


```
T Q_Novo_D4403_p 161 WSPRGTVDIRYGTNRPFLGKRIDFTEQAEEKLAPVIARLERELPGQLGKLEVRQRVERAUNSAFTTLSLNRDNPPV 240 (489)
T ss_pred ceEEEeeeEeCCeEEEechHchHHHHHHHHHHHHHHHHHHHHHHHHhhccCeCCCCCCe
```

```
Q ss_pred EEEeeeecccCCeEEEEeeCCCCEEEEEE
Q Q_LactoD2140_p 173 VLIKLSQFKLQNGMTLRATKLDPNDLLEFAVYL 205 (205)
Q Consensus 173 ~i~l~~~~~ik~~~idl~d~i~f~l~i 205 (205)
    ++.++- -.+..+.++|+.+.+
T Consensus 241 wL~~~P~~~~~v~~~s~~~~~l~~~l 267 (489)
T Q_Novo_D4403_p 241 WMRVSP-----RELQYGGYELDGKRLVRLGV 267 (489)
T ss_pred EEEEec----cEEEecCeEEEEE
```

Rv0817c vs. YceB

```
Query Q_Rv0817c_p3
Match_columns 270
No_of_seqs 122 out of 126
Neff 8.86375
Searched_HMMs 1
Date Wed Aug 15 00:33:21 2018
Command hhsearch -cpu 8 -i ../results/full.a3m -d ..../results/db -o ..../results/Rv0817c_v_YceB.hhr -oa3m
..../results/Rv0817c_v_YceB.a3m -p 20 -Z 250 -loc -z 1 -b 1 -B 250 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -
-contxt /cluster/toolkit/production/biopros/tools/hh-suite-build/data/context_data.crf

No Hit Prob E-value P-value Score SS Cols Query HMM Template HMM
1 Q_YceB_p3 52.7 0.0032 0.0032 23.7 8.1 135 121-256 24-185 (186)

No 1
>Q_YceB_p3
Probab=52.68 E-value=0.0032 Score=23.72 Aligned_cols=135 Identities=11% Similarity=0.151 Sum_probs=0.0 Template_Neff=8.100

Q ss_pred EEEeeHHHHHHHHh-----cchhhccCcccccccCCCCCccccccccceEEEEeeCcCcceeEEEEEE
Q Q_Rv0817c_p3 121 RIIDSMHLGRYL-----GISDMVAAPRQESENDAATGGTTESGISRGVLVFSGTFISANFAHRVSLVLDLS 187 (270)
Q Consensus 121 ~~~l~~~~L~~~~~l~~~~~g~~~~v~g~~~~v~~~~~ 187 (270)
    .+|||||+||+.+
T Consensus 24 ~~~ise~lq~~l~~~P~k~~~~~1~~~v~1~~~v~1~~~v~r~1~~~~~g~~~g~~~l~ 103 (186)
T Q_YceB_p3 24 QVTITEQEINQSLAKHNNSFSKDIGLPGVADAHIVLTNLTSIGREPNKVLTGDNALDMNSLFGSQATMCLKLKALPV 103 (186)
T ss_pred eeeeCHHHHHHHHHHHCCCCcccCCcccEEEEEecCeeecccCCCCeEEEEEEecCCCCeeeEEEEEEEEE
```



```
Q ss_pred EeeCCCCeEEEcceCCCCCCCCC---HHHHHHHHHHhcccCCCCC-CCCc---ceEEEEeeCCeEEE
Q Q_Rv0817c_p3 188 VASDDRATLVITPTAVTGPDTADQPFP----DDKRDAVLHAFASKLKNQKL-PFGVV----PNTVGARGSDVII 253 (270)
Q Consensus 188 ~~~~l~~~1~~~lp~~~~~L~p~~~~~L~p~gl~~~~~v~v~~~~~ 253 (270)
    .+...+.++..++-.-..+..-+....+...+...|.-|.|+..+
T Consensus 104 Y~d~~~aiyL~~~i~~~i~~~i~~~v~1~~~v~1~~~v~1~~~v~1~~~PVY~L~~~i~~~v~g~L~l 182 (186)
T Q_YceB_p3 104 F-DKEKGAIFLKEMEVVDATVQPEKMQTLLPYLNQALRNYFNQQPAYVLREDGSQGEAMAKKLAKGIEVKPGEIVI 182 (186)
T ss_pred E-eCCCCeEEEcceCCCCcccEChHHHHHHHHHHHHHHHhcccCCCCeCCCCcccHHHHHHHHHhcCcccEEEEE
```



```
Q ss_pred EEE
Q Q_Rv0817c_p3 254 EGI 256 (270)
Q Consensus 254 ~~ 256 (270)
    ++
T Consensus 183 ~ls 185 (186)
T Q_YceB_p3 183 PFT 185 (186)
T ss_pred eeC
```

