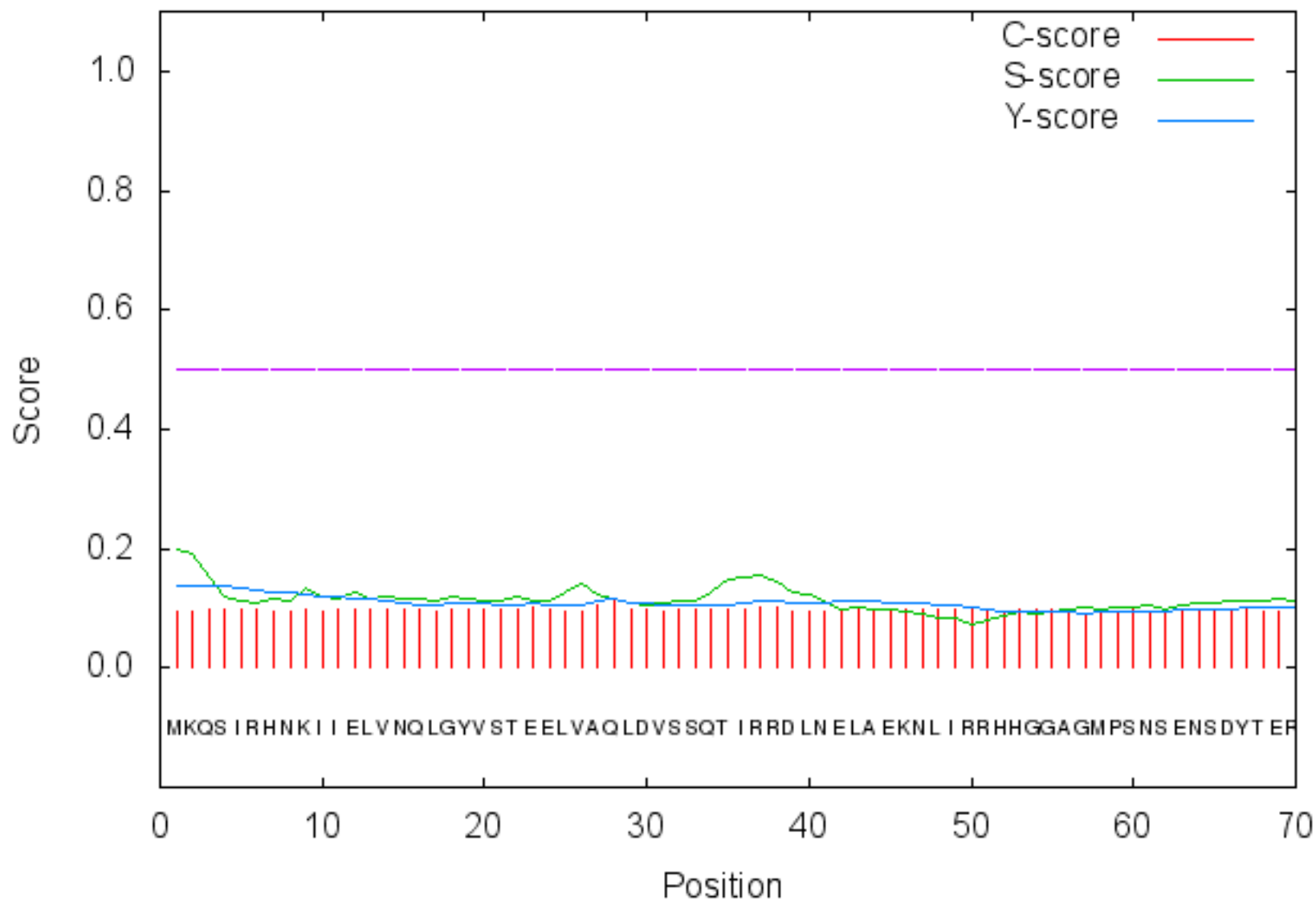
```

# Measure  Position  Value  Cutoff  signal peptide?
max. C     27         0.139
max. Y     11         0.174
max. S     7          0.373
mean S     1-10       0.311
D          1-10       0.238   0.570   NO
Name=murD  SP='NO' D=0.238 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script

```

>glpR

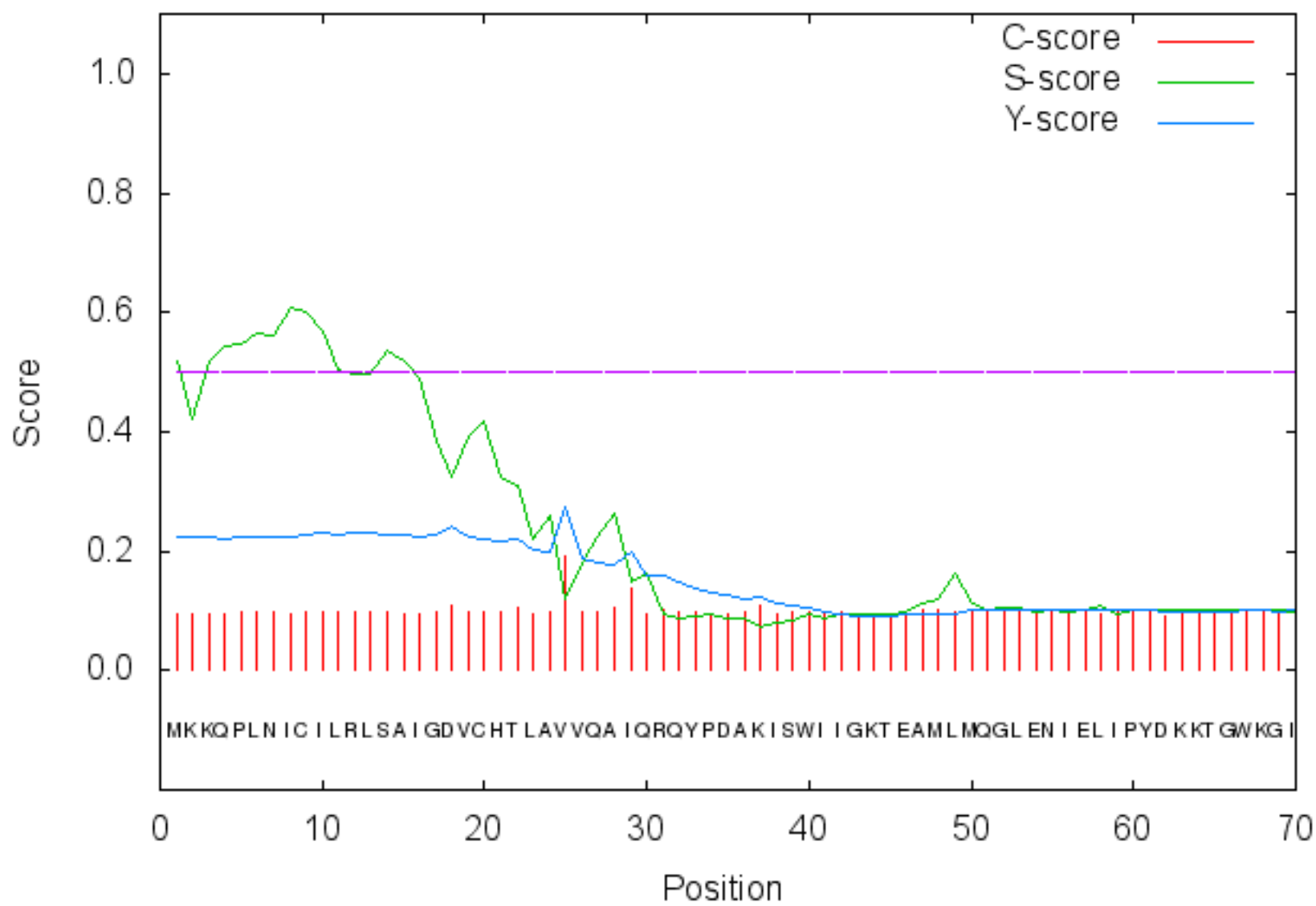
SignalP-4.1 prediction (gram- networks): glpR



```
# Measure  Position  Value  Cutoff  signal peptide?
max. C     28       0.113
max. Y     11       0.119
max. S     1        0.197
mean S     1-10     0.136
D         1-10     0.127  0.570  NO
Name=glpR      SP='NO' D=0.127 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script
```

>rfaC

SignalP-4.1 prediction (gram- networks): rfaC



```
# Measure  Position  Value  Cutoff  signal peptide?
max. C     25       0.191
max. Y     25       0.273
```

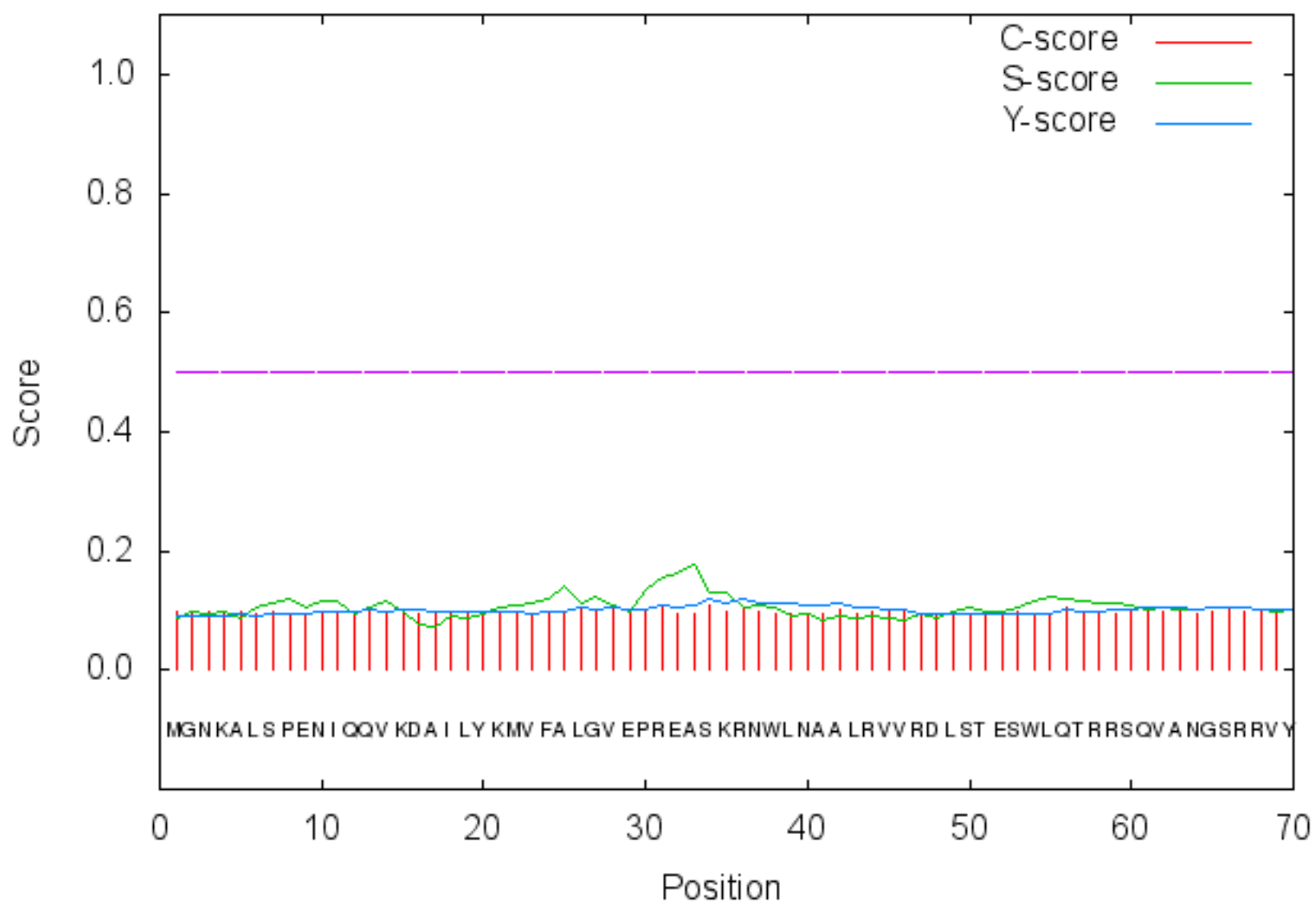
```

max. S      8      0.608
mean S     1-24    0.464
D          1-24    0.362    0.570    NO
Name=rfaC   SP='NO' D=0.362 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script

```

>malP

SignalP-4.1 prediction (gram- networks): malP



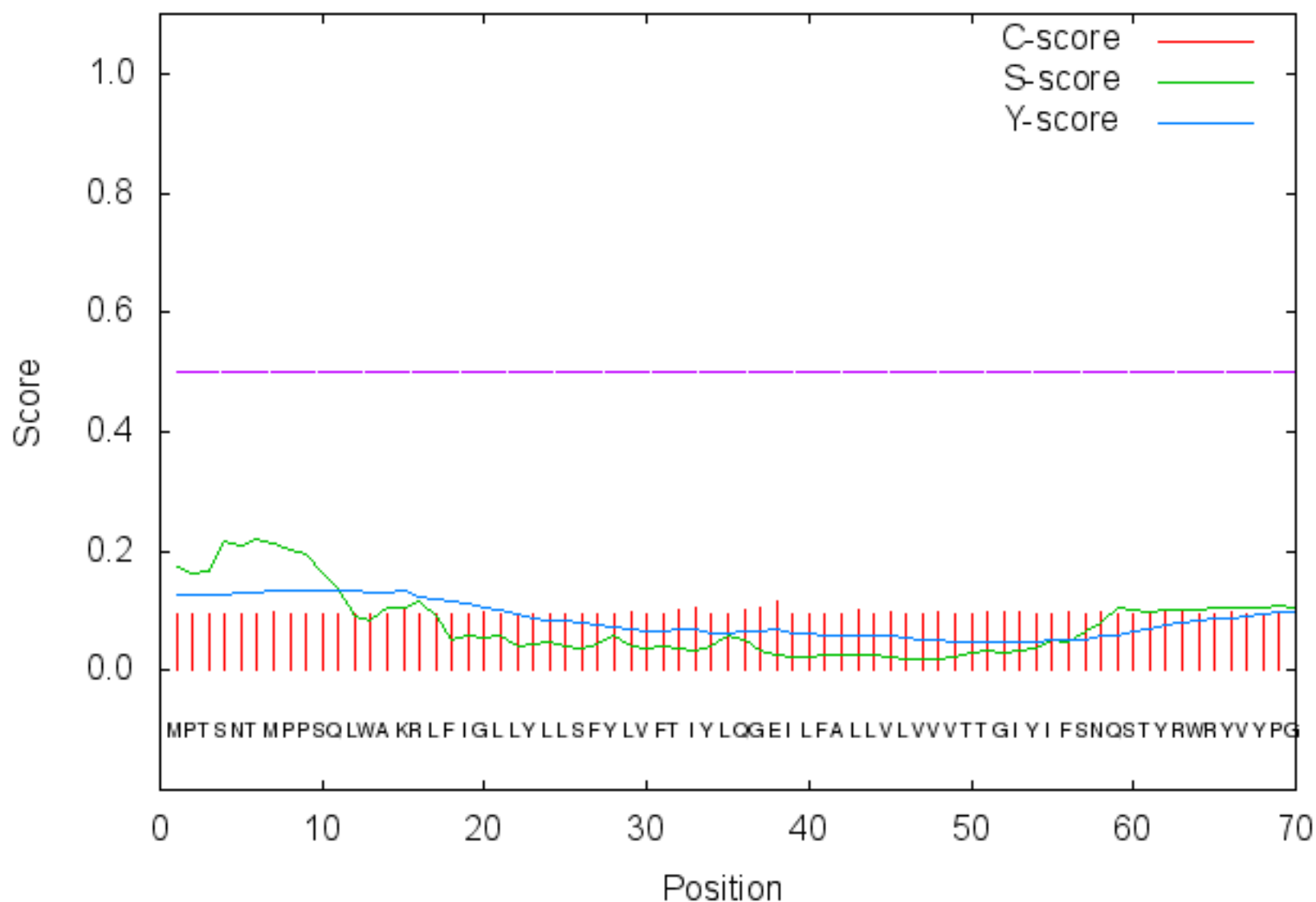
```

# Measure  Position  Value    Cutoff  signal peptide?
max. C     28      0.110
max. Y     34      0.119
max. S     33      0.176
mean S     1-33    0.110
D          1-33    0.115    0.570    NO
Name=malP   SP='NO' D=0.115 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script

```

>malF

SignalP-4.1 prediction (gram- networks): malF



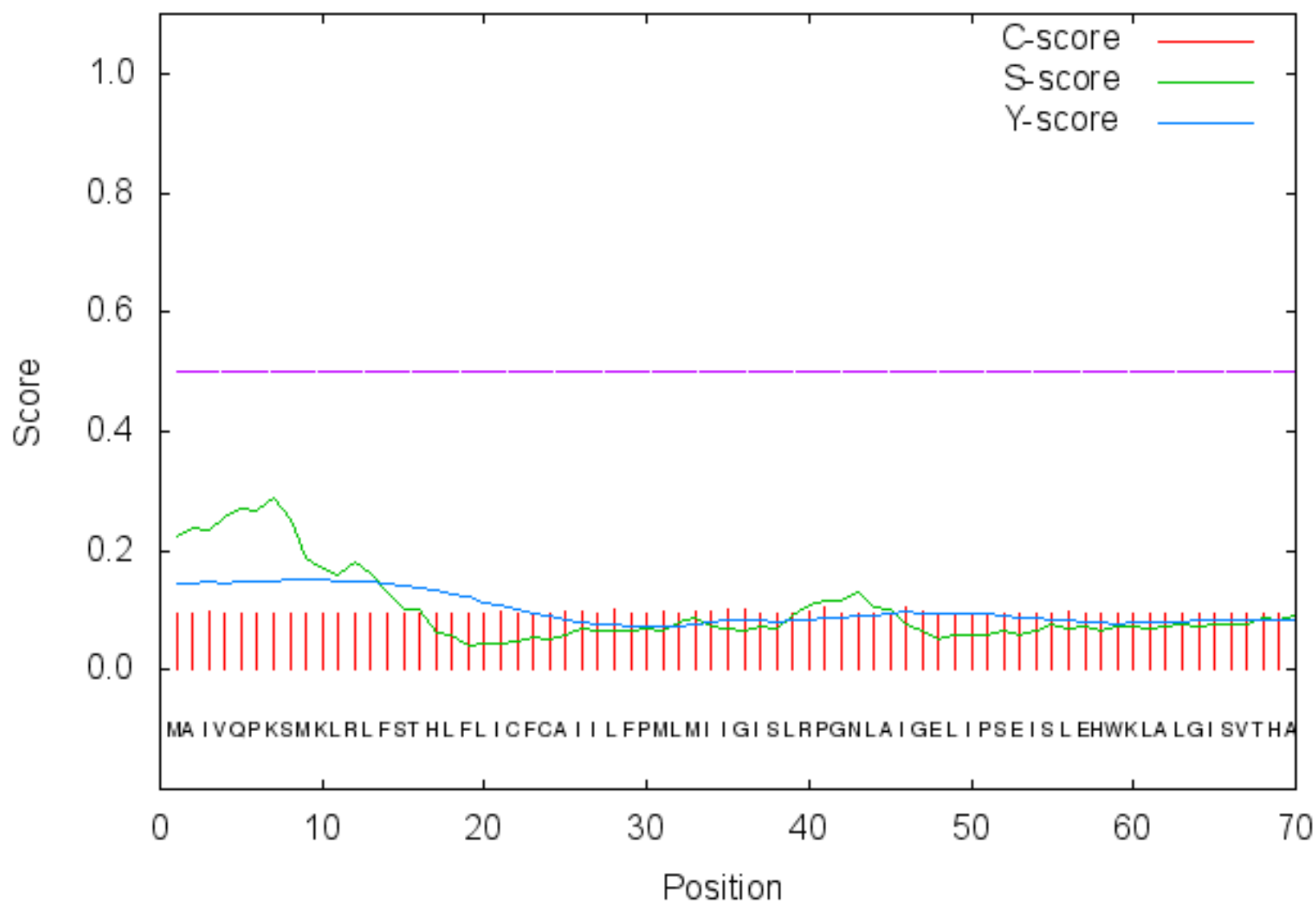
# Measure	Position	Value	Cutoff	signal peptide?
max. C	38	0.115		
max. Y	15	0.134		
max. S	6	0.221		
mean S	1-14	0.167		
D	1-14	0.146	0.510	NO

Name=malF SP='NO' D=0.146 D-cutoff=0.510 Networks=SignalP-TM

[data](#)
[gnuplot script](#)

>malG

SignalP-4.1 prediction (gram- networks): malG



# Measure	Position	Value	Cutoff	signal peptide?
max. C	46	0.106		
max. Y	11	0.150		

```

max. S      7      0.289
mean S     1-10    0.239
D          1-10    0.183  0.510  NO

