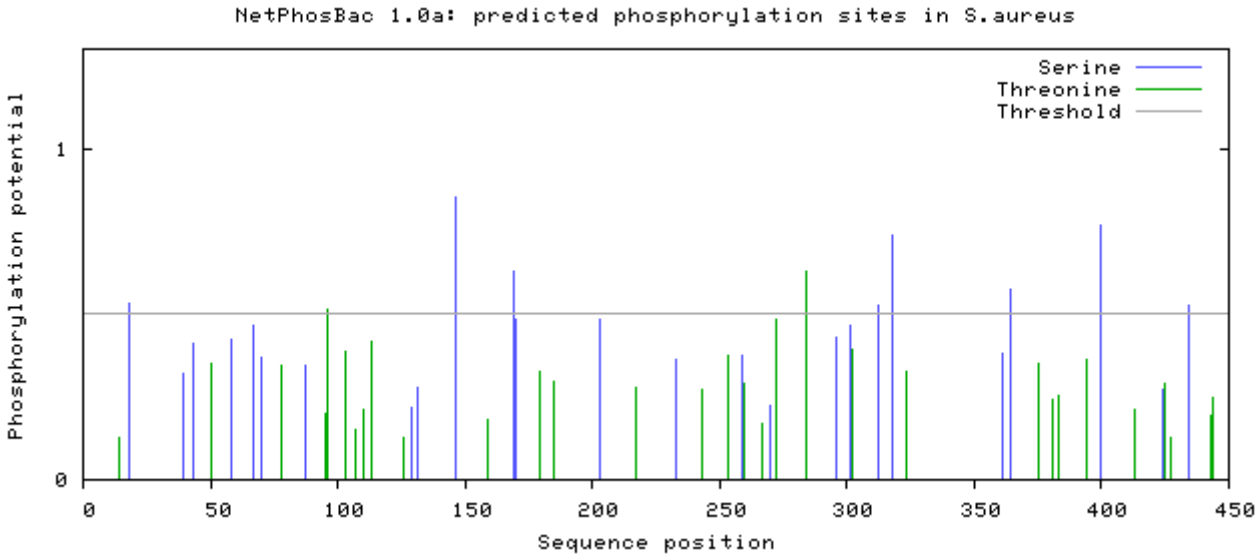# NetPhosBac 1.0 Server - prediction results

Technical University of Denmark