Rv0817c vs. DUF4403-C

```
Query Q_Novo_D4403C_p3
Match_columns 202
No_of_seqs 100 out of 113
Neff 8.36093
Searched_HMMs 1
Date Wed Aug 15 00:34:40 2018
Command hhsearch -cpu 8 -i ../results/full.a3m -d ..../results/db -o ..../results/NovoD4403C_v_Rv0817c.hhr -oa3m
..../results/NovoD4403C_v_Rv0817c.a3m -p 0 -Z 250 -loc -z 1 -b 1 -B 250 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000
-contxt /cluster/toolkit/production/biopros/tools/hh-suite-build/data/context_data.crf

No Hit Prob E-value P-value Score SS Cols Query HMM Template HMM
1 Q_Rv0817c_p3 1.6 0.11 0.11 14.6 13.5 141 14-196 117-259 (270)

No 1
>Q_Rv0817c_p3
Probab=1.59 E-value=0.11 Score=14.57 Aligned_cols=141 Identities=11% Similarity=0.028 Sum_probs=0.0 Template_Neff=8.900

Q ss_pred EEEEEEeCHHHHHHHHHhcccCCCCcccCCCCCCCCCCCCcccCCCCcEEEEEeeEcCcCcceeEEEEEE
Q Q_Novo_D4403C_ 14 AFFIPVVADYVQLEPVL-MKALHKRSARPFEVPGVPVKADFRKVTYGTHGGRIVAVGVEFTATDQAGRVTGKTVWMT 92 (202)
Q Consensus 14 ~~~vp~~~v~y~~~l~~~l~~~l~~~~~g~~~i~i~~v~1~g~~~g~~~l~l~~~a~~~~~g~~~G~iy~ 92 (202)
    +...+...+.+|+.+.+..-..+...+.+...+...|...+.+..+...+...+...+...+...
T Consensus 117 ~~~~l~~~~~L~~~~~l~~~~~g~~~~~g~~~~~v~~~~~g~~~~~v~~~~~ 183 (270)
T Q_Rv0817c_p3 117 ELESRIIIDSMHLGRYLGISDLMVAAAPRQESENDAATGGTTESGIS-----GSRGLVFSGTPIS-----ANFAHRVSL 183 (270)
T ss_pred EEEEEEecHHHHHHHHhcccCCCCCCCCCCCCCCC-----ccccceEEeeeec-----CcCcceeEEE
```



```
Q ss_pred EEEEE-cCCCCCEEEEEEeeEcCcchHHHHHHHHhcccCCCCCCCCCCCCCCCCCCC-----ccccceEEEEE
Q Q_Novo_D4403C_ 93 GVPVN-ADNSRRIGFENFEVSGTDMGGNLLIRLANTPGMATHIAADLAQNFENDYNNKLVLKIDRATEDKREGDILLRA 171 (202)
Q Consensus 93 g~P~~~D~~~l~l~dl~~~t~~~l~~~a~~~l~~~i~~~l~~~l~~~a~~~l~~~i~~~L~~~~~l~~~ 171 (202)
    +...+.+...+.+...+...+...+.+...+.+...+.+...+.+...+.+...
T Consensus 184 ~~~~l~~~l~~~~~l~~~~~-----1~~~~~l~~~~~1~~~~~l~~~~~l~~~~~l~~~~~ 234 (270)
T Q_Rv0817c_p3 184 VDLSVASDDRATLVITPTAVTGPDTA-----DQPVPDDKRDA-----VLHAFASKLKNQK 234 (270)
T ss_pred EEEEEEccccCCCCeeEcCCCC-----CCCCCCCCCCCC-----ccccCCCCCCCC-----HHHHhcccCCCC
```



```
Q ss_pred EEeeeEeeEEEeeCcEEEeeeEe
Q Q_Novo_D4403C_ 172 EVTRIRTRGRIAAGQGLYLPVWADG 196 (202)
Q Consensus 172 ~~~~i~~~i~~~i~~~i~~~G 196 (202)
    -.+|||||.+|||||.+.+...
T Consensus 235 LP~gl~~~v~v~~~gl~v~~~g~~ 259 (270)
```

```
T Q_Rv0817c_p3    235 LPFGVVNPNTVGARGSDVIIIEGITRG 259 (270)
T ss_pred          CCCCcceEEEEeCCeEEEEEEec
```