```

Name=malG SP='NO' D=0.183 D-cutoff=0.510 Networks=SignalP-TM

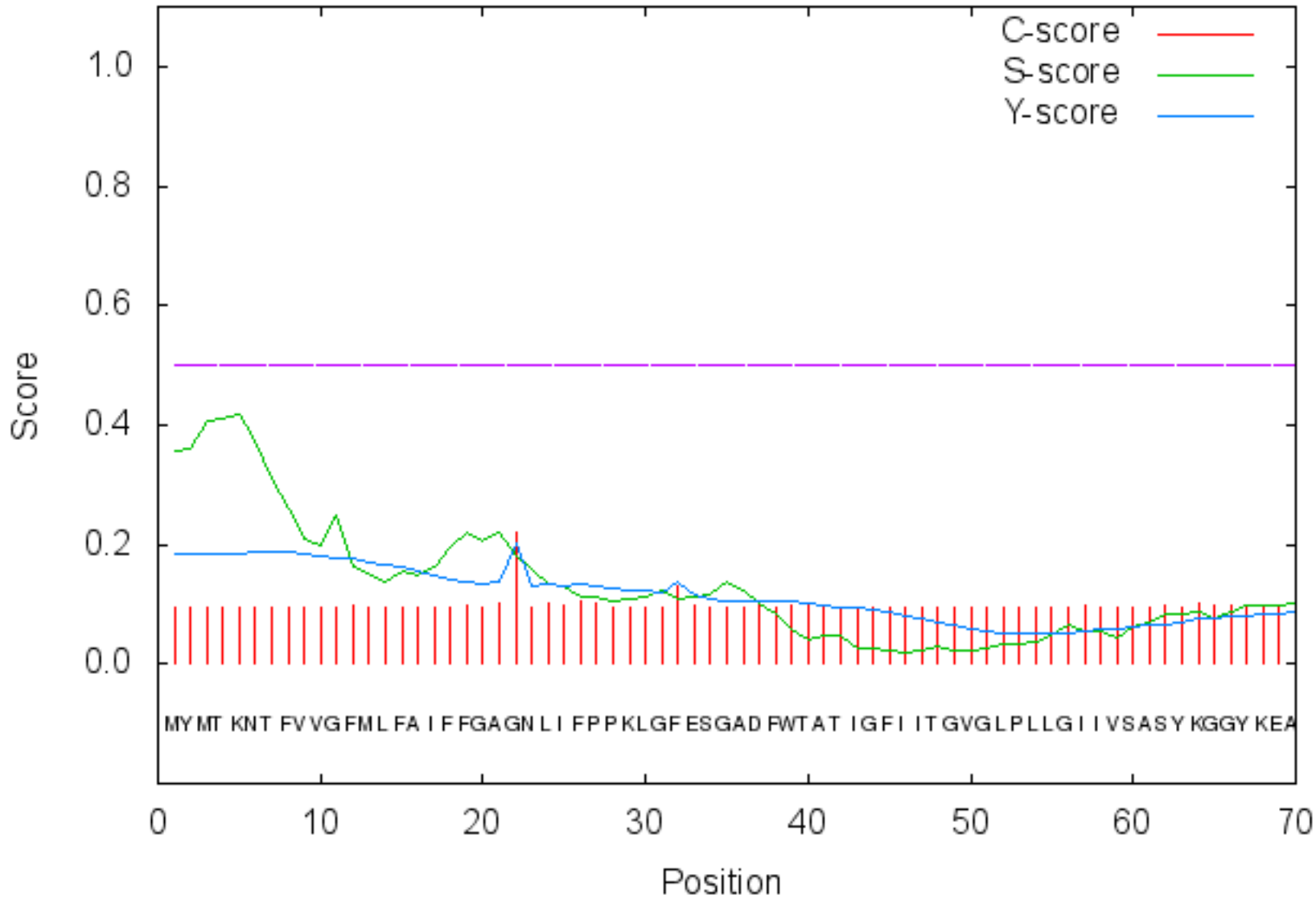
```

# data
# gnuplot script

```

>brnQ

SignalP-4.1 prediction (gram- networks): brnQ



```

# Measure  Position  Value  Cutoff  signal peptide?
max. C     22      0.219
max. Y     22      0.201
max. S      5      0.419
mean S     1-21    0.253
D          1-21    0.220  0.510  NO

```

Name=brnQ SP='NO' D=0.220 D-cutoff=0.510 Networks=SignalP-TM

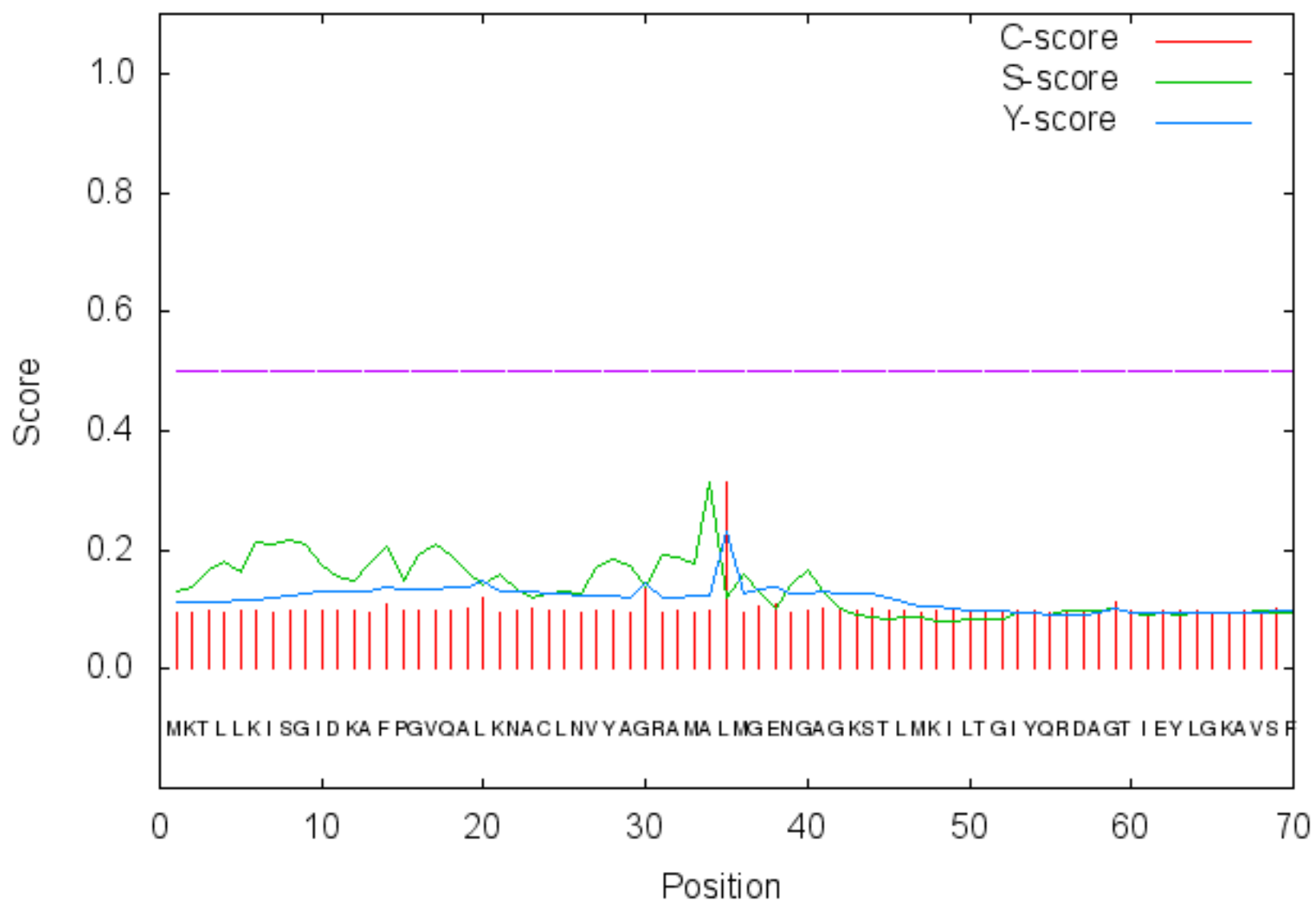
```

# data
# gnuplot script

```

>rbsA

SignalP-4.1 prediction (gram- networks): rbsA



# Measure	Position	Value	Cutoff	signal peptide?
max. C	35	0.312		
max. Y	35	0.230		
max. S	34	0.315		
mean S	1-34	0.173		
D	1-34	0.203	0.570	NO

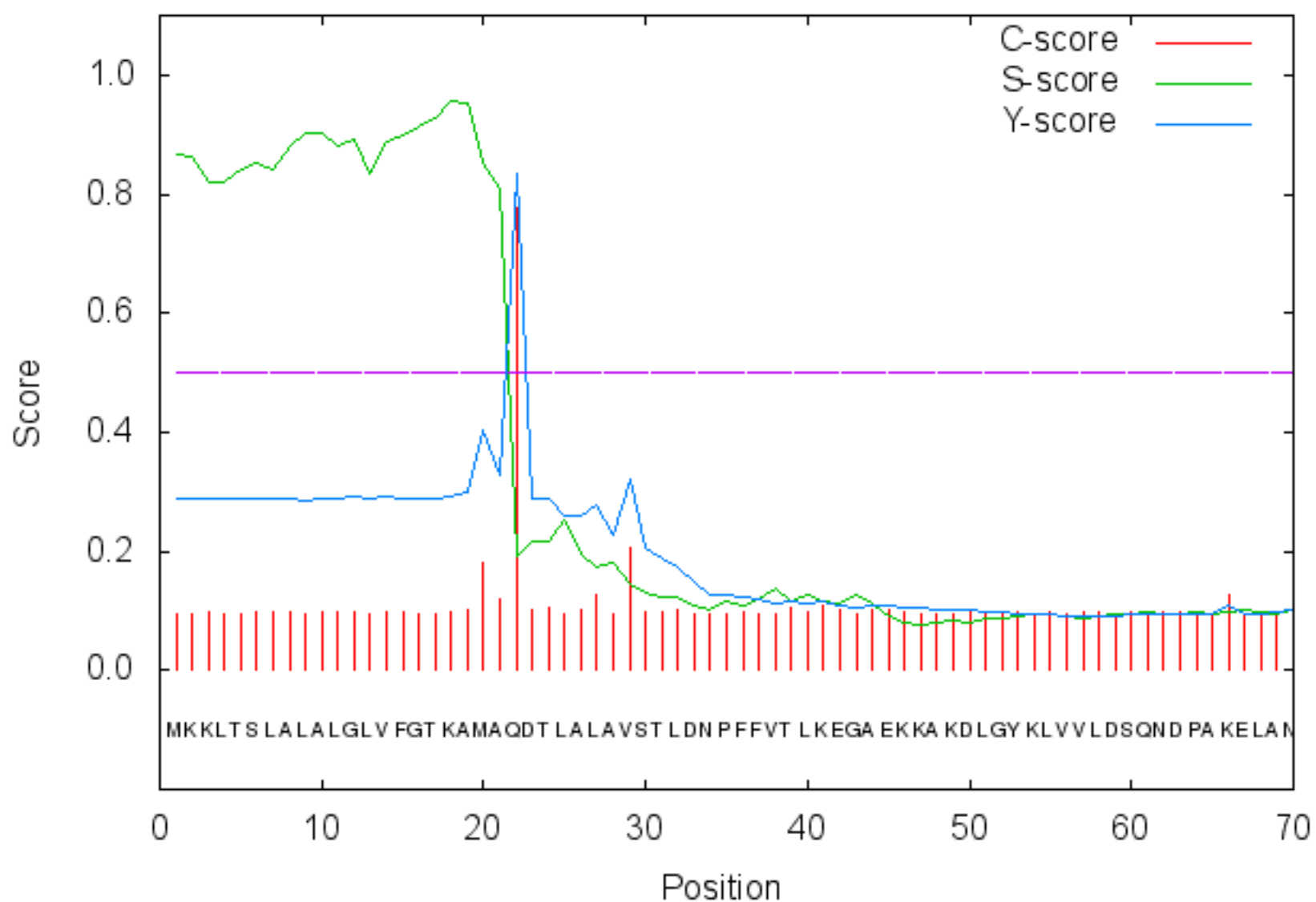
Name=rbsA SP='NO' D=0.203 D-cutoff=0.570 Networks=SignalP-noTM

[data](#)

[gnuplot script](#)

>rbsB

SignalP-4.1 prediction (gram- networks): rbsB



# Measure	Position	Value	Cutoff	signal peptide?
max. C	22	0.777		
max. Y	22	0.833		

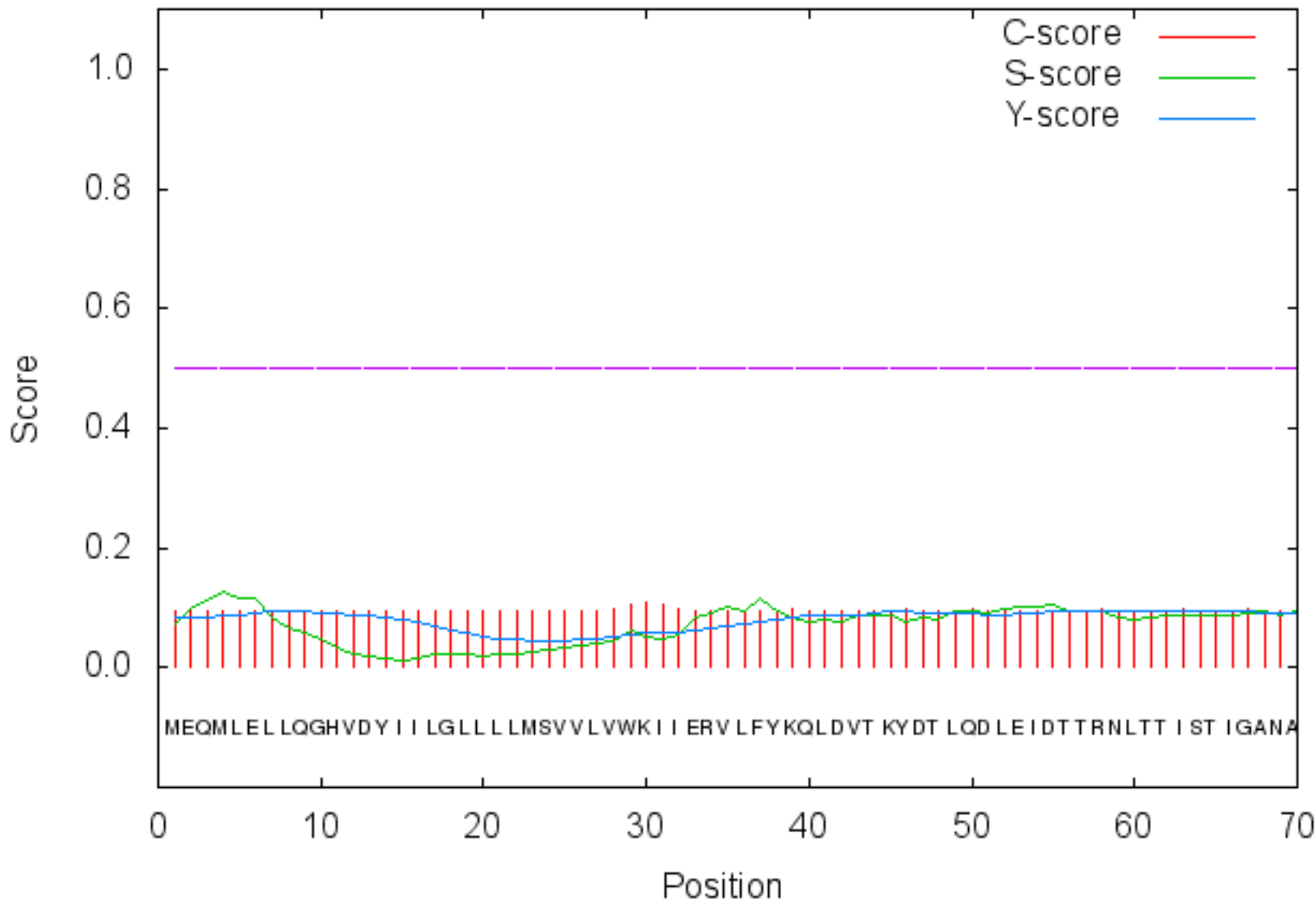

```
max. S 18 0.956
mean S 1-21 0.876
D 1-21 0.853 0.570 YES
```

Name=rbsB SP='YES' Cleavage site between pos. 21 and 22: AMA-QD D=0.853 D-cutoff=0.570 Networks=SignalP-noTM

```
# data
# gnuplot script
```

>exbB

SignalP-4.1 prediction (gram- networks): exbB



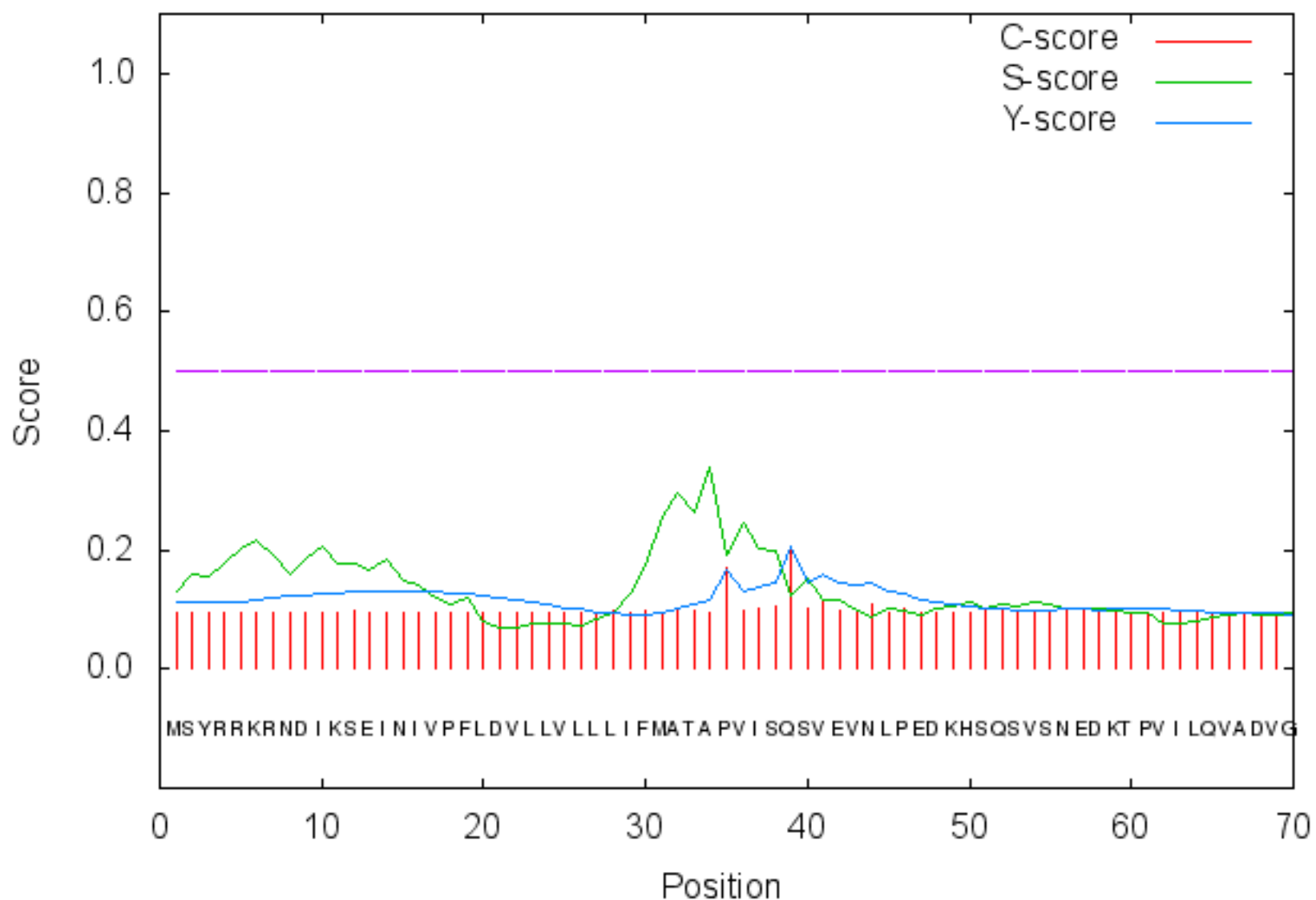
```
# Measure Position Value Cutoff signal peptide?
max. C 30 0.108
max. Y 59 0.095
max. S 4 0.127
mean S 1-58 0.068
D 1-58 0.085 0.510 NO
```

Name=exbB SP='NO' D=0.085 D-cutoff=0.510 Networks=SignalP-TM

```
# data
# gnuplot script
```

>exbD

SignalP-4.1 prediction (gram- networks): exbD



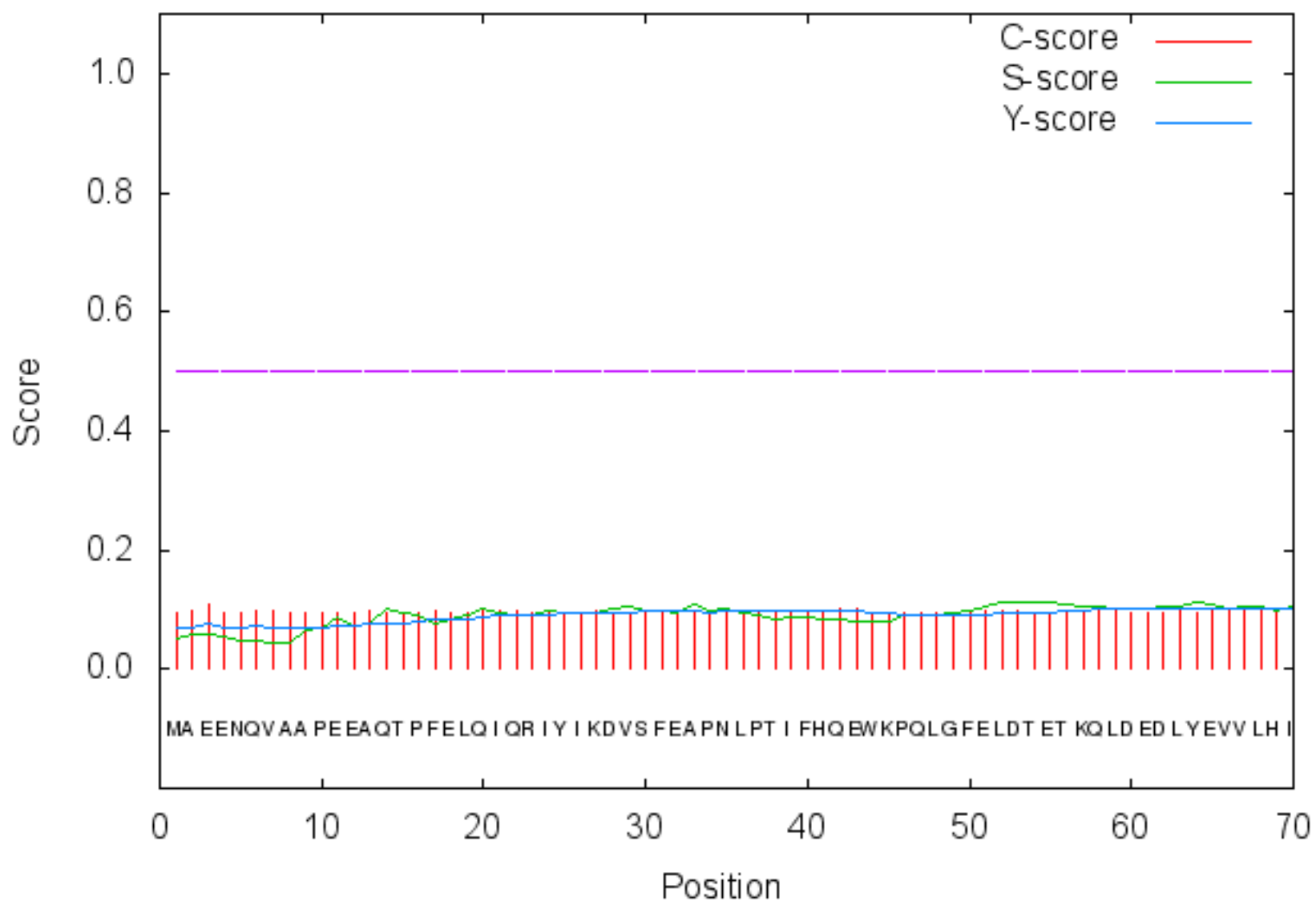
# Measure	Position	Value	Cutoff	signal peptide?
max. C	39	0.205		
max. Y	39	0.205		
max. S	34	0.337		
mean S	1-38	0.161		
D	1-38	0.189	0.510	NO

