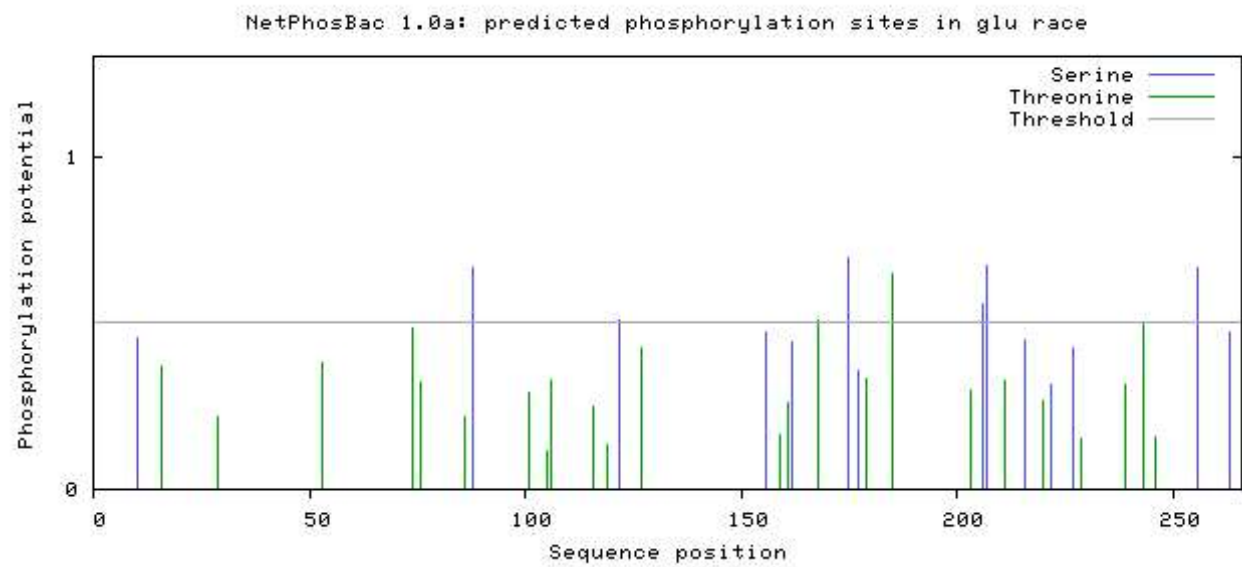




NetPhosBac 1.0 Server - prediction results

Technical University of Denmark

```
>glu_race      266 amino acids
#
# netphosbac-1.0a prediction results
#
# Sequence          # x   Context    Score   Kinase   Answer
# -----
# glu_race          10 S   GVIDSGVGG   0.456   main     .
# glu_race          16 T   VGGLTVAKE   0.368   main     .
# glu_race          29 T   LPNETIYYL   0.219   main     .
# glu_race          53 T   VKQYTVIEIA  0.379   main     .
# glu_race          74 T   IACNTATAV   0.482   main     .
# glu_race          76 T   CNTATAVAL   0.323   main     .
# glu_race          86 T   YLQKTLSIP   0.216   main     .
# glu_race          88 S   QKTLSIPVI   0.665   main     Y
# glu_race         101 T   PGARTAIMT   0.293   main     .
# glu_race         105 T   TAIMTTRNQ   0.117   main     .
# glu_race         106 T   AIMTTRNQN   0.327   main     .
# glu_race         116 T   LVLGTEGTI   0.245   main     .
# glu_race         119 T   GTEGTIKSE   0.135   main     .
# glu_race         122 S   GTIKSEAYR   0.506   main     Y
# glu_race         127 T   EAYRTHIKR   0.424   main     .
# glu_race         156 S   QMRYSDPTI   0.471   main     .
# glu_race         159 T   YSDPTITSI   0.162   main     .
# glu_race         161 T   DPTITSIVI   0.260   main     .
# glu_race         162 S   PTITSIVIH   0.440   main     .
# glu_race         168 T   VIHQTILKRW  0.506   main     Y
# glu_race         175 S   RWRNSESMT   0.694   main     Y
# glu_race         177 S   RNSESMTVI   0.359   main     .
# glu_race         179 T   SESMTVILG   0.332   main     .
# glu_race         185 T   ILGCTHYPL   0.644   main     Y
# glu_race         203 T   GGKKTVISS   0.296   main     .
# glu_race         206 S   KTVISSGLE   0.556   main     Y
# glu_race         207 S   TVISSGLET   0.670   main     Y
# glu_race         211 T   SGLETAREV   0.329   main     .
# glu_race         216 S   AREVSALLT   0.444   main     .
# glu_race         220 T   SALLTFSNE   0.268   main     .
# glu_race         222 S   LLTFSNEHA   0.314   main     .
# glu_race         227 S   NEHASYTEH   0.423   main     .
# glu_race         229 T   HASYTEHPD   0.154   main     .
# glu_race         239 T   RFFATGDPT   0.316   main     .
# glu_race         243 T   TGDPTHITN   0.500   main     Y
# glu_race         246 T   PTHITNIIK   0.159   main     .
# glu_race         256 S   WLNLSVNVE   0.664   main     Y
# glu_race         263 S   VERISVND-   0.471   main     .
#
# MNKPIGVIDSGVGLTVAKEIMRQLPNETIYYLGDIGRCPPYGRPGEQVK # 50
# QYTVEIARKLMEFDIKMLVIACNTATAVALEYLQKTLSIPVIGVIEPGAR # 100
# TAIMTTRNQNLVLVLGTEGTIKSEAYRTHIKRINPHVEVHGVACPGFVPLV # 150
# EQMRYSDPTITSIVIHQTLKRWNRNSESMTVILGCTHYPLLYKPIYDYFGG # 200
# KKTVISSGLETAREVSALLTFSNEHASYTEHPDHRFFATGDPTHITNIIK # 250
# EWLNLNVNVERISVND # 300
%1 ..... # 50
%1 .....S..... # 100
%1 .....S..... # 150
%1 .....T.....S.....T..... # 200
%1 .....SS.....T..... # 250
%1 .....S.....
```



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