Rv0817c vs. DUF4403-N

```
Query          Q_Rv0817c_p3
Match_columns  270
No_of_seqs    122 out of 126
Neff          8.86375
Searched_HMMs 1
Date           Sun Oct 28 23:23:55 2018
Command        hhsearch -cpu 8 -i ..../results/full.a3m -d ..../results/db -o ..../results/D4403Nv0816c_v_.hhr -oa3m
..../results/D4403Nv0816c_v_.a3m -p 0 -Z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -context /cluster/toolkit/production/biopros/tools/hh-suite-build/data/context_data.crf

No Hit          Prob E-value P-value Score   SS Cols Query HMM  Template HMM
1 Q_Novo_D4403_p3/1-287 16.8  0.0035  0.0035  25.2  2.4  22   1-22   1-22  (287)
2 Q_Novo_D4403_p3/1-287 2.0   0.058   0.058   17.4  2.4  21   236-256 246-266 (287)

No 1
>Q_Novo_D4403_p3/1-287
Probab=16.84  E-value=0.0035  Score=25.16  Aligned_cols=22  Identities=14%  Similarity=0.181  Sum_probs=0.0  Template_Neff=8.900

Q ss_pred          CCCcchHHHHHHHHHHHHHHHHHHHHHHH
Q Q_Rv0817c_p3    1 MPMRKVLVGTVGAIVVAVLIV  22 (270)
Q Consensus        1 m~~rr~~r~~~lvvvvl~~  22 (270)
                  |+|+|...+.++||||||+.++
T Consensus        1 M~~~~~l~~~l~~~C  22 (287)
T Q_Novo_D4403_p  1 MRTRRYVTAAALTASLLTLPAC 22 (287)
T ss_pred          CchHHHHHHHHHHHHHHHHHHHHHc

No 2
>Q_Novo_D4403_p3/1-287
Probab=1.97  E-value=0.058  Score=17.39  Aligned_cols=21  Identities=10%  Similarity=0.039  Sum_probs=0.0  Template_Neff=8.900

Q ss_pred          CCCccceEEEEeCCeEEEEEE
Q Q_Rv0817c_p3    236 PFGVVNPNTVGARGSDVIIEGI 256 (270)
Q Consensus        236 P~g1~~~v~v~~g1~v~~~ 256 (270)
                  |..+..+..+..++..+
T Consensus        246 P~~v~~~~~l~~~l~~~ 266 (287)
T Q_Novo_D4403_p  246 PRELQYGGYELDGKRLVRLRG 266 (287)
T ss_pred          ceEEEEeCCeEEEEEE
```