Name=exbD SP='NO' D=0.189 D-cutoff=0.510 Networks=SignalP-TM

[data](#)
[gnuplot script](#)

>secB

SignalP-4.1 prediction (gram- networks): secB



# Measure	Position	Value	Cutoff	signal peptide?
max. C	3	0.108		
max. Y	65	0.103		

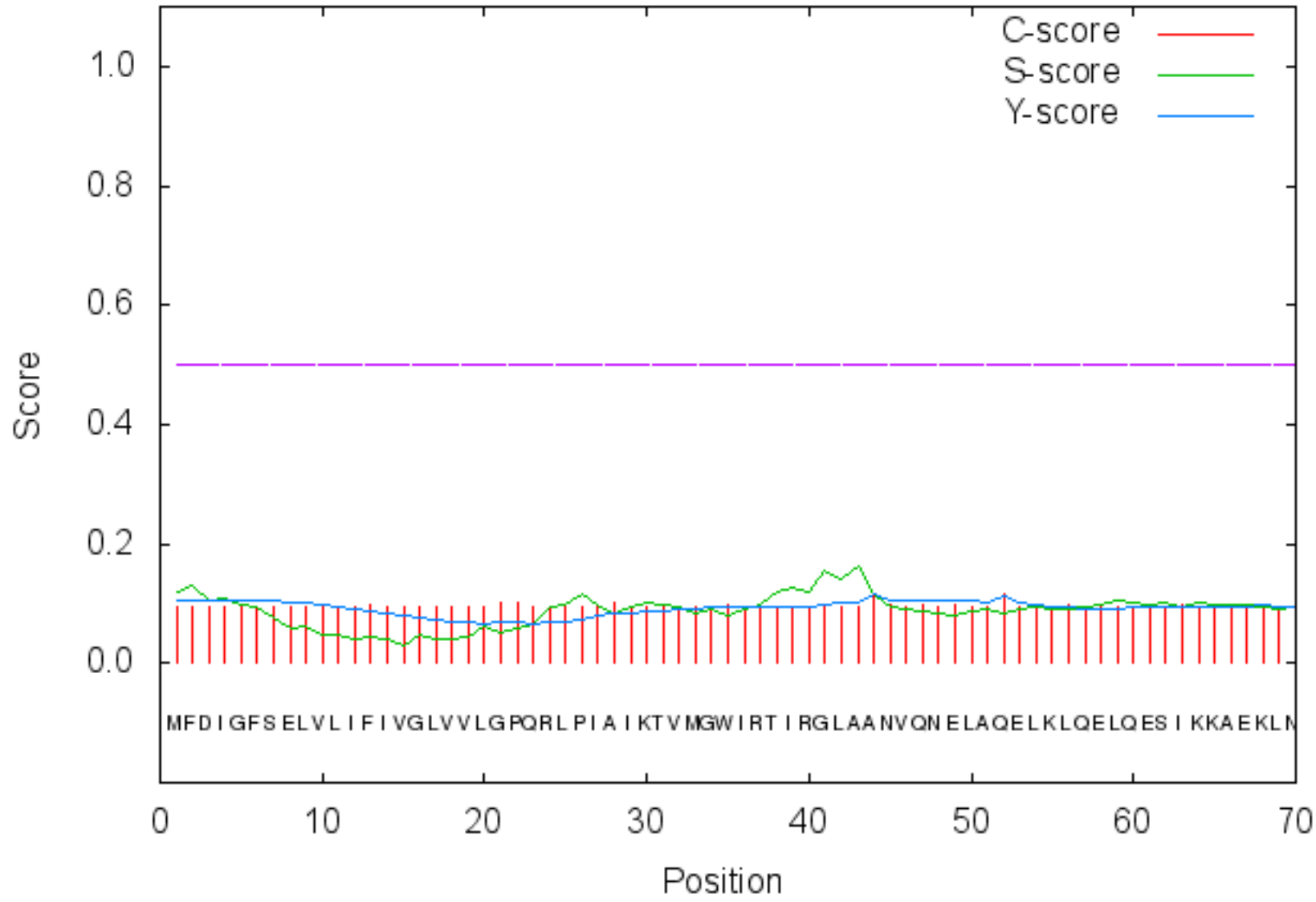
```
max. S 54 0.114
mean S 1-64 0.089
D 1-64 0.096 0.570 NO
```

Name=secB SP='NO' D=0.096 D-cutoff=0.570 Networks=SignalP-noTM

```
# data
# gnuplot script
```

>tatB

SignalP-4.1 prediction (gram- networks): tatB



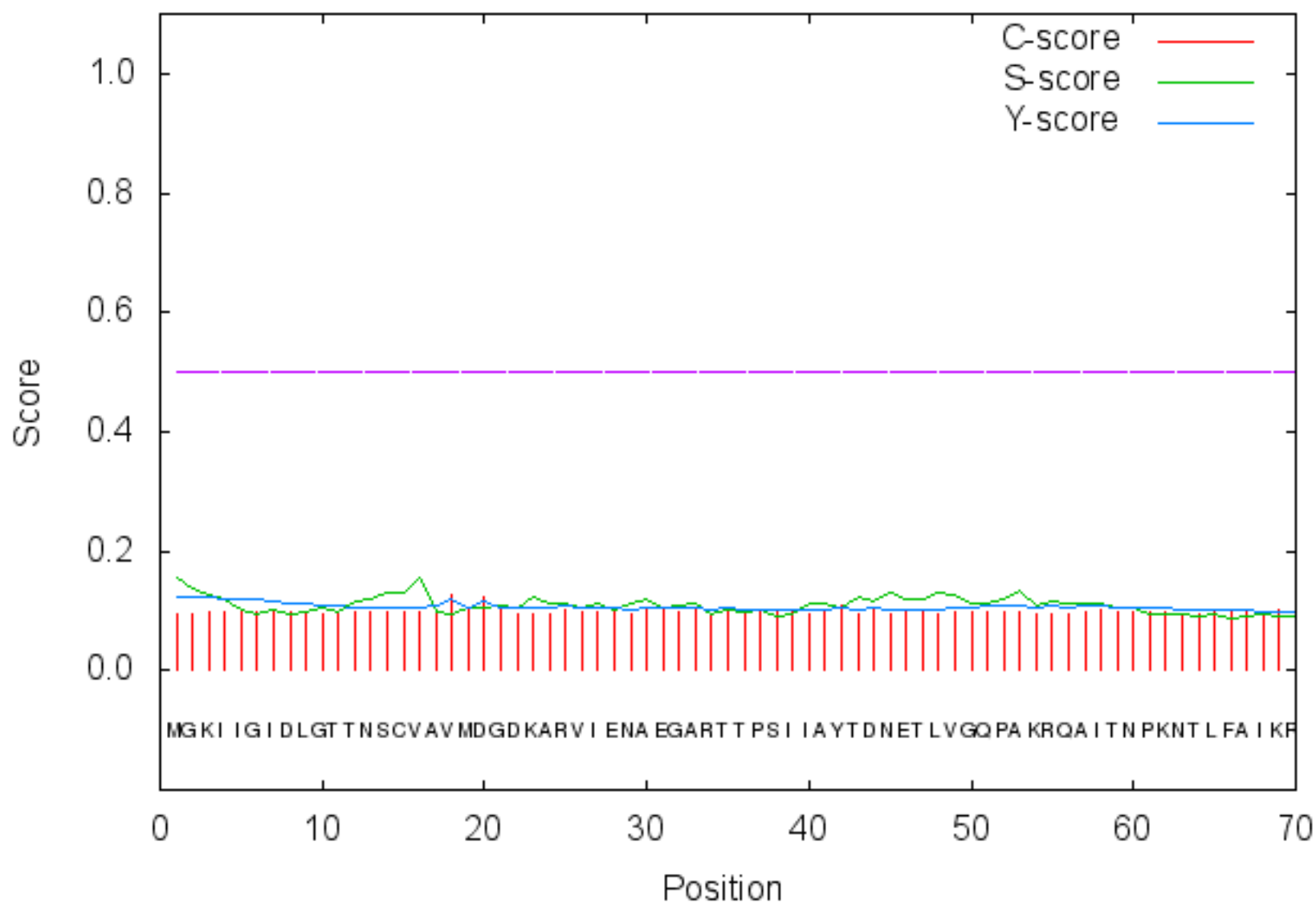
# Measure	Position	Value	Cutoff	signal peptide?
max. C	44	0.117		
max. Y	44	0.116		
max. S	43	0.162		
mean S	1-43	0.085		
D	1-43	0.104	0.510	NO

Name=tatB SP='NO' D=0.104 D-cutoff=0.510 Networks=SignalP-TM

```
# data
# gnuplot script
```

>dnaK

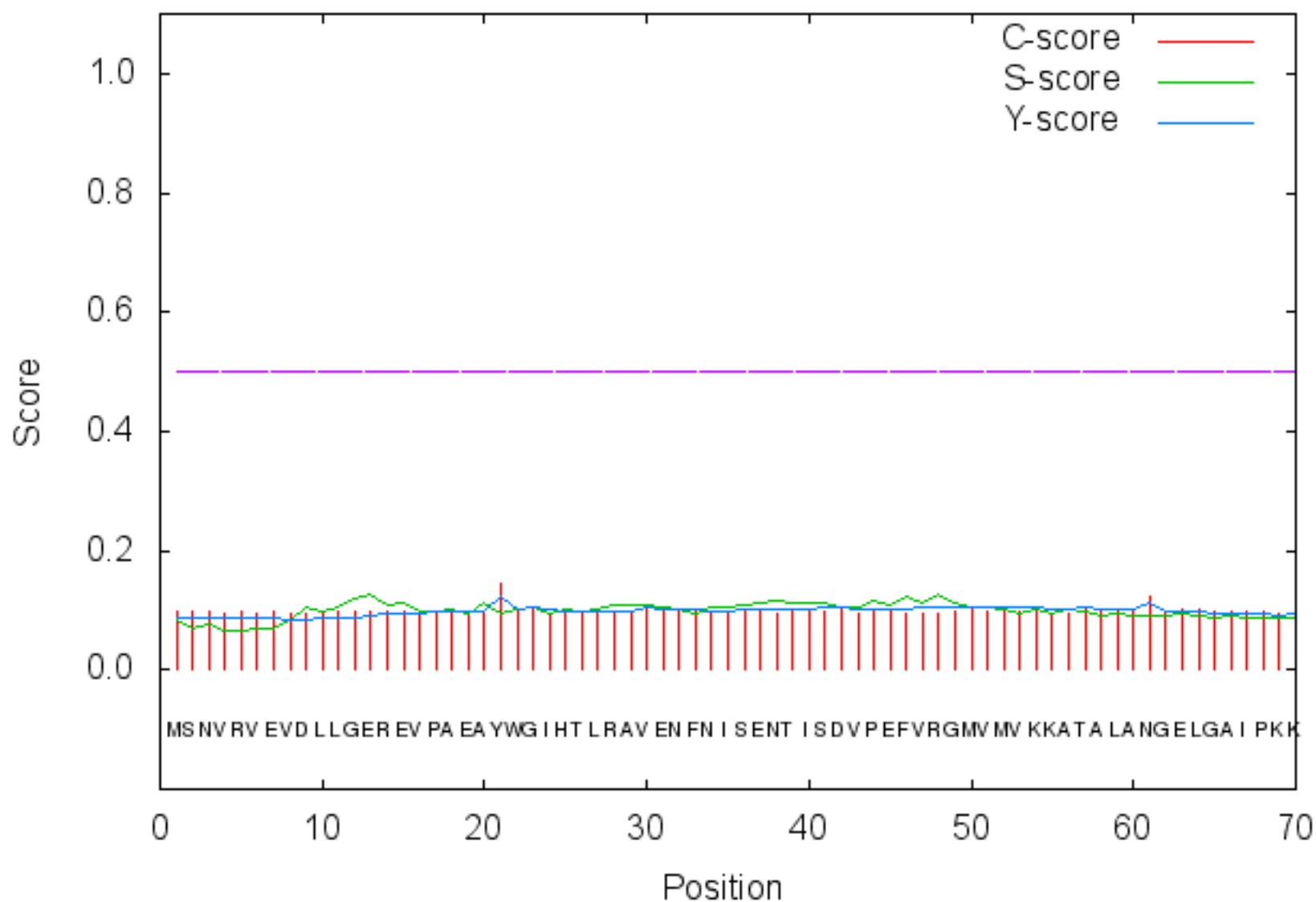
SignalP-4.1 prediction (gram- networks): dnaK



```
# Measure  Position  Value  Cutoff  signal peptide?
max. C     18       0.125
max. Y     18       0.119
max. S     16       0.156
mean S     1-17     0.117
D         1-17     0.118   0.570   NO
Name=dnaK      SP='NO' D=0.118 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script
```

>aspA

SignalP-4.1 prediction (gram- networks): aspA



```
# Measure  Position  Value  Cutoff  signal peptide?
max. C     21       0.144
max. Y     21       0.124
```

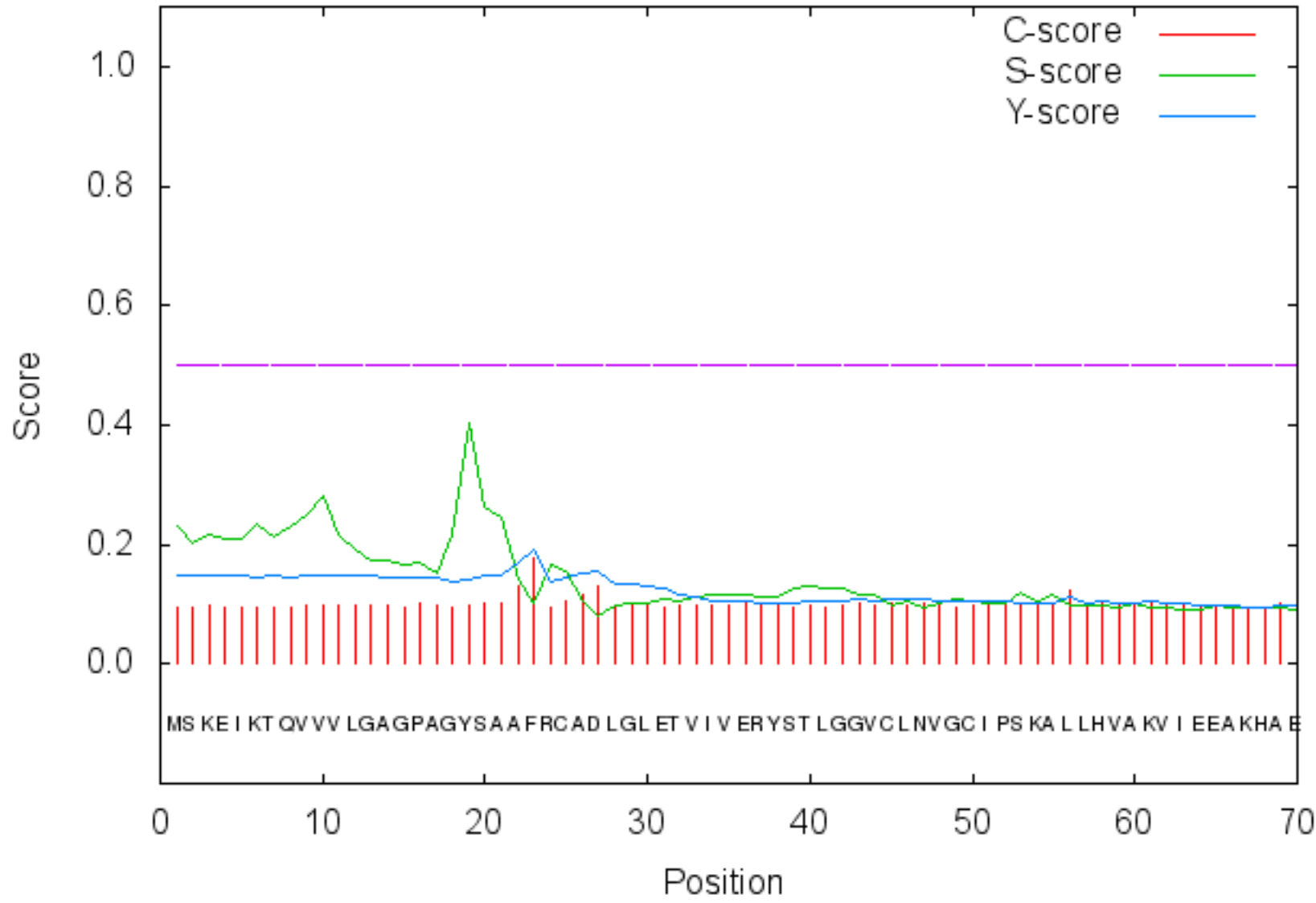
```
max. S 48 0.127
mean S 1-20 0.093
D 1-20 0.109 0.570 NO
```

Name=aspA SP='NO' D=0.109 D-cutoff=0.570 Networks=SignalP-noTM

```
# data
# gnuplot script
```

>lpdA

SignalP-4.1 prediction (gram- networks): lpdA



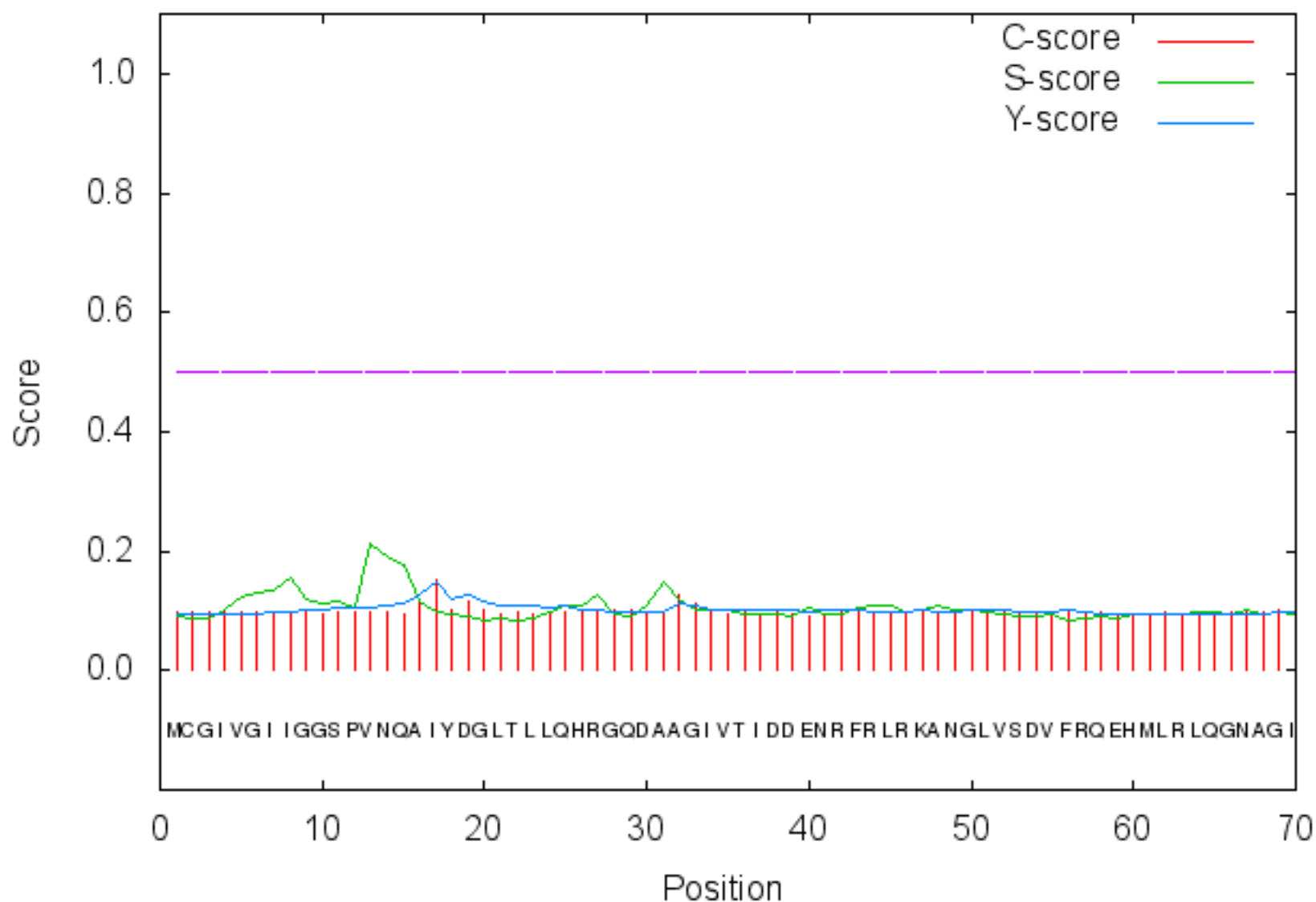
```
# Measure Position Value Cutoff signal peptide?
max. C 23 0.178
max. Y 23 0.193
max. S 19 0.403
mean S 1-22 0.218
D 1-22 0.205 0.570 NO
```

