A

```
 No Hit                                        Prob E-value  P-value  Score    SS  Cols Query HMM  Template HMM
  1 YP_026208.1 DUF3971-AsmA2 doma             99.6 5.3E-13  6.4E-18  112.4  21.2  144    1-145     30-174 (1266) YhdP
  2 NP_416568.1 suppressor of OmpF             99.4 1.6E-11    2E-16   96.5  14.7  124    5-130     29-163 (617)  AsmA
  3 NP_417981.2 putative inner mem             99.4 1.5E-11  1.9E-16   98.0  12.5  125    4-130     31-179 (686)  YhjG
  4 NP_418112.1 putative inner mem             99.1 1.3E-08  1.6E-13   79.8  14.3  122    1-144     25-148 (569)  YicH
  5 NP_418642.1 translocation and              98.7 6.2E-07  7.5E-12   76.8  12.6  117    5-128     29-149 (1259) TamB
  6 NP_012064.1 Mdm31p [Saccharomy             97.7  0.0034  4.2E-08   50.2  12.5  135    5-143    145-322 (579)  Mdm31
  7 NP_415899.1 putative membrane-             97.6 0.00091  1.1E-08   56.2   9.5  131    5-145     28-177 (879)  YdbH
  8 NP_014790.4 Mdm32p [Saccharomy             96.9   0.066    8E-07   43.7  11.5  132   10-143    171-318 (622)  Mdm32
  9 6A9J_A Endolysin,Autophagy-rel             81.7      13  0.00016   28.9   6.4   83    7-95     172-265 (389)  Atg2
 10 NP_013060.1 membrane morphogen             77.5 1.3E+02   0.0016   31.0  17.0  141    3-151      1-200 (3144) Vps13
 11 6CBC_A Putative vacuolar prote             62.8      98   0.0012   23.5  12.4  135    7-149      6-190 (336)  Vps13
```