Rv0817c vs. DUF2140

```
Query          Q_LactoD2140_p3
Match_columns  205
No_of_seqs    105 out of 112
Neff          7.36164
Searched_HMMs 1
Date           Wed Aug 15 00:04:20 2018
Command        hhsearch -cpu 8 -i ..../results/full.a3m -d ..../results/db -o ..../results/LactoD2140_v_Rv0817c.hhr -oa3m
..../results/LactoD2140_v_Rv0817c.a3m -p 20 -Z 250 -loc -z 1 -b 1 -B 250 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -context /cluster/toolkit/production/biopros/tools/hh-suite-build/data/context_data.crf

No Hit          Prob E-value P-value Score   SS Cols Query HMM  Template HMM
1 Q_Rv0817c_p3  95.0 8.9E-06 8.9E-06  40.3  14.7  162   16-177  2-256 (270)

No 1
>Q_Rv0817c_p3
Probab=95.02  E-value=8.9e-06  Score=40.31  Aligned_cols=162  Identities=11%  Similarity=-0.004  Sum_probs=0.0  Template_Neff=8.900

Q ss_pred          ccCCHHHHHHHHHHHHHHHHHHHHHHhCCC-----
Q Q_LactoD2140_p  16 SMINWWKWAFLILIGLILGSIWFTKTVLAP----- 47 (205)
Q Consensus        16 ~~N-WK-AF~~L1~l~----- 47 (205)
                  .++||++..++|||||||||++. -. ....
T Consensus        2 ~~~rr~~r~~~~ivvvvl~~l~v~ad~a~~ae~~ia~~l~~~~l~~~p~v~i~g~PfL~qL~~G~~~v~v~~~ 81 (270)
T Q_Rv0817c_p3    2 PMRKVLVGTVGAIVVAVLIVGAVGADFGASIAYEYRLSTTVRKAANLRSDFVAILRFFFIPQAMREHYAELEIKAFAV 81 (270)
T ss_pred          CCcchHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCCeEEccCccHHHhcccCeEEEEecccc

Q ss_pred          -----CcCcccccccccCCCCeEEEEeCHHHHHHHHHHH-----HHHHhccCCCCceEEEEE
Q Q_LactoD2140_p  48 -----SLNTATETKTISNDPVFTVKVTSSANRIMAH-----YLTKYLKDSPIKYAVTLG 97 (205)
Q Consensus        48 -----~~~~~v~v~ln~li~~~l~~~~y~v~~~ 97 (205)
                  .....+....++..+||+++. -.....-.....
T Consensus        82 ~~~~~V~~~~~a~~~~~l~~~L~~~~~g~~~~~ 161 (270)
T Q_Rv0817c_p3    82 EHAGSGTATEATMHSIDLSYASWLRFDALKPVGELRESRIIDSMHGRYLGISDLMVAPRQESNDATGGTTESGISG 161 (270)
T ss_pred          eCCCCeEEEEeccccCHHHhccCCCCCeEEEEEeccccCCCCCCCCcccccccc

Q ss_pred          CCCCCCCCCCCcCCCCeEEEEeEE--cCCCCeEEeEEc---cccCCHHHHHHHHHh----cCCCCeEE
Q Q_LactoD2140_p  98 NNEAALNSFKPLGNNVFKQLTFDPLV--LNKGVDLLKSKKLNVG----TLPVPISFVMSYIGH-----YKIPSWSL 165 (205)
Q Consensus        98 ~d~v~l~g~~~lg~~~l~~~p~V~~~nGn1~L~~~i~vG~~~l~LP~~~vL~~~i~~~~~lP~wV~i 165 (205)
                  .+.+.+.|++..+..++...+. +..|.++..+..+ +..+|...-..+. ..|+.+
T Consensus        162 ~~~~g~~~g~~~v~~~v~~~l~~~1~~~1~~~~~1p~~~LP~g1~~ 241 (270)
T Q_Rv0817c_p3    162 SRGLVFSGTPISANFAHRVSVLVDSLVSASDDRATLVIPTAVTGPDTADQPVPDDKRDAVLFHAFASKLPNQKLPGVVP 241 (270)
T ss_pred          ccceEEeeeecCCCCeEEEEEecCCCCeEEEEEecCCCCeEEEEEecCCCCCCCCCCCCCCCCCCCCCCCC
```

Takeout vs. YceB

```

Query          Q_Takeout_p3
Match_columns  249
No_of_seqs    110 out of 115
Neff          9.96623
Searched_HMMs 1
Date          Sun Oct 28 23:38:53 2018
Command        hhsearch -cpu 8 -i ../../results/full.a3m -d ../../results/db -o ../../results/Takeout_v_YceB.hhr -oa3m
../../results/Takeout_v_YceB.a3m -p 0 -Z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -
-contxt /cluster/toolkit/production/biopros/tools/hh-suite-build/data/context_data.crf

No Hit           Prob E-value P-value  Score   SS Cols Query HMM  Template HMM
1 Q_YceB_p3     2.7   0.067  0.067   15.0  7.7   68 109-177  52-119 (186)

No 1
>Q_YceB_p3
Probab=2.72  E-value=0.067  Score=15.04  Aligned_cols=68  Identities=9%  Similarity=0.067  Sum_probs=0.0  Template_Neff=8.100

Q ss_pred       eEEEEEEEEEccEEEEEEEEEeeeecccccccccccccccccccccccccccccccccccccccc
Q Q_Takeout_p3  109 AKHEVKIVTKTFSLVGPVNIQGKVLILPISGTVQSNMTMVNRRAIVSFSGKPLVKNGETYLVDVLK 177 (249)
Q Consensus     109 ~~~~~p~l~~~g~y~~~g~~~~i~g~g~~~~~l~i~~~~~ 177 (249)
T Consensus     52 ~~~v~l~~~v~l~~~~r~l~~~~~s~l~~~~~a~l~~~~~Yd~~~~~aiyl~~~~~i~ 119 (186)
T Q_YceB_p3     52 ADAHIVLTNLTSQI-GREEPNPKVTLTGDNLMNSLFGSQRATMKLKALPVDFEKGAIFLKEMEVV 119 (186)
T ss_pred        eeEEEEEEecCeeee-cccccccccEEEEEeeeeccccCCCCcEEEecCCCeEEEecEEE