Name=lpdA SP='NO' D=0.205 D-cutoff=0.570 Networks=SignalP-noTM

```
# data
# gnuplot script
```

>purF

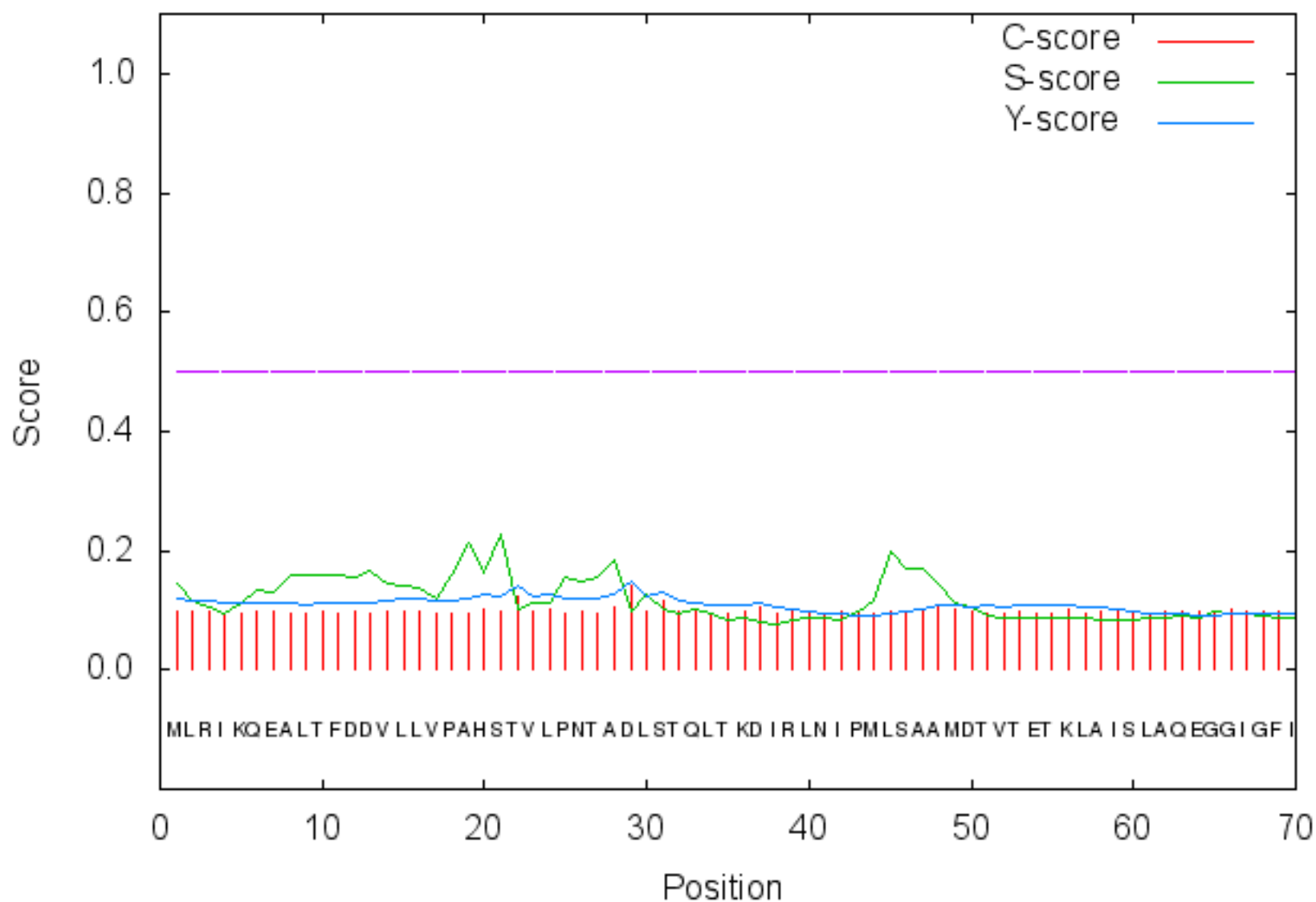
SignalP-4.1 prediction (gram- networks): purF



```
# Measure  Position  Value  Cutoff  signal peptide?
max. C     17         0.153
max. Y     17         0.147
max. S     13         0.213
mean S     1-16       0.129
D          1-16       0.138   0.570   NO
Name=purF  SP='NO' D=0.138 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script
```

>guaB

SignalP-4.1 prediction (gram- networks): guaB



```
# Measure  Position  Value  Cutoff  signal peptide?
max. C     29         0.141
max. Y     29         0.147
```

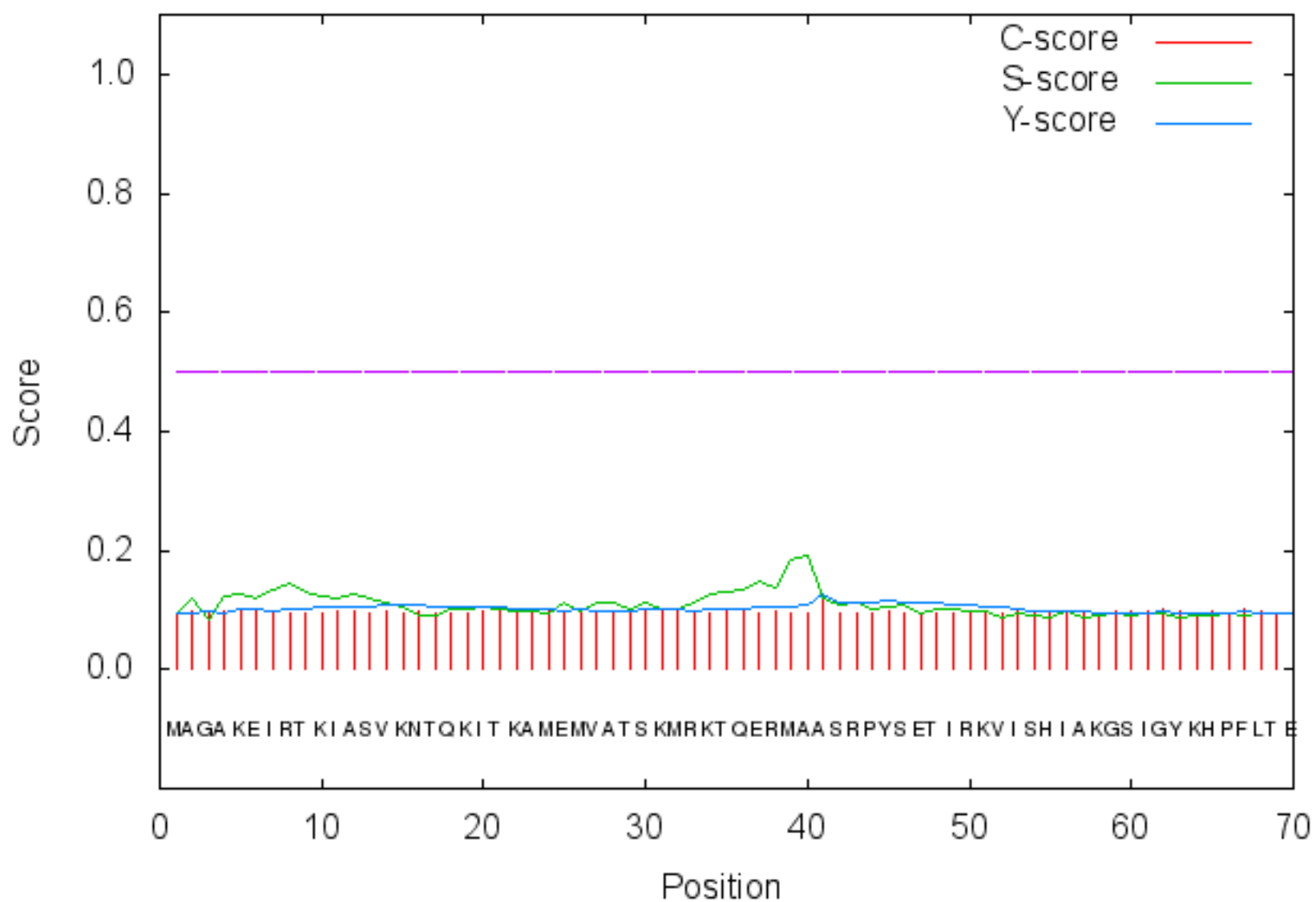
```

max. S    21    0.228
mean S    1-28   0.145
D         1-28   0.146   0.570   NO
Name=guaB      SP='NO' D=0.146 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script

```

>atpG

SignalP-4.1 prediction (gram- networks): atpG



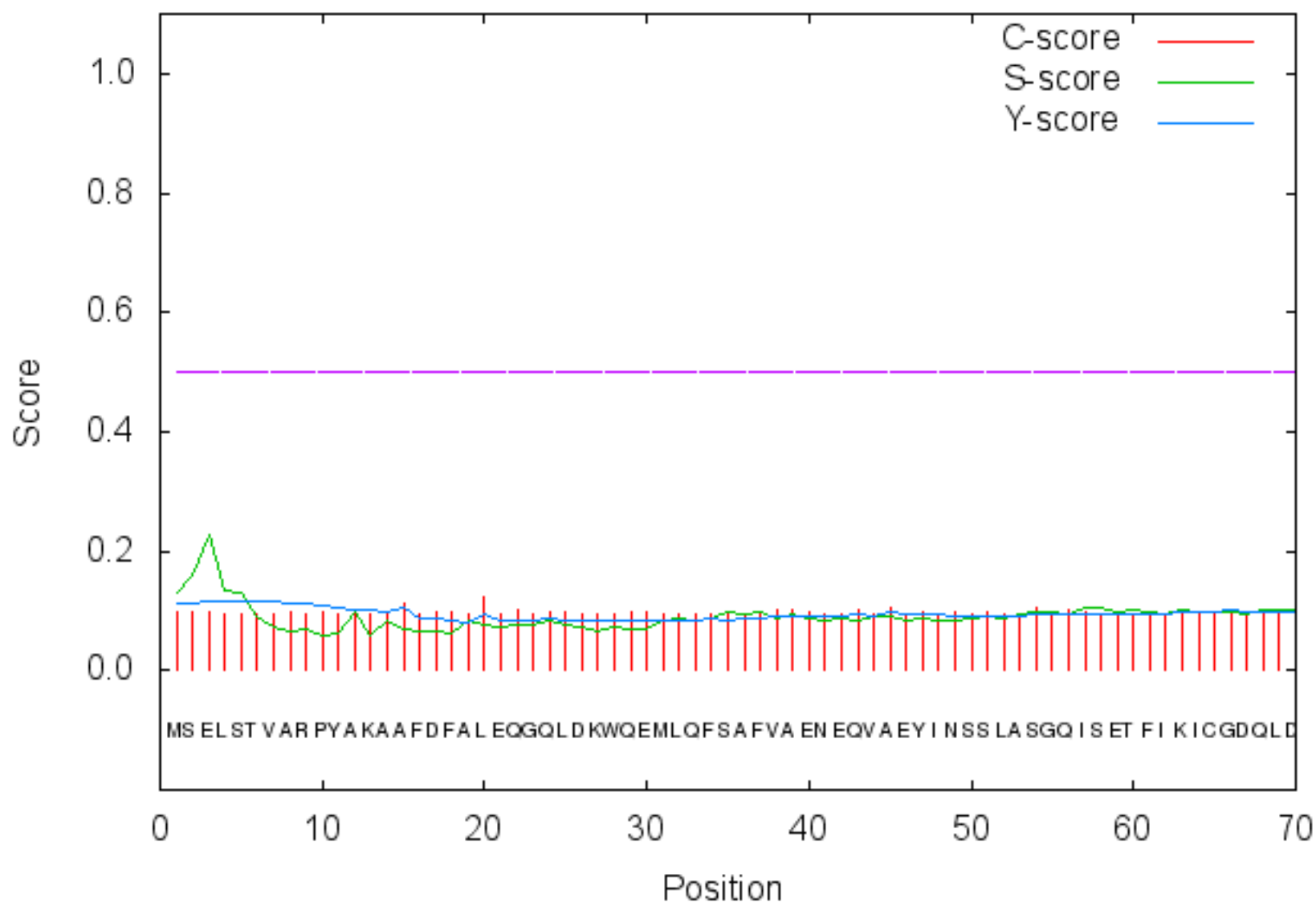
```

# Measure  Position  Value    Cutoff  signal peptide?
max. C     41         0.124
max. Y     41         0.128
max. S     40         0.191
mean S     1-40       0.117
D         1-40       0.123   0.570   NO
Name=atpG      SP='NO' D=0.123 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script

```

>atpH

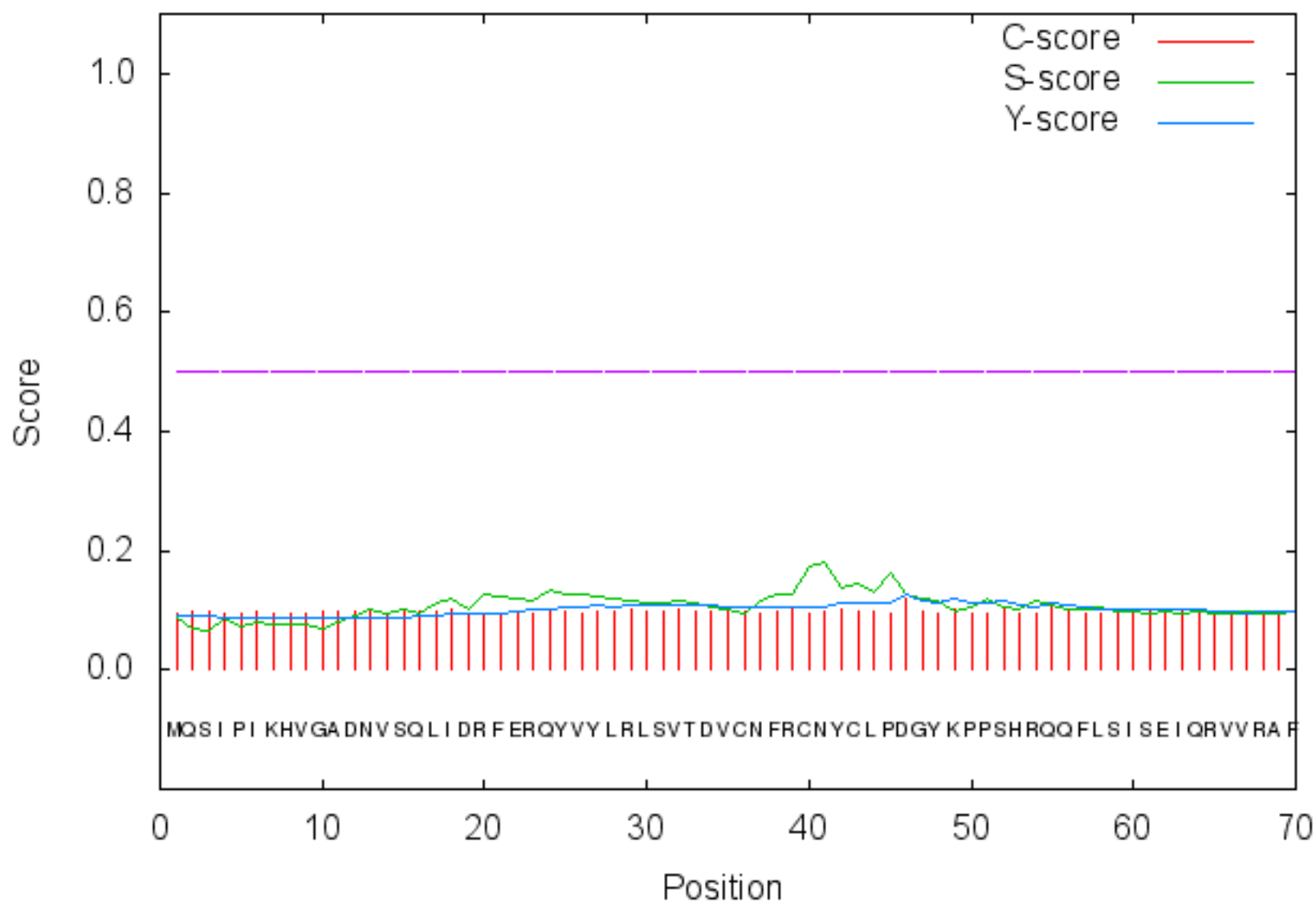
SignalP-4.1 prediction (gram- networks): atpH



```
# Measure  Position  Value  Cutoff  signal peptide?
max. C     20         0.123
max. Y     11         0.106
max. S      3         0.228
mean S     1-10       0.115
D          1-10       0.110  0.570  NO
Name=atpH      SP='NO' D=0.110 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script
```

>moaA

SignalP-4.1 prediction (gram- networks): moaA



```
# Measure  Position  Value  Cutoff  signal peptide?
max. C     46         0.119
max. Y     46         0.126
```



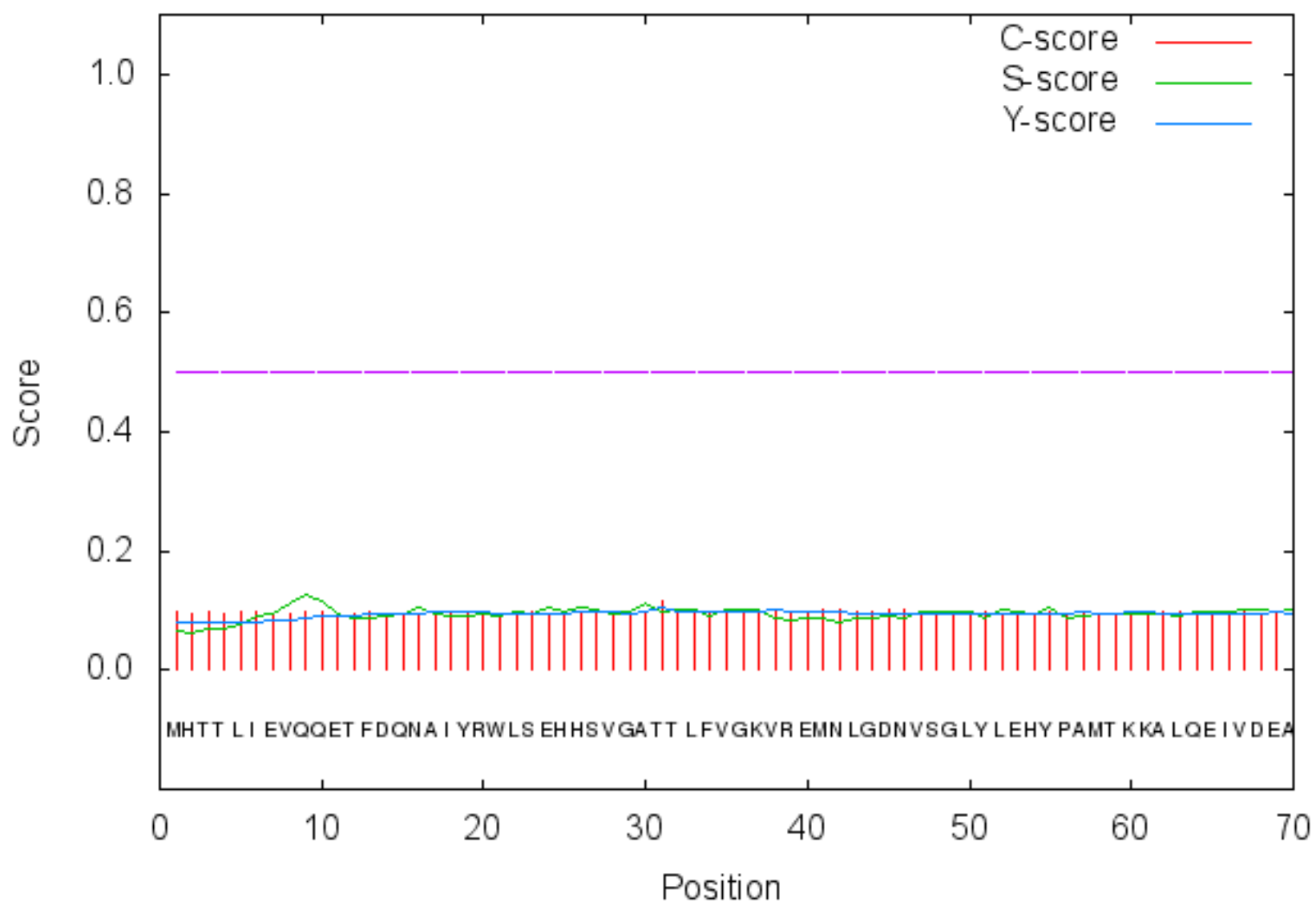
```

max. S    41    0.182
mean S    1-45   0.110
D         1-45   0.118   0.570   NO
Name=moaA      SP='NO' D=0.118 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script