```
>S.aureus          450 amino acids
#
# netphosbac-1.0a prediction results
#
# Sequence              # x    Context   Score  Kinase   Answer
# ----------------------------------------------------------------
# S.aureus             14 T   AGKGTRMKS  0.130  main       .
# S.aureus             18 S   TRMKSKKYK  0.534  main       Y
# S.aureus             39 S   HVLESVKGS  0.322  main       .
# S.aureus             43 S   SVKGSGVDQ  0.410  main       .
# S.aureus             50 T   DQVVTIVGH  0.352  main       .
# S.aureus             58 S   HGAESVKGH  0.422  main       .
# S.aureus             67 S   LGERSLYSF  0.463  main       .
# S.aureus             70 S   RSLYSFQEK  0.369  main       .
# S.aureus             78 T   KQLGTAHAV  0.344  main       .
# S.aureus             87 S   QMAKSHLED  0.347  main       .
# S.aureus             95 T   DKEGTTIVV  0.197  main       .
# S.aureus             96 T   KEGTTIVVC  0.516  main       Y
# S.aureus            103 T   VCGDTPLIT  0.388  main       .
# S.aureus            107 T   TPLITKETL  0.153  main       .
# S.aureus            110 T   ITKETLETL  0.212  main       .
# S.aureus            113 T   ETLETLIAH  0.415  main       .
# S.aureus            126 T   NAQATVLSA  0.128  main       .
# S.aureus            129 S   ATVLSASIQ  0.221  main       .
# S.aureus            131 S   VLSASIQQP  0.277  main       .
# S.aureus            146 S   VRNASGRLE  0.852  main       Y
# S.aureus            159 T   EKDATQAEK  0.182  main       .
# S.aureus            169 S   INEISSGIF  0.629  main       Y
# S.aureus            170 S   NEISSGIFA  0.481  main       .
# S.aureus            179 T   FNNKTLFEK  0.328  main       .
# S.aureus            185 T   FEKLTQVKN  0.293  main       .
# S.aureus            203 S   PDVLSLILN  0.482  main       .
# S.aureus            217 T   EVYRTNDVE  0.280  main       .
# S.aureus            233 S   RVMLSQAEK  0.365  main       .
# S.aureus            243 T   MQRRTNHYH  0.275  main       .
# S.aureus            253 T   LNGVTIIDP  0.375  main       .
# S.aureus            259 S   IDPDSTFIG  0.373  main       .
# S.aureus            260 T   DPDSTFIGP  0.291  main       .
# S.aureus            267 T   GPDVTIGSD  0.169  main       .
# S.aureus            270 S   VTIGSDTVI  0.225  main       .
# S.aureus            272 T   IGSDTVIEP  0.484  main       .
# S.aureus            284 T   INGRTEIGE  0.632  main       Y
# S.aureus            296 S   IGQYSEINN  0.429  main       .
# S.aureus            301 S   EINNSTIEN  0.468  main       .
# S.aureus            302 T   INNSTIENG  0.394  main       .
# S.aureus            312 S   CIQQSVVND  0.524  main       Y
# S.aureus            318 S   VNDASVGAN  0.736  main       Y
# S.aureus            323 T   VGANTKVGP  0.329  main       .
# S.aureus            361 S   GAKVSHLSY  0.380  main       .
# S.aureus            364 S   VSHLSYIGD  0.575  main       Y
# S.aureus            375 T   IGERTNIGC  0.348  main       .
# S.aureus            381 T   IGCGTITVN  0.242  main       .
# S.aureus            383 T   CGTITVNYD  0.254  main       .
# S.aureus            394 T   NKFKTIVGK  0.363  main       .
# S.aureus            400 S   VGKDSFVGC  0.770  main       Y
# S.aureus            413 T   VAPVTIGDD  0.210  main       .
# S.aureus            424 S   VAAGSTITD  0.273  main       .
# S.aureus            425 T   AAGSTITDD  0.291  main       .
```

```
# S.aureus              427 T    GSTITDDVP   0.127    main        .
# S.aureus              434 S    VPNDSLAVA   0.525    main        Y
# S.aureus              443 T    RARQTTKEG   0.195    main        .
# S.aureus              444 T    ARQTTKEGY   0.250    main        .
#
    MRRHAIILAAGKGTRMKSKKYKVLHEVAGKPMVEHVLESVKGSGVDQVVT    #     50
    IVGHGAESVKGHLGERSLYSFQEKQLGTAHAVQMAKSHLEDKEGTTIVVC    #    100
    GDTPLITKETLETLIAHHEDANAQATVLSASIQQPYGYGRIVRNASGRLE    #    150
    RIVEEKDATQAEKDINEISSGIFAFNNKTLFEKLTQVKNDNAQGEYYLPD    #    200
    VLSLILNDGGIVEVYRTNDVEEIMGVNDRVMLSQAEKAMQRRTNHYHMLN    #    250
    GVTIIDPDSTFIGPDVTIGSDTVIEPGVRINGRTEIGEDVVIGQYSEINN    #    300
    STIENGACIQQSVVNDASVGANTKVGPFAQLRPGAQLGADVKVGNFVEIK    #    350
    KADLKDGAKVSHLSYIGDAVIGERTNIGCGTITVNYDGENKFKTIVGKDS    #    400
    FVGCNVNLVAPVTIGDDVLVAAGSTITDDVPNDSLAVARARQTTKEGYRK    #    450
%1  ................S.................................    #     50
%1  .................................................T....    #    100
%1  .............................................S....    #    150
%1  ................S................................    #    200
%1  .................................................    #    250
%1  .............................T...................    #    300
%1  .........S.....S.................................    #    350
%1  ..........S...............................S        #    400
%1  .............................S...................    #    450
```


NetPhosBac 1.0a: predicted phosphorylation sites in S.aureus