```

>moaE

SignalP-4.1 prediction (gram- networks): moaE



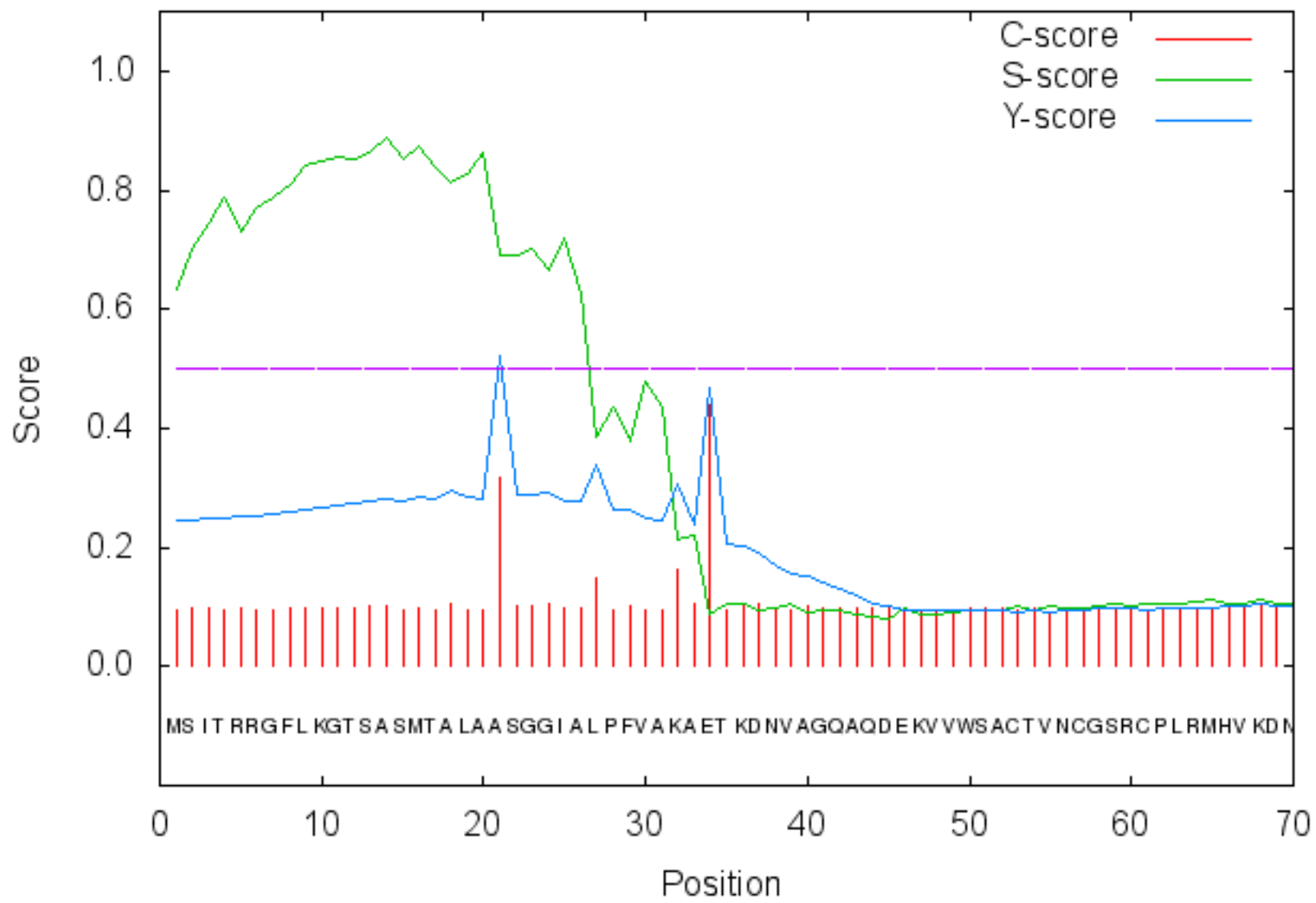
```

# Measure  Position  Value    Cutoff  signal peptide?
max. C     31         0.117
max. Y     31         0.107
max. S     9          0.127
mean S     1-30       0.094
D         1-30       0.101   0.570   NO
Name=moaE      SP='NO' D=0.101 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script

```

>dmsA

SignalP-4.1 prediction (gram- networks): dmsA



# Measure	Position	Value	Cutoff	signal peptide?
max. C	34	0.441		
max. Y	21	0.521		
max. S	14	0.887		
mean S	1-20	0.809		
D	1-20	0.656	0.570	YES

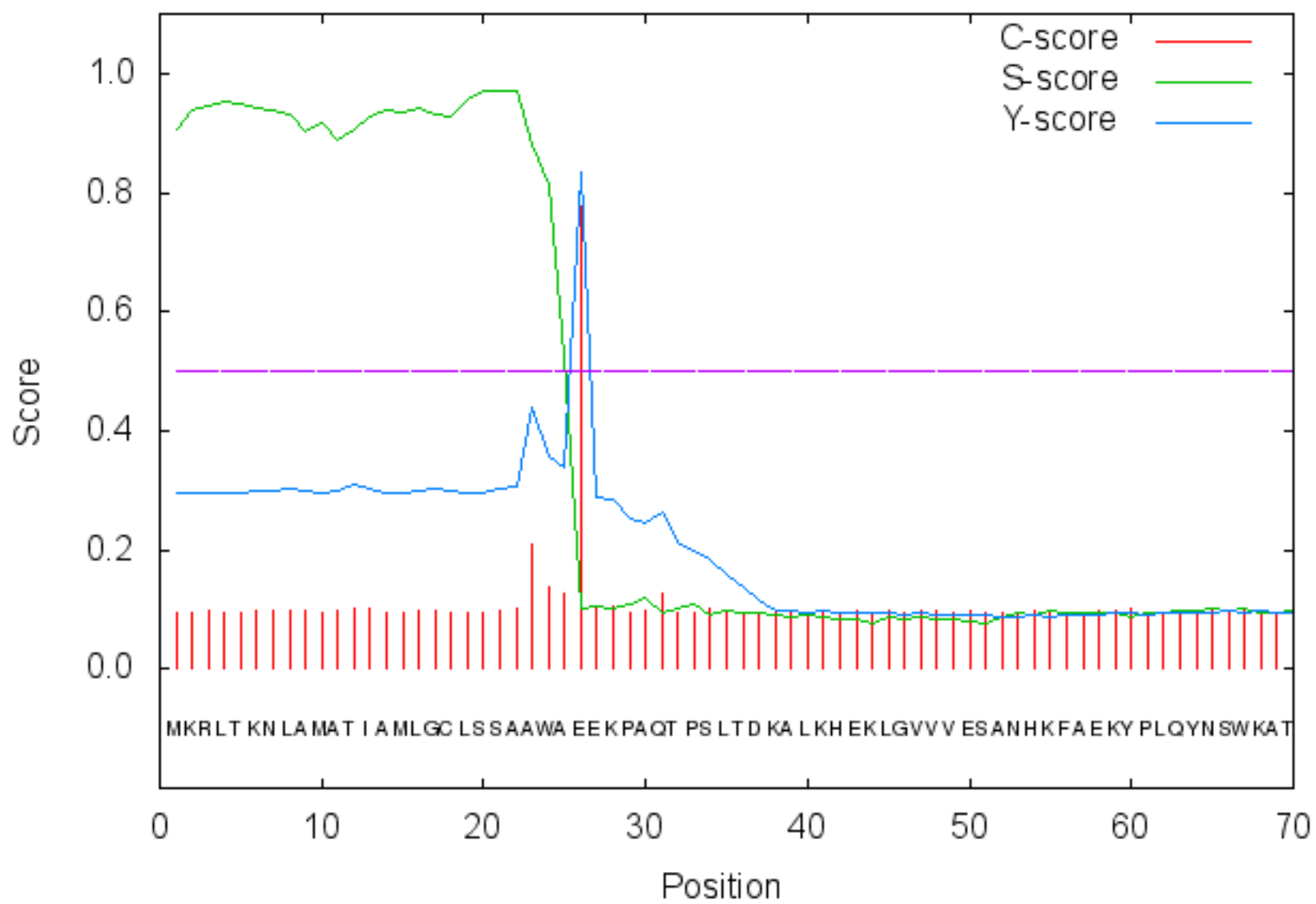
Name=dmsA SP='YES' Cleavage site between pos. 20 and 21: ALA-AS D=0.656 D-cutoff=0.570 Networks=SignalP-noTM

[data](#)

[gnuplot script](#)

>nrfA

SignalP-4.1 prediction (gram- networks): nrfA



# Measure	Position	Value	Cutoff	signal peptide?
max. C	26	0.777		
max. Y	26	0.835		

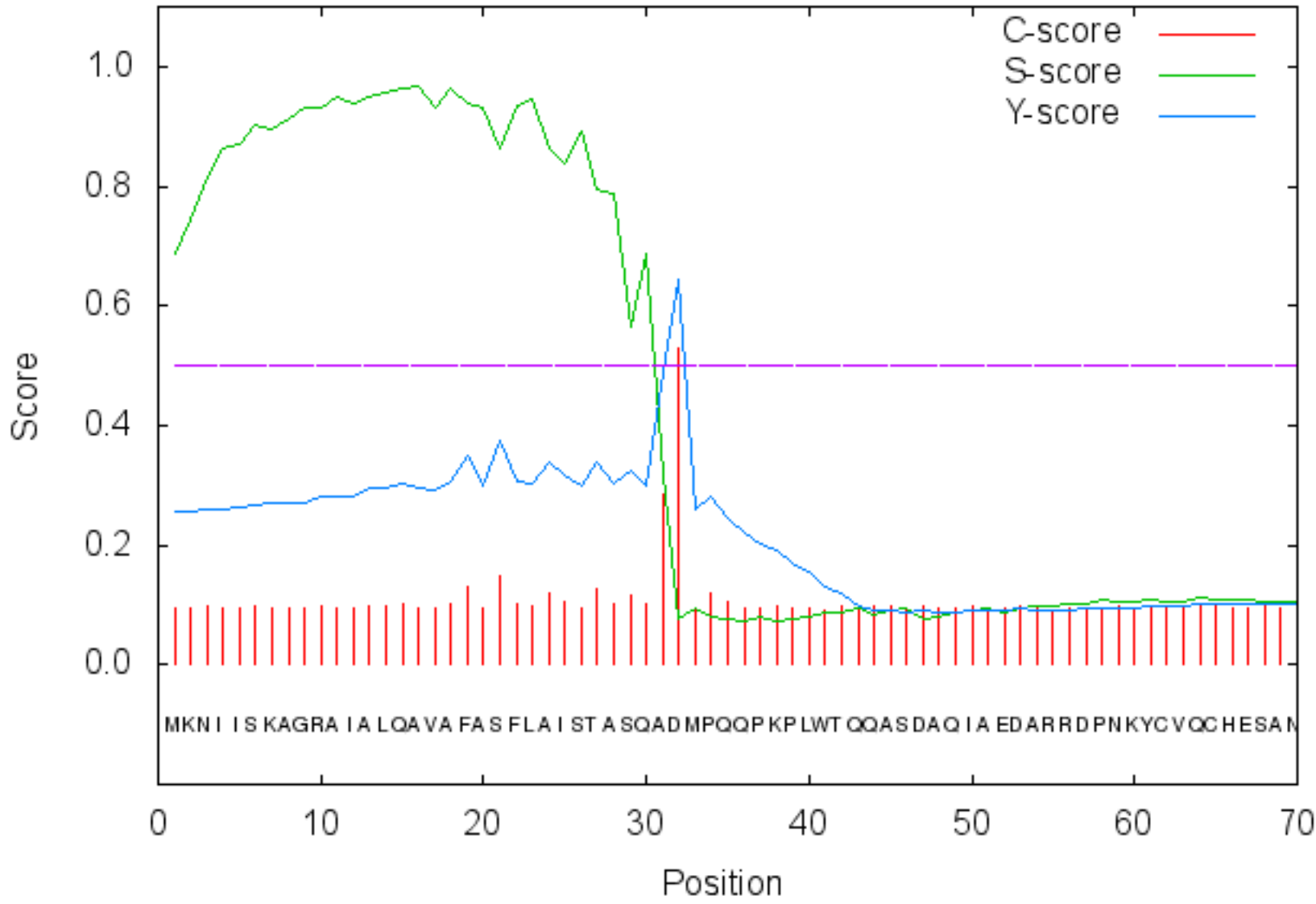
max. S 21 0.972
mean S 1-25 0.912
D 1-25 0.871 0.570 YES

Name=nrfA SP='YES' Cleavage site between pos. 25 and 26: AWA-EE D=0.871 D-cutoff=0.570 Networks=SignalP-noTM

[data](#)
[gnuplot script](#)

>nrfB

SignalP-4.1 prediction (gram- networks): nrfB



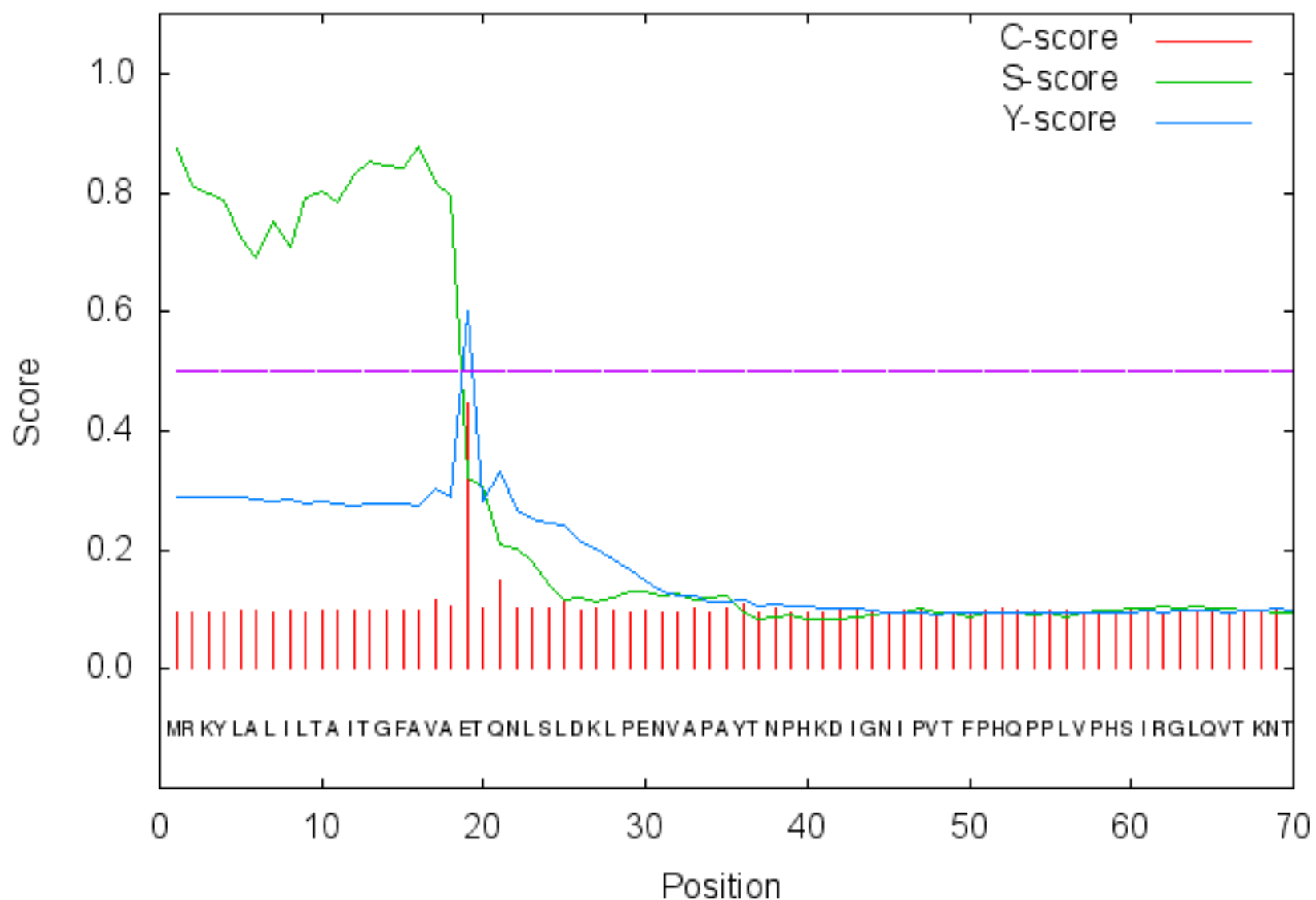
# Measure	Position	Value	Cutoff	signal peptide?
max. C	32	0.528		
max. Y	32	0.644		
max. S	16	0.968		
mean S	1-31	0.856		
D	1-31	0.744	0.570	YES

Name=nrfB SP='YES' Cleavage site between pos. 31 and 32: SQA-DM D=0.744 D-cutoff=0.570 Networks=SignalP-noTM

[data](#)
[gnuplot script](#)

>napB

SignalP-4.1 prediction (gram- networks): napB



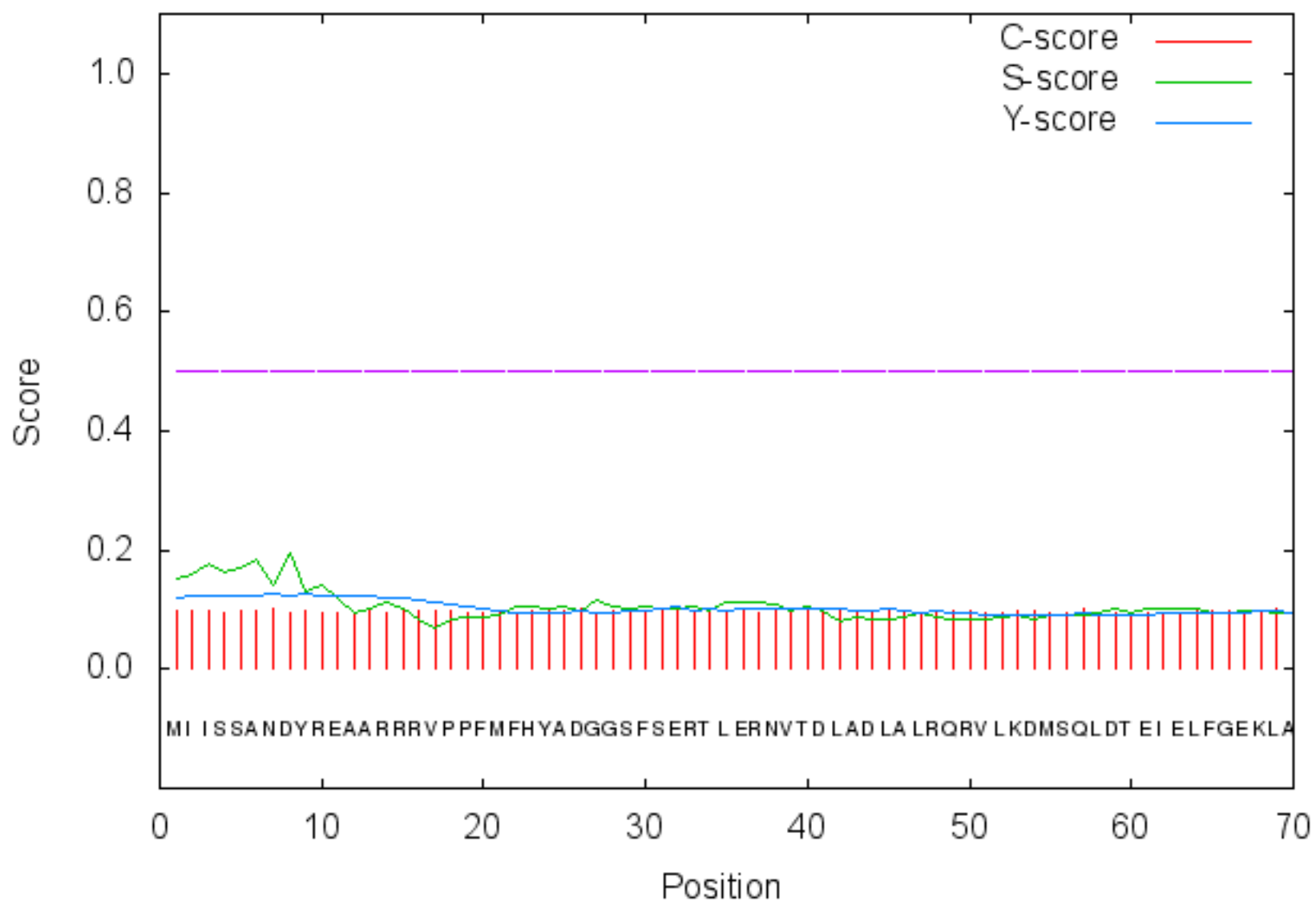
# Measure	Position	Value	Cutoff	signal peptide?
max. C	19	0.447		
max. Y	19	0.601		
max. S	16	0.878		
mean S	1-18	0.798		
D	1-18	0.694	0.570	YES

Name=napB SP='YES' Cleavage site between pos. 18 and 19: AVA-ET D=0.694 D-cutoff=0.570 Networks=SignalP-noTM

[data](#)
[gnuplot script](#)

>11dd

SignalP-4.1 prediction (gram- networks): IldD



# Measure	Position	Value	Cutoff	signal peptide?
max. C	32	0.106		
max. Y	11	0.123		

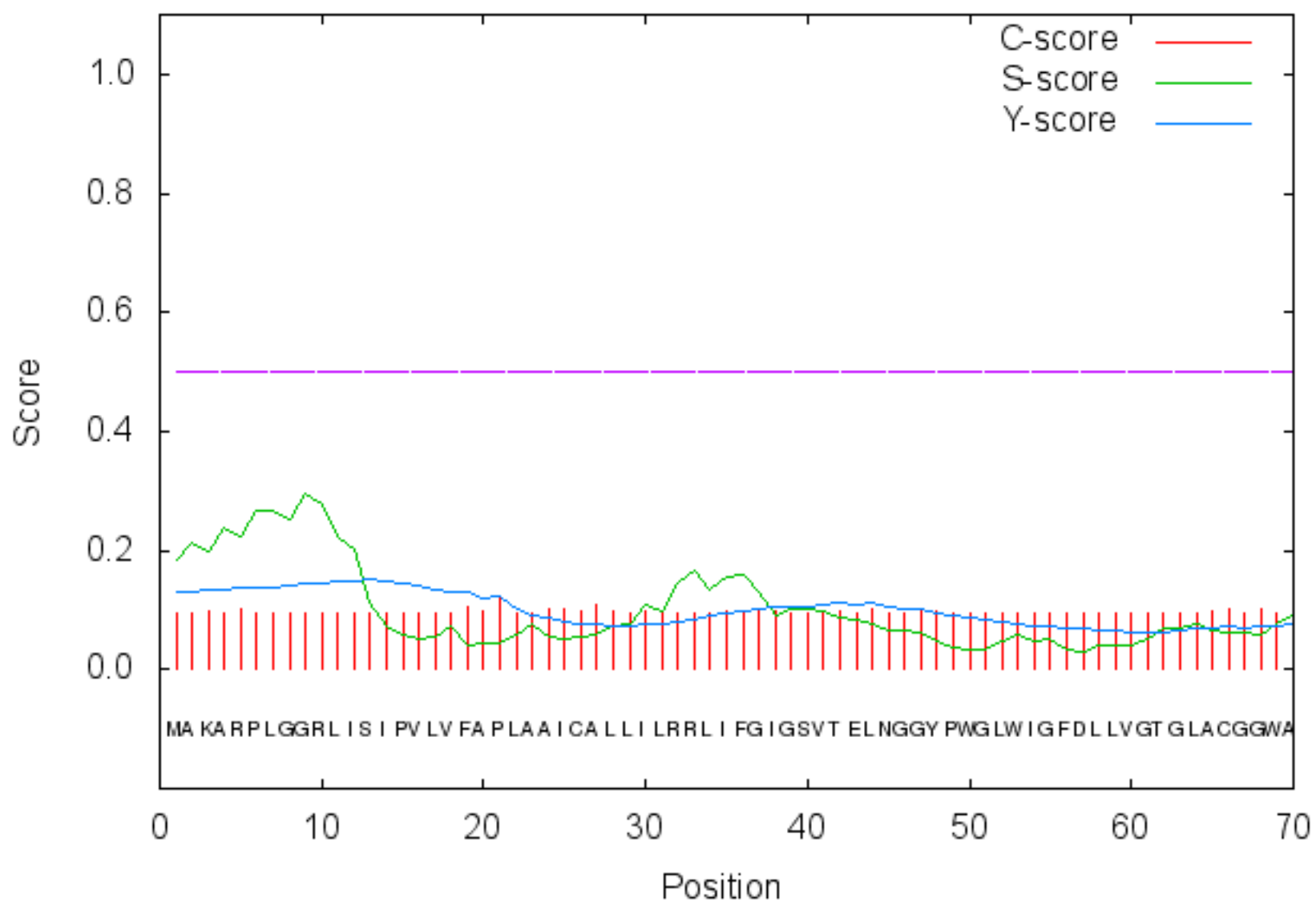
```

max. S      8      0.196
mean S     1-10    0.161
D          1-10    0.141  0.570  NO
Name=lldD   SP='NO' D=0.141 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script

```

>hybB

SignalP-4.1 prediction (gram- networks): hybB



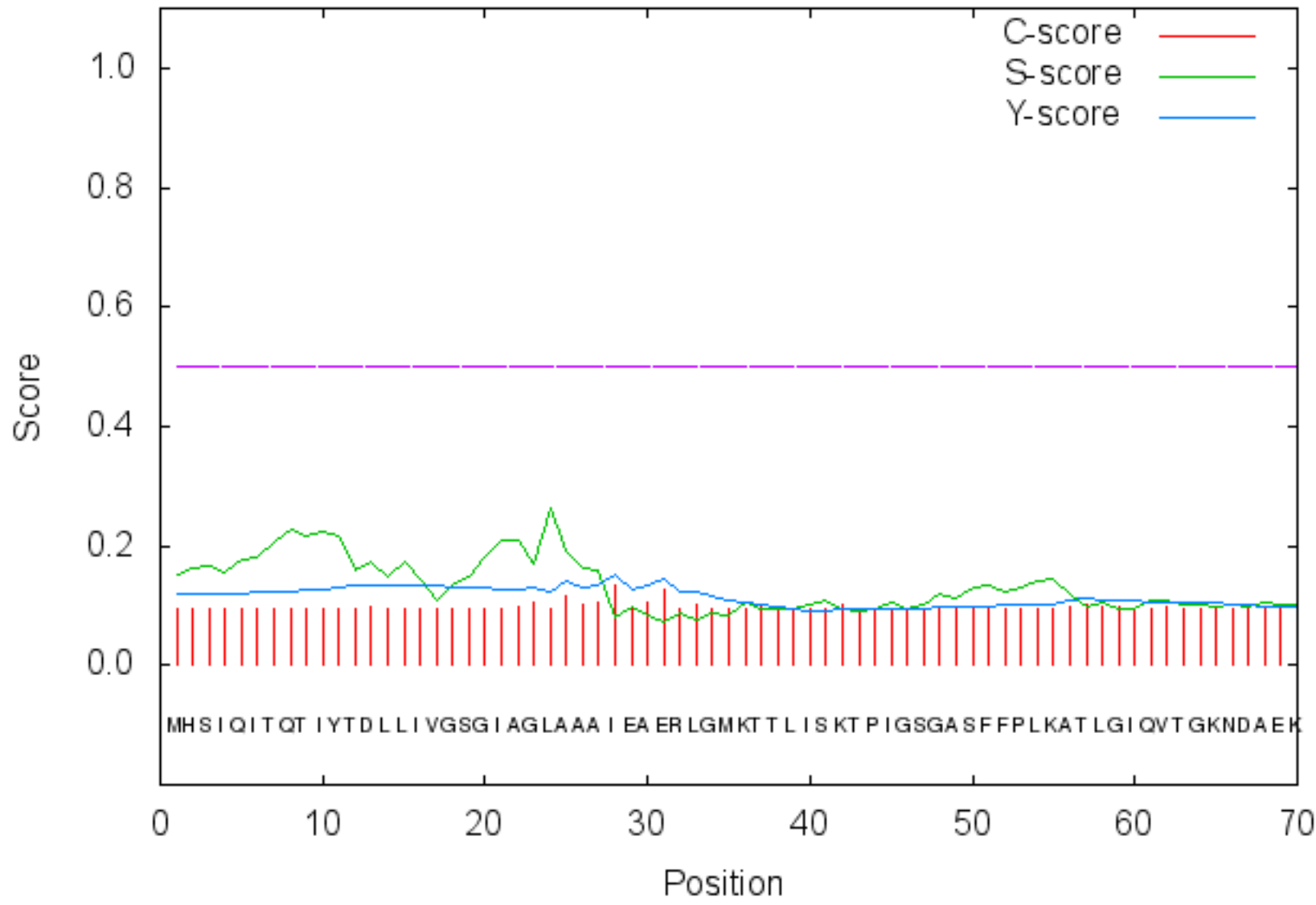
```

# Measure  Position  Value  Cutoff  signal peptide?
max. C     21         0.121  0.510  NO
max. Y     13         0.151  0.510  NO
max. S     9          0.296  0.510  NO
mean S    1-12        0.237  0.510  NO
D         1-12        0.183  0.510  NO
Name=hybB  SP='NO' D=0.183 D-cutoff=0.510 Networks=SignalP-TM
# data
# gnuplot script

```

>frdA

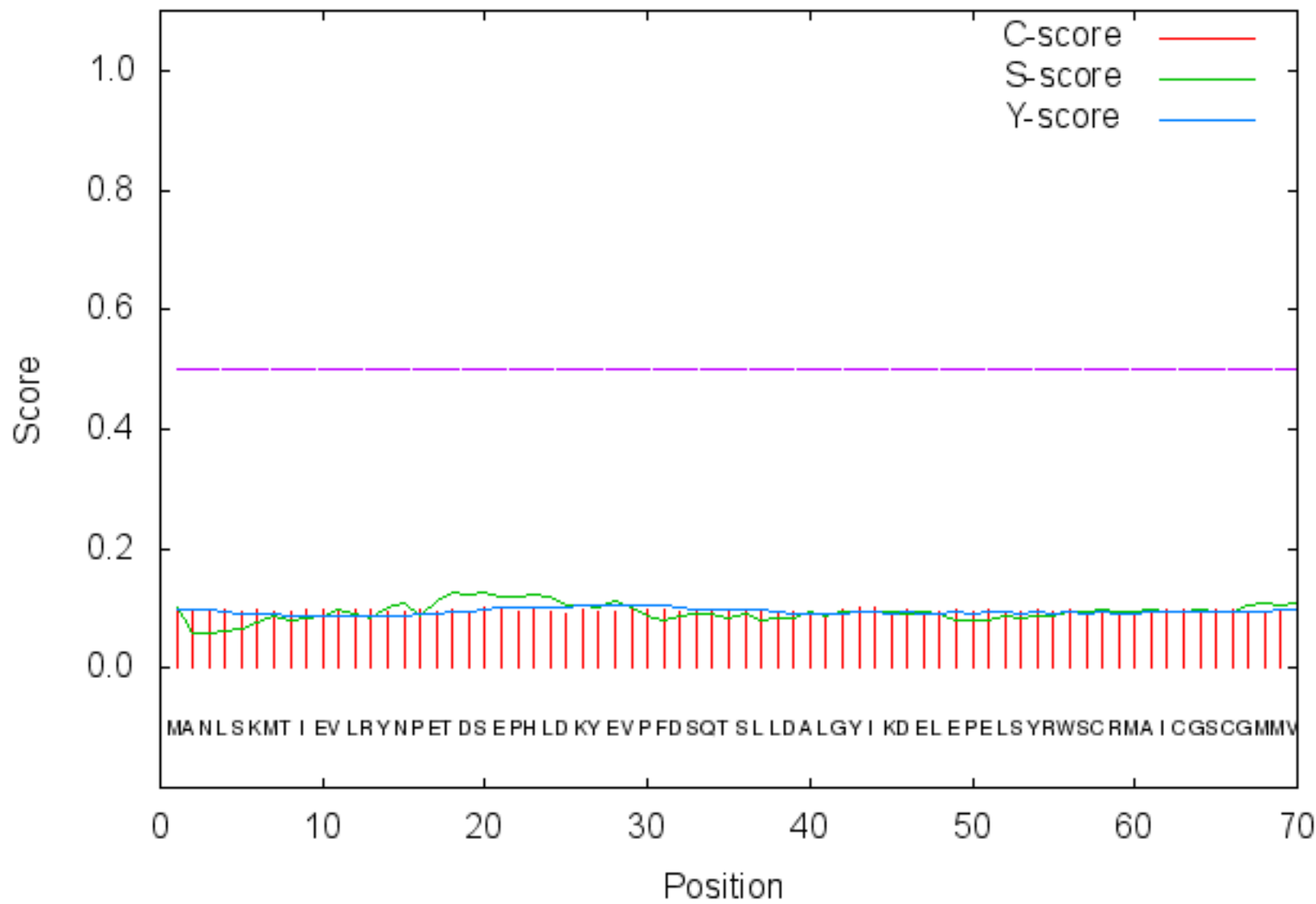
SignalP-4.1 prediction (gram- networks): frdA



```
# Measure  Position  Value  Cutoff  signal peptide?
max. C     28       0.133
max. Y     28       0.152
max. S     24       0.265
mean S     1-27     0.178
D         1-27     0.162  0.510  NO
Name=frdA      SP='NO' D=0.162 D-cutoff=0.510 Networks=SignalP-TM
# data
# gnuplot script
```

>frdB

SignalP-4.1 prediction (gram- networks): frdB



```
# Measure  Position  Value  Cutoff  signal peptide?
max. C     43       0.101
max. Y     29       0.106
```

```

max. S    20    0.126
mean S    1-28   0.097
D         1-28   0.102   0.570   NO

```

Name=frdB SP='NO' D=0.102 D-cutoff=0.570 Networks=SignalP-noTM

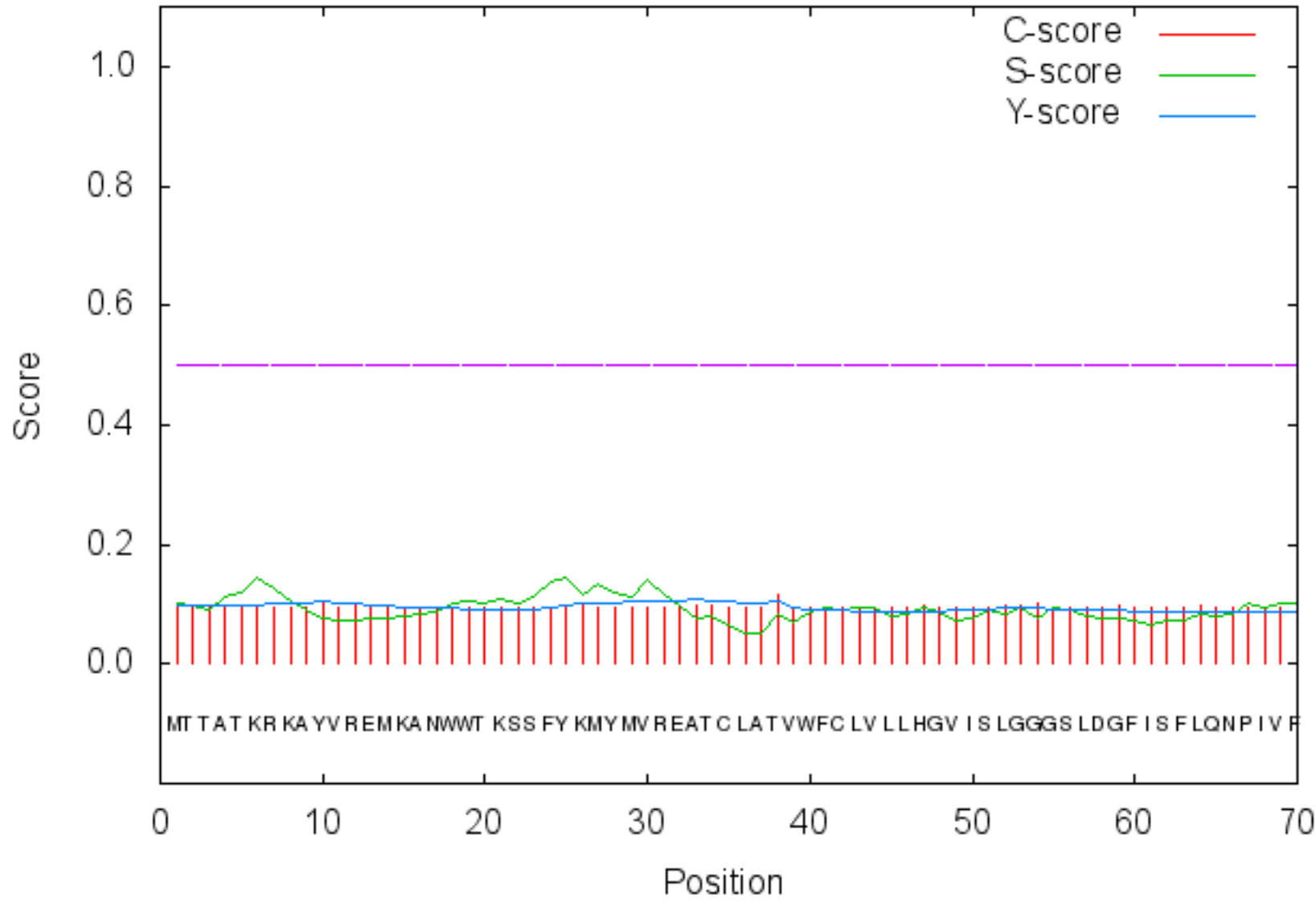
```

# data
# gnuplot script

```

>frdC

SignalP-4.1 prediction (gram- networks): frdC



```

# Measure  Position  Value  Cutoff  signal peptide?
max. C     38         0.117
max. Y     33         0.108
max. S     25         0.146
mean S     1-32       0.105
D         1-32       0.107   0.510   NO

```

Name=frdC SP='NO' D=0.107 D-cutoff=0.510 Networks=SignalP-TM

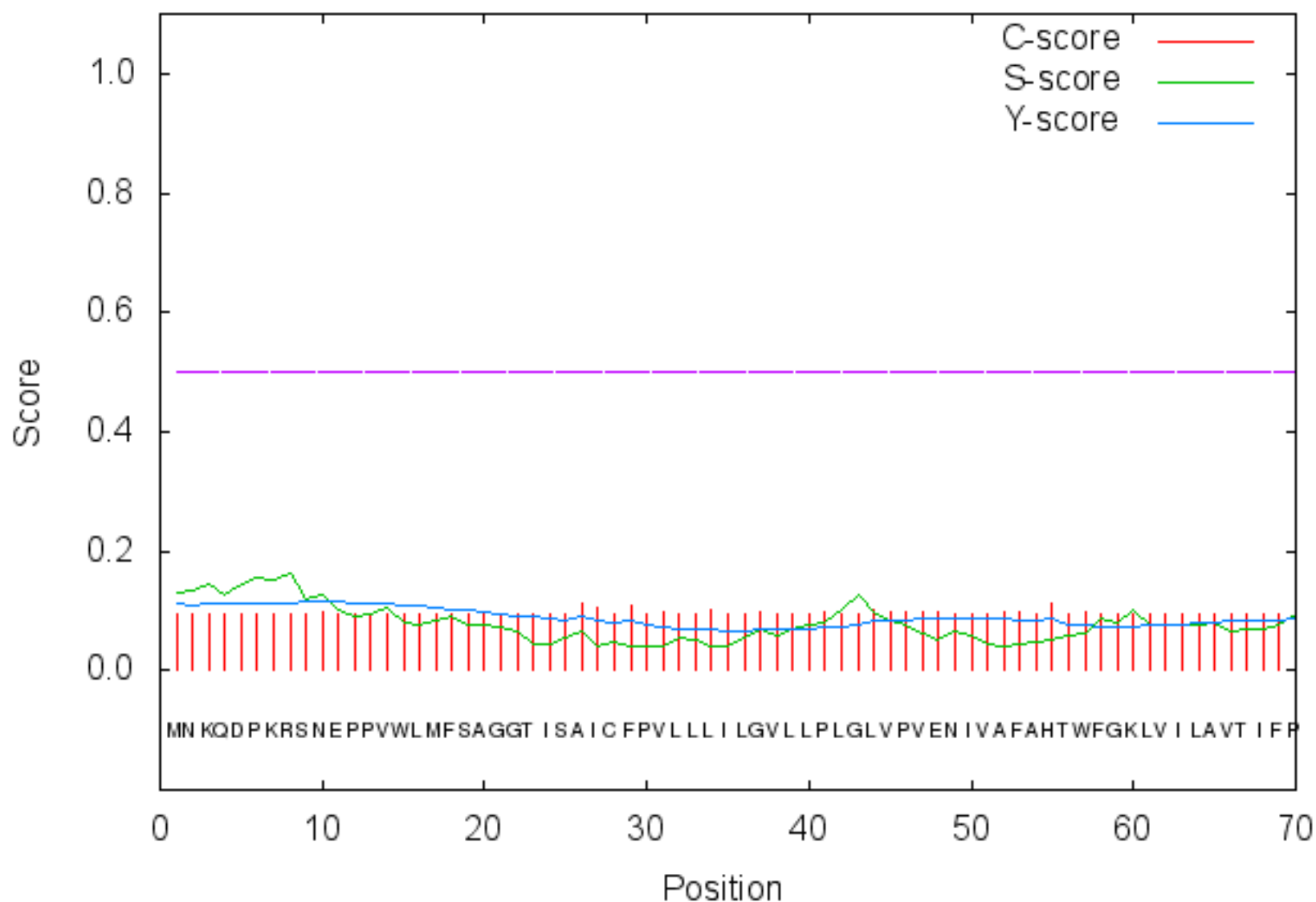
```

# data
# gnuplot script

```

>frdD

SignalP-4.1 prediction (gram- networks): frdD



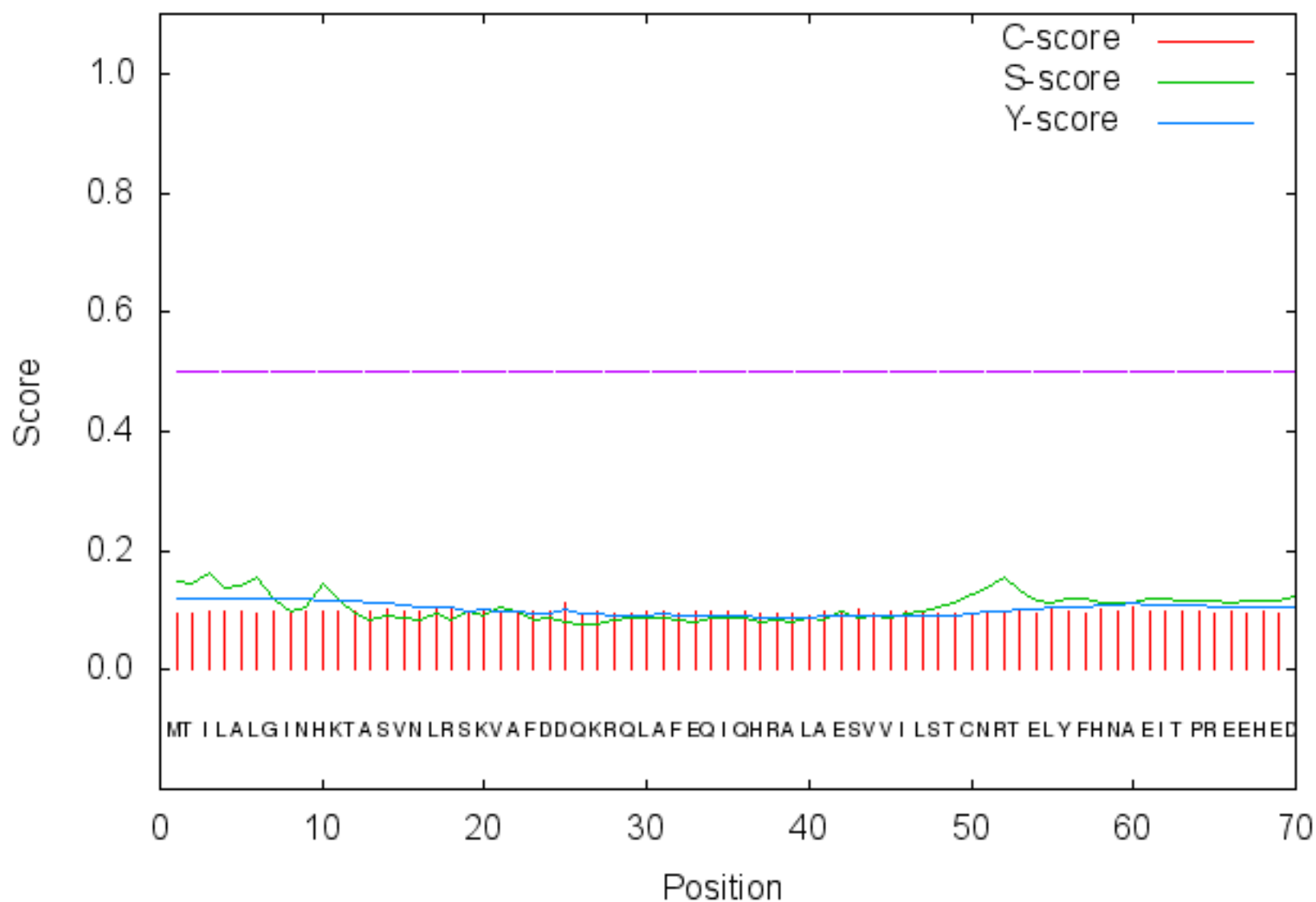
# Measure	Position	Value	Cutoff	signal peptide?
max. C	26	0.113		
max. Y	11	0.115		
max. S	8	0.162		
mean S	1-10	0.139		
D	1-10	0.124	0.510	NO

Name=frdD SP='NO' D=0.124 D-cutoff=0.510 Networks=SignalP-TM

[data](#)
[gnuplot script](#)

>hemA

SignalP-4.1 prediction (gram- networks): hemA



# Measure	Position	Value	Cutoff	signal peptide?
max. C	25	0.114		
max. Y	11	0.116		

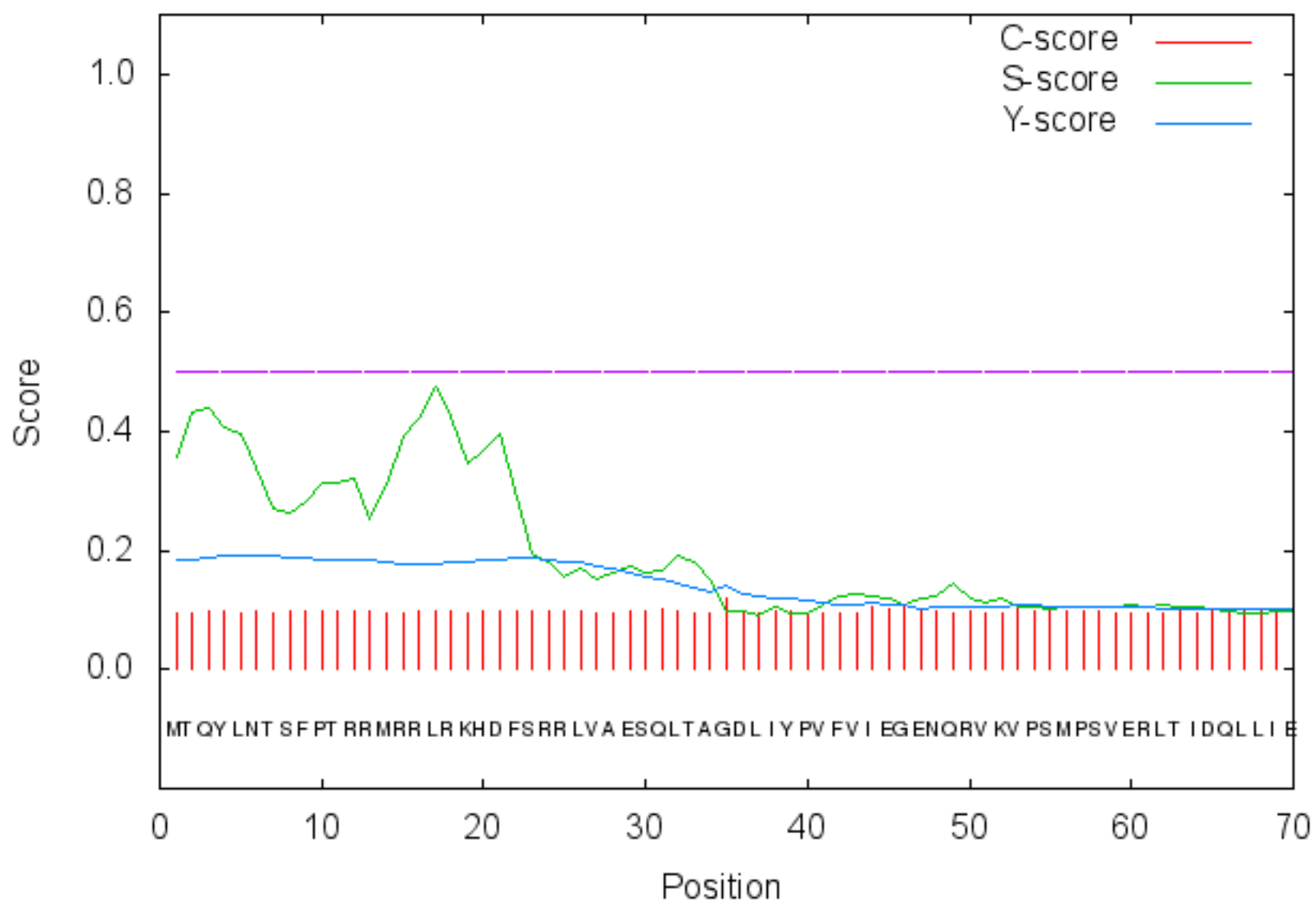

```

max. S      3      0.161
mean S     1-10    0.136
D         1-10    0.125  0.570  NO
Name=hemA   SP='NO' D=0.125 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script

```

>hemB

SignalP-4.1 prediction (gram- networks): hemB



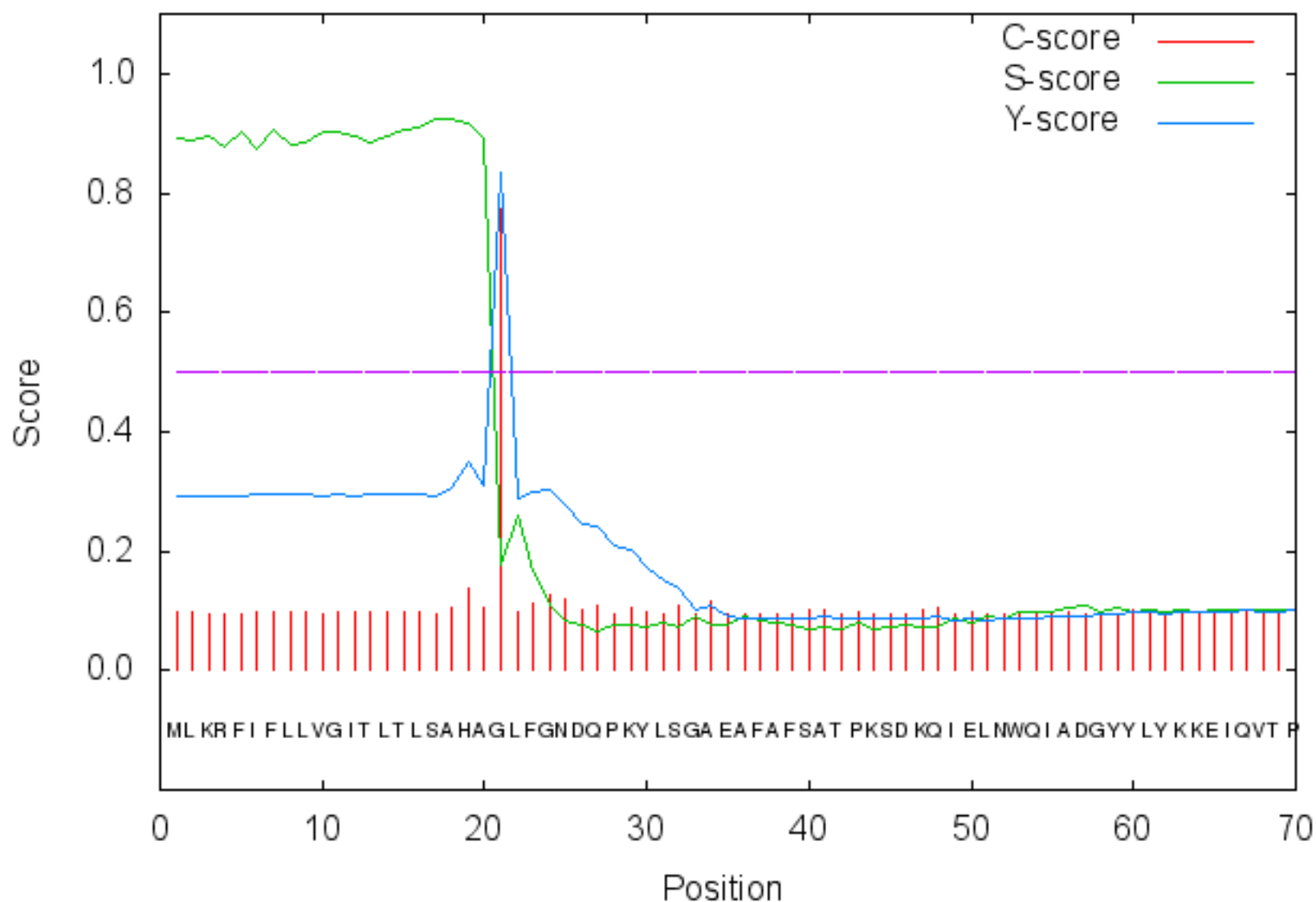
```

# Measure  Position  Value  Cutoff  signal peptide?
max. C     35         0.118
max. Y     22         0.189
max. S     17         0.475
mean S     1-21       0.358
D         1-21       0.268  0.570  NO
Name=hemB   SP='NO' D=0.268 D-cutoff=0.570 Networks=SignalP-noTM
# data
# gnuplot script

```

>dsb

SignalP-4.1 prediction (gram- networks): dsb



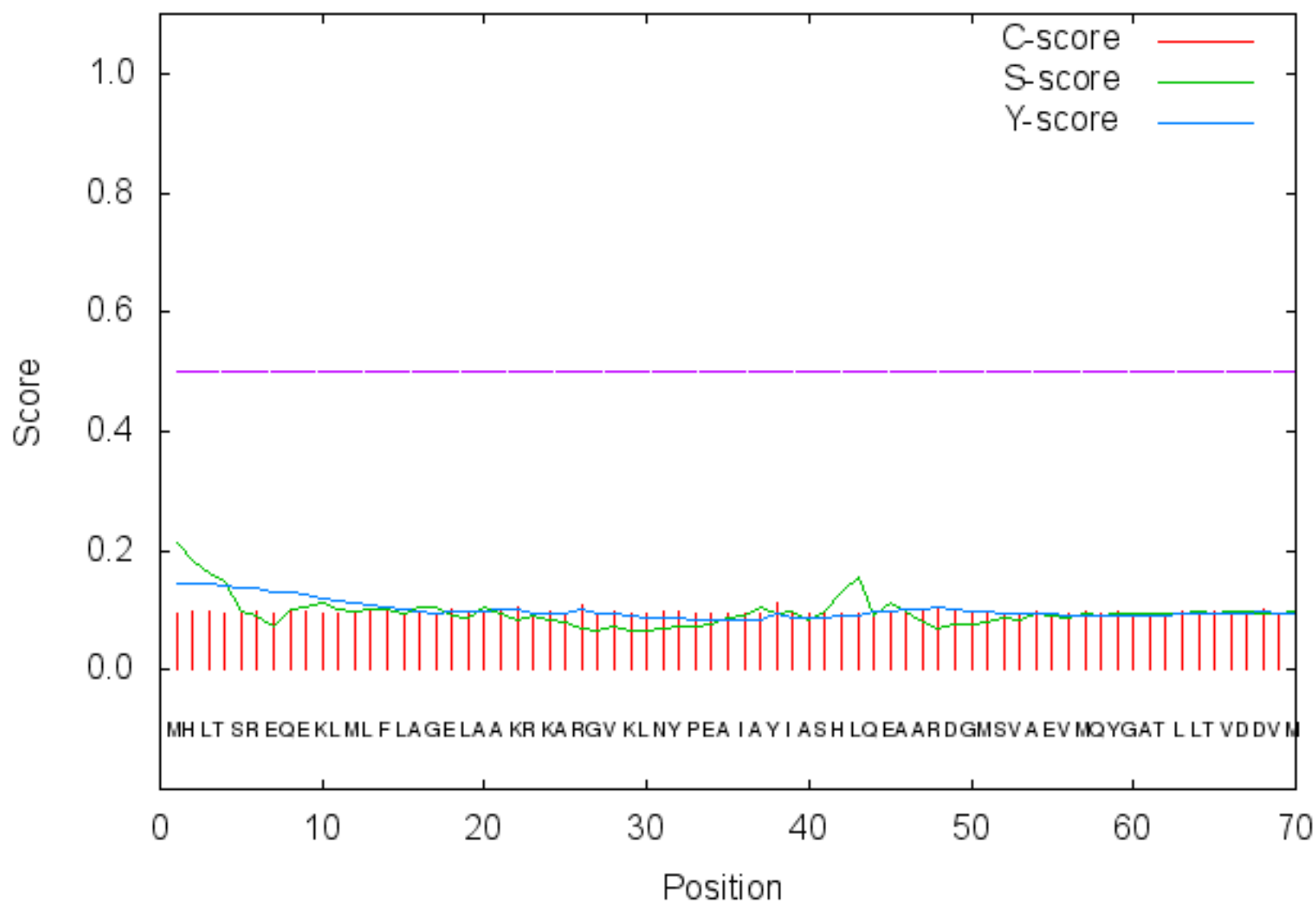
# Measure	Position	Value	Cutoff	signal peptide?
max. C	21	0.772		
max. Y	21	0.835		
max. S	17	0.925		
mean S	1-20	0.897		
D	1-20	0.864	0.570	YES

Name=dsb SP='YES' Cleavage site between pos. 20 and 21: AHA-GL D=0.864 D-cutoff=0.570 Networks=SignalP-noTM

[data](#)
[gnuplot script](#)

>ureA

SignalP-4.1 prediction (gram- networks): ureA



# Measure	Position	Value	Cutoff	signal peptide?
max. C	38	0.114		
max. Y	11	0.117		

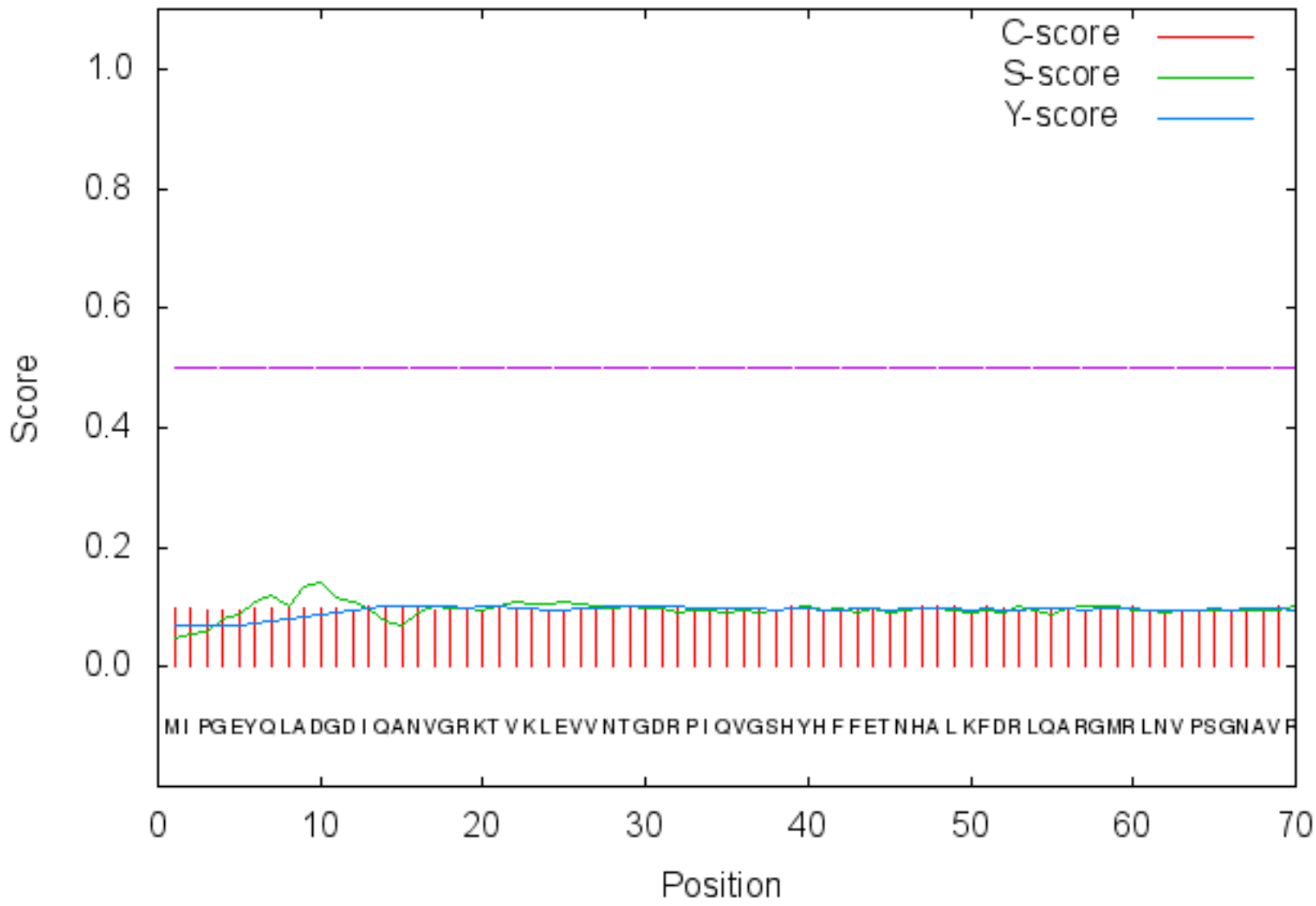
```
max. S 1 0.212
mean S 1-10 0.129
D 1-10 0.122 0.570 NO
```

```
Name=ureA SP='NO' D=0.122 D-cutoff=0.570 Networks=SignalP-noTM
```

```
# data
# gnuplot script
```

>ureB

SignalP-4.1 prediction (gram- networks): ureB



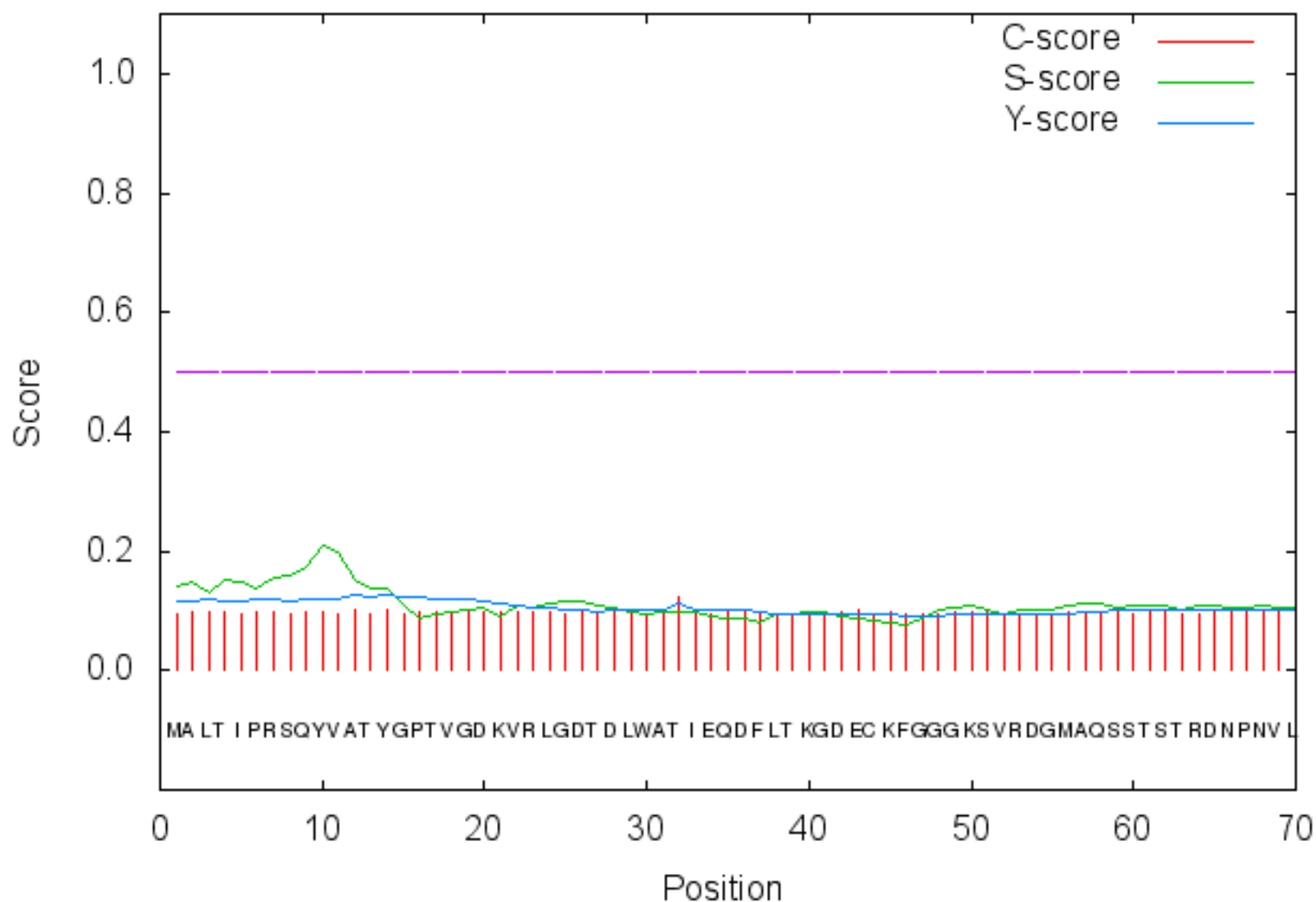
```
# Measure Position Value Cutoff signal peptide?
max. C 51 0.102
max. Y 16 0.102
max. S 10 0.140
mean S 1-15 0.094
D 1-15 0.098 0.570 NO
```

```
Name=ureB SP='NO' D=0.098 D-cutoff=0.570 Networks=SignalP-noTM
```

```
# data
# gnuplot script
```

>ureC

SignalP-4.1 prediction (gram- networks): ureC



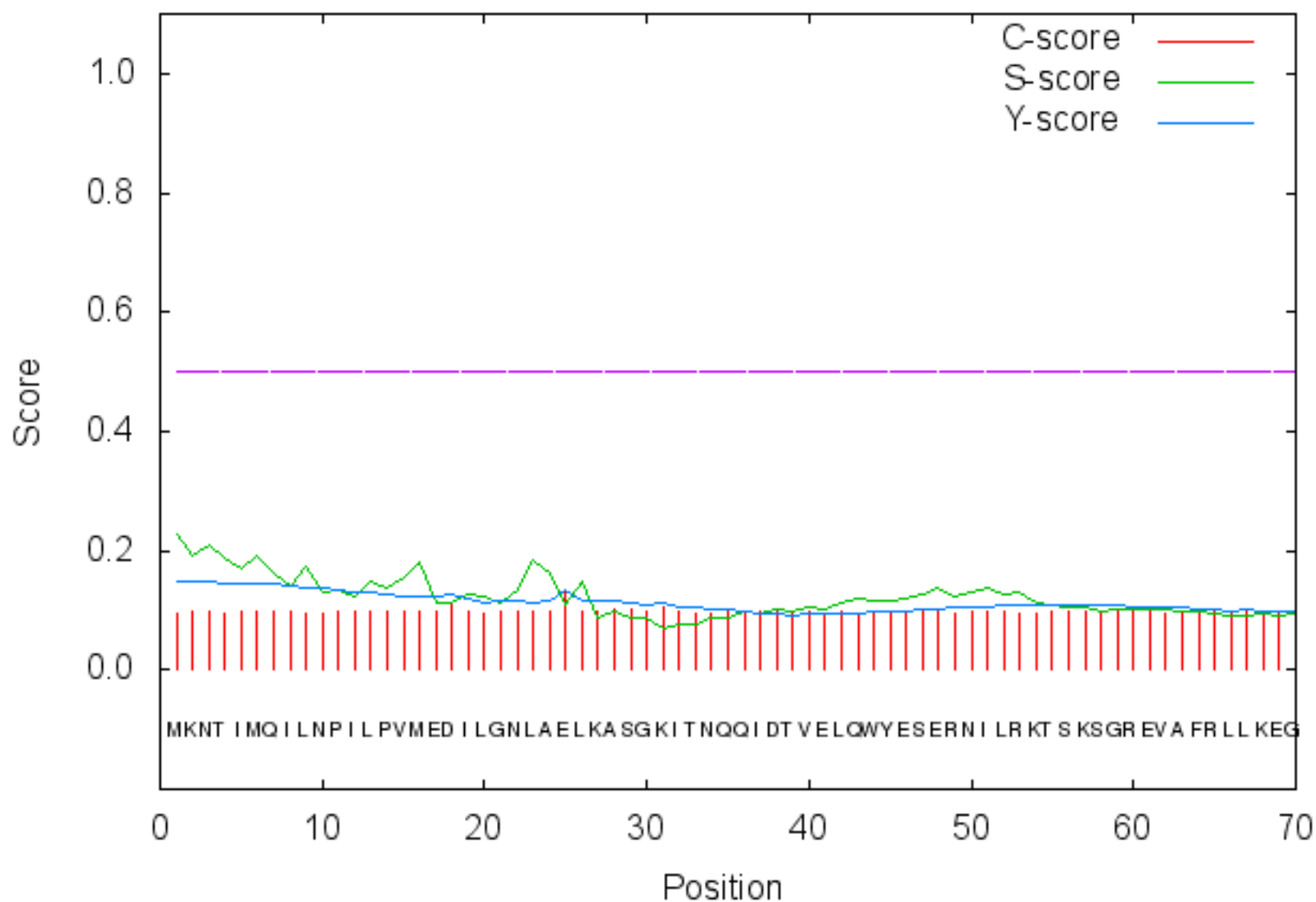
# Measure	Position	Value	Cutoff	signal peptide?
max. C	32	0.123		
max. Y	12	0.127		
max. S	10	0.208		
mean S	1-11	0.159		
D	1-11	0.142	0.570	NO

Name=ureC SP='NO' D=0.142 D-cutoff=0.570 Networks=SignalP-noTM

[data](#)
[gnuplot script](#)

>ureE

SignalP-4.1 prediction (gram- networks): ureE



# Measure	Position	Value	Cutoff	signal peptide?
max. C	25	0.130		
max. Y	25	0.135		

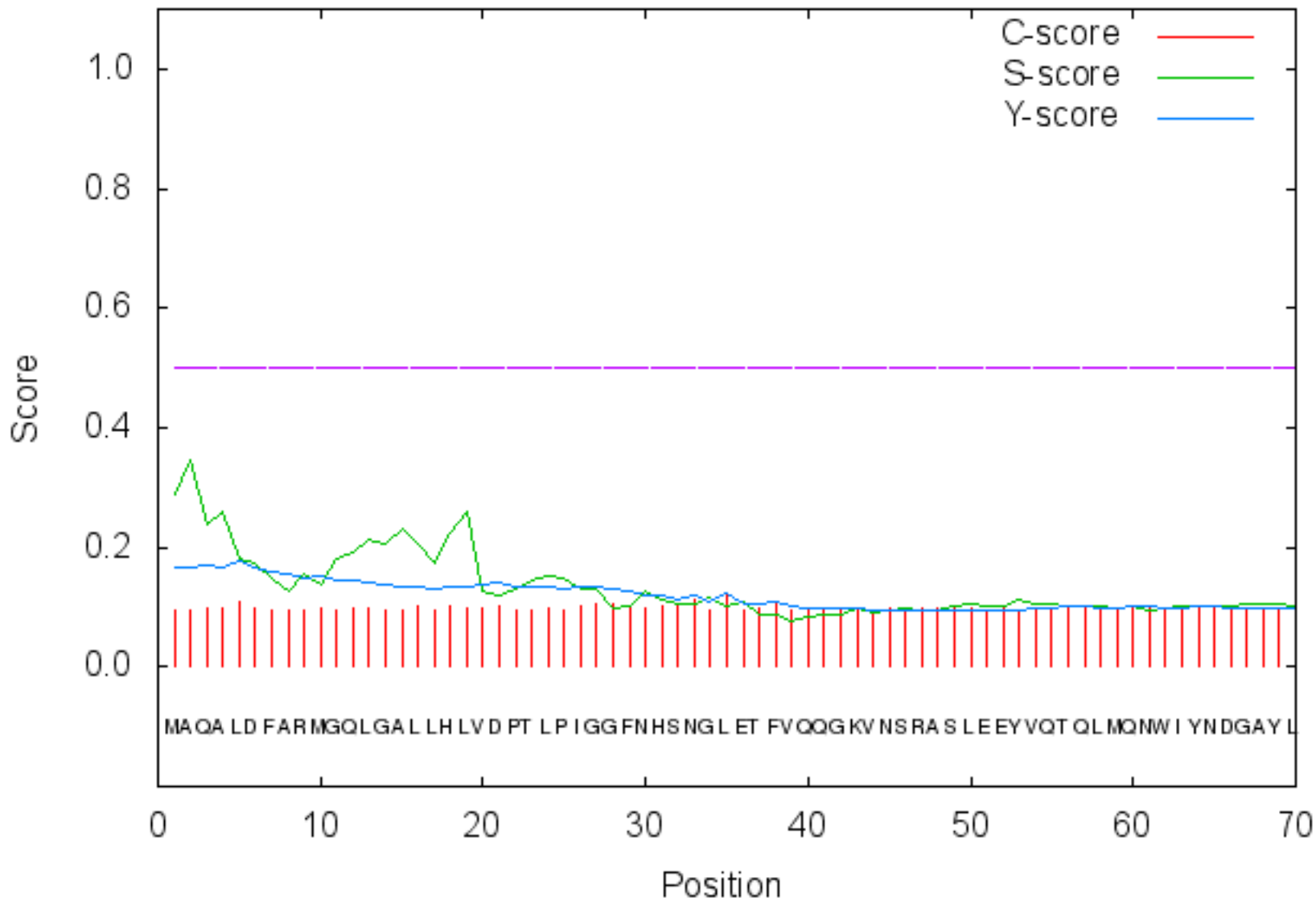
```
max. S 1 0.226
mean S 1-24 0.155
D 1-24 0.145 0.570 NO
```

```
Name=ureE SP='NO' D=0.145 D-cutoff=0.570 Networks=SignalP-noTM
```

```
# data
# gnuplot script
```

>ureF

SignalP-4.1 prediction (gram- networks): ureF



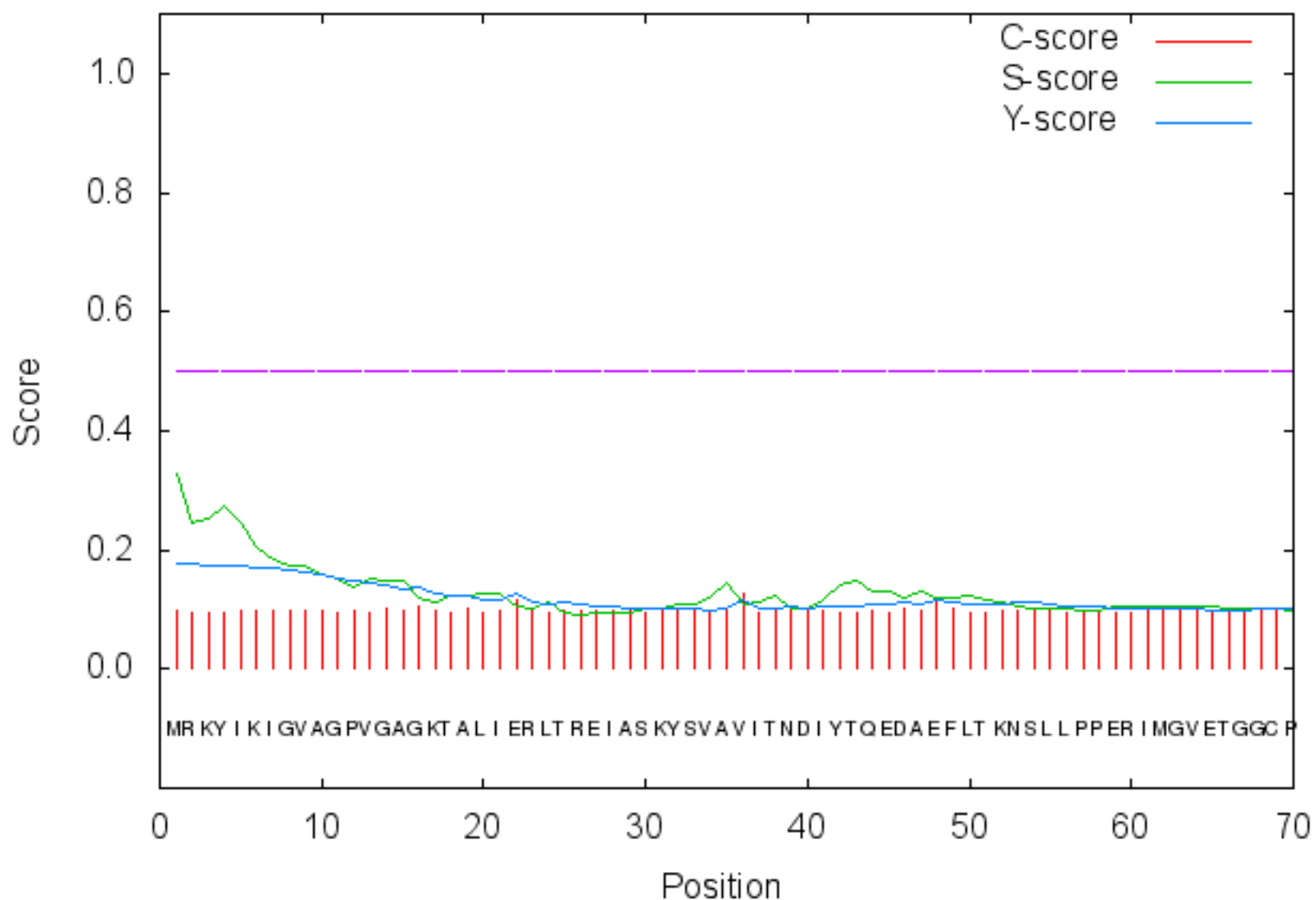
```
# Measure Position Value Cutoff signal peptide?
max. C 35 0.122
max. Y 11 0.145
max. S 2 0.347
mean S 1-10 0.205
D 1-10 0.173 0.570 NO
```

```
Name=ureF SP='NO' D=0.173 D-cutoff=0.570 Networks=SignalP-noTM
```

```
# data
# gnuplot script
```

>ureG

SignalP-4.1 prediction (gram- networks): ureG



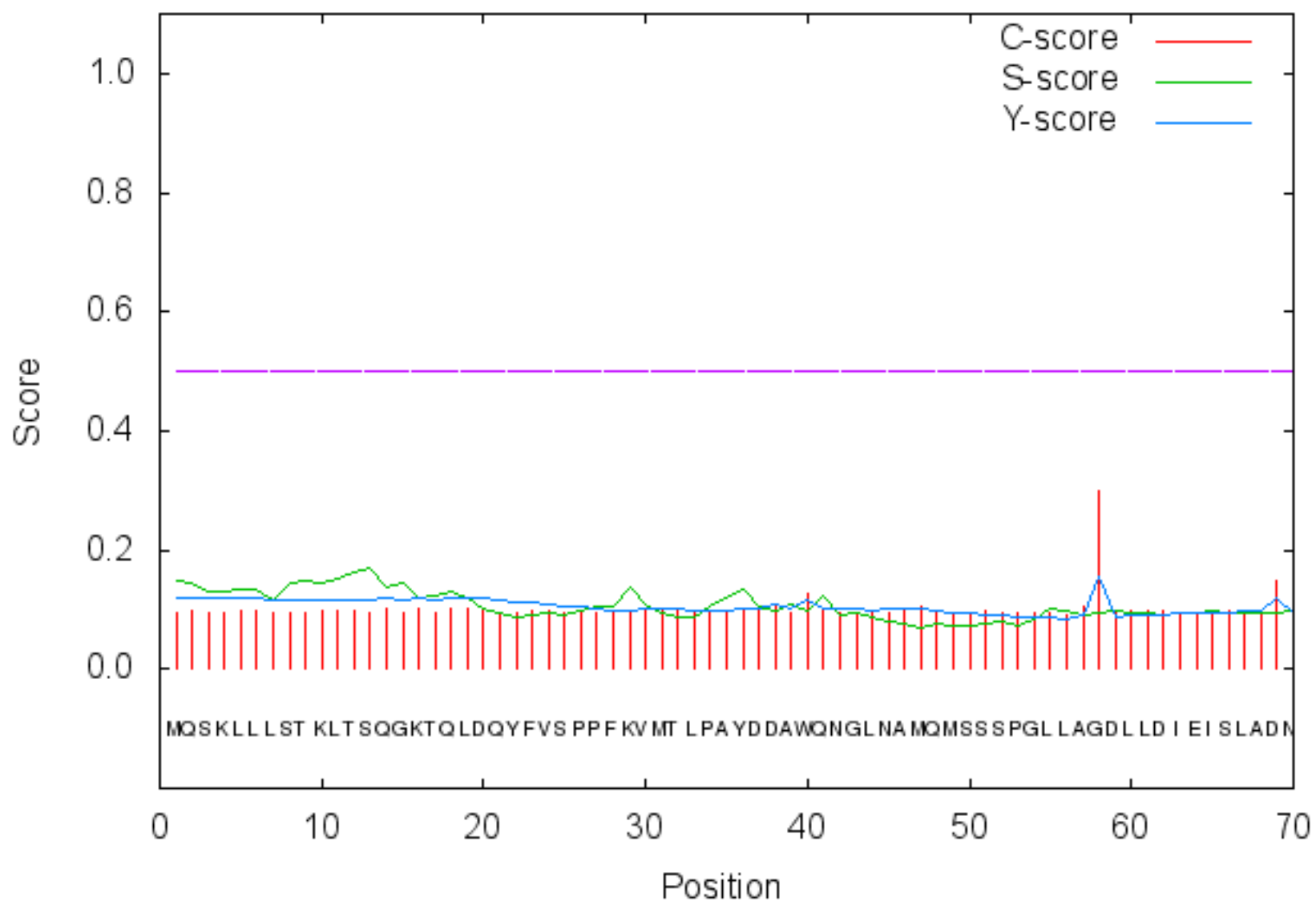
# Measure	Position	Value	Cutoff	signal peptide?
max. C	36	0.127		
max. Y	11	0.152		
max. S	1	0.327		
mean S	1-10	0.224		
D	1-10	0.186	0.570	NO

Name=ureG SP='NO' D=0.186 D-cutoff=0.570 Networks=SignalP-noTM

[data](#)
[gnuplot script](#)

>ureH

SignalP-4.1 prediction (gram- networks): ureH



# Measure	Position	Value	Cutoff	signal peptide?
max. C	58	0.298		
max. Y	58	0.155		

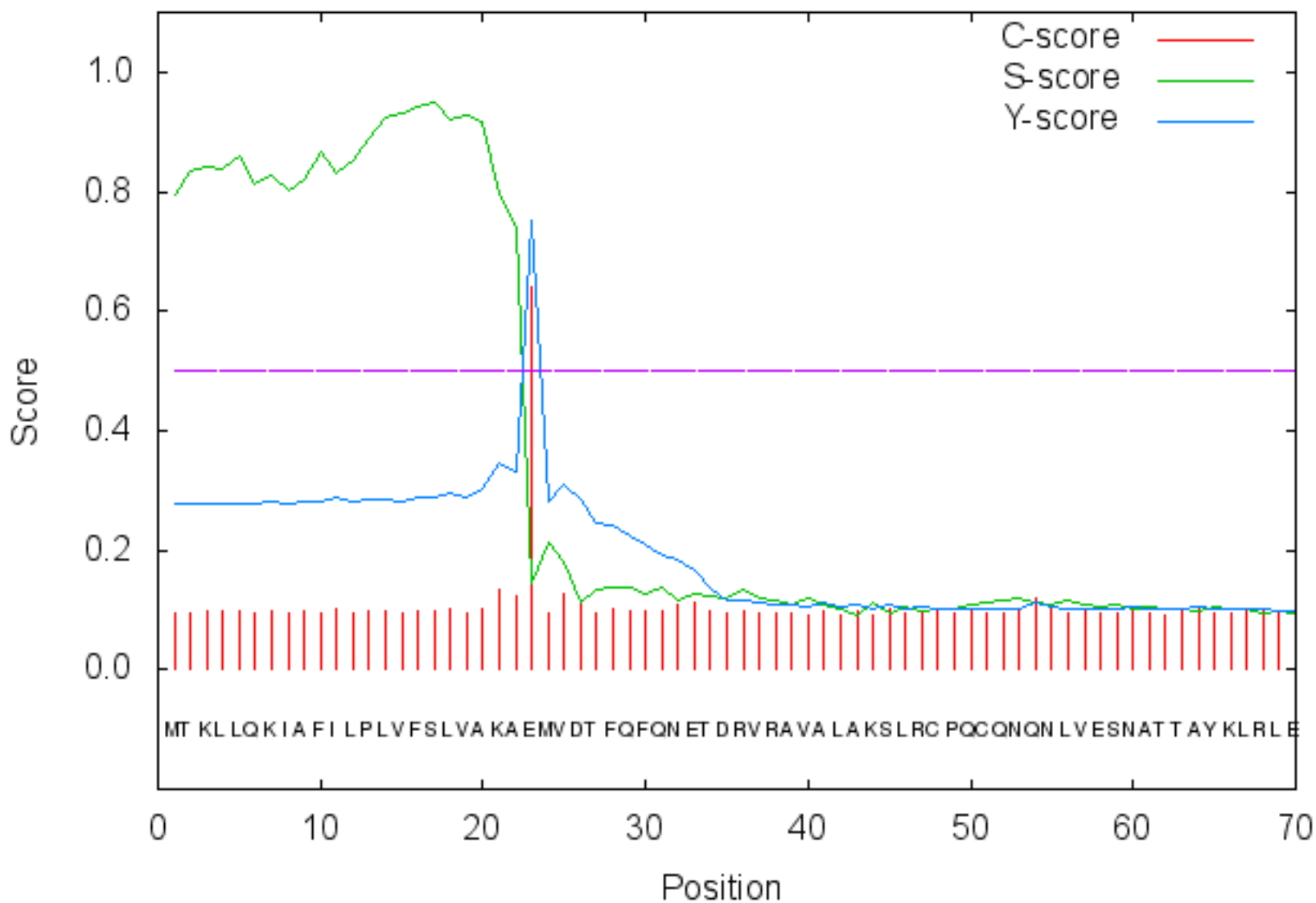
```
max. S 13 0.170
mean S 1-57 0.109
D 1-57 0.133 0.570 NO
```

Name=ureH SP='NO' D=0.133 D-cutoff=0.570 Networks=SignalP-noTM

```
# data
# gnuplot script
```

>ccmH

SignalP-4.1 prediction (gram- networks): ccmH



```
# Measure Position Value Cutoff signal peptide?
max. C 23 0.640
max. Y 23 0.753
max. S 17 0.950
mean S 1-22 0.860
D 1-22 0.803 0.570 YES
```

Name=ccmH SP='YES' Cleavage site between pos. 22 and 23: AKA-EM D=0.803 D-cutoff=0.570 Networks=SignalP-noTM

```
# data
# gnuplot script
```

Signal peptides: 9

```
# processed fasta entries
# gff file of processed entries
```

Please cite:

SignalP 4.0: discriminating signal peptides from transmembrane regions
Petersen TN., Brunak S., von Heijne G. & Nielsen H.
Nature Methods, 8:785-786, 2011

[Explain](#) the output. Go [back](#).