```

Takeout vs. DUF4403-C

```

Query          Q_Novo_D4403C_p3
Match_columns  202
No_of_seqs    100 out of 113
Neff          8.36093
Searched_HMMs 1
Date          Wed Aug 15 08:41:35 2018
Command        hhsearch -cpu 8 -i ../../results/full.a3m -d ../../results/db -o ../../results/NovoD4403C_v_Takeout.hhr -oa3m
../../results/NovoD4403C_v_Takeout.a3m -p 0 -Z 250 -loc -z 1 -b 1 -B 250 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -
-contxt /cluster/toolkit/production/biopros/tools/hh-suite-build/data/context_data.crf

No Hit           Prob E-value P-value  Score   SS Cols Query HMM  Template HMM
1 Q_Takeout_p3  30.8  0.0072  0.0072  21.1  6.9  99 50-161  128-226 (249)
2 Q_Takeout_p3  0.1   0.58   0.58   8.9   5.2  36 167-202  111-147 (249)

No 1
>Q_Takeout_p3
Probab=30.77  E-value=0.0072  Score=21.12  Aligned_cols=99  Identities=13%  Similarity=0.233  Sum_probs=0.0  Template_Neff=10.000

Q ss_pred       cEEEEEEEEEccEEEEEEEEEccCCCCcccccEEEEEeeeeccccCCCCCCCCCCcCcchHHHHHHHHHhC
Q Q_Novo_D4403C_ 50 VKADFRKVITIYGTGGRIVAVGEFTATDQAGRVTGKCTVWMTGVPVNADESRRIGFENFVEVSGTDDMTGGLNLIRLANT 129 (202)
Q Consensus     50 ~~i~i~~v~i~g~y~l~l~~a~~~~~g~~~~G~iy~l~g~P~~D~~~~~l~d~~~~~t~~~l~~~a~l~~~ 129 (202)
T Consensus     128 ~~g~~~~~i~g~g~~~~~l~~~~~a~~~~~n~~~~~a~~~~~n~~~~~i~~~~~ 194 (249)
T Q_Takeout_p3  128 IQGKVLLILPISTGQSNMTM-----VNVRAlVSFSGKPLVKNGETYLVDVLKITMKPESSHYHFSNLFNGD 194 (249)
T ss_pred        EEEEEEeeeeccccEEEEE-----EEEEEeeeeccccEEEEEecCCCC

Q ss_pred       cchHHHHHHHHccccchHHHHHHHHHHHHHHHHHC
Q Q_Novo_D4403C_ 130 PGMAHTIAALAQNPFENDYNKLLVKIDRAIED 161 (202)
Q Consensus     130 ~~i~~~l~~~l~~~l~~~l~~~i~~~L~~ 161 (202)
T Consensus     195 ~~~~~n~~~in~~~~~i~~~~~ 226 (249)
T Q_Takeout_p3  195 KALGDNMNVLNENSEA1YKETAKAIDRSFGK 226 (249)
T ss_pred        HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH


```

Takeout vs. DUF4403-N

```

Query          Q_Takeout_p3
Match_columns  249
No_of_seqs    110 out of 115
Neff          9.96623
Searched_HMMs 1
Date          Sun Oct 28 23:33:50 2018
Command        hhsearch -cpu 8 -i ../../results/full.a3m -d ../../results/db -o ../../results/Takeout_v_D4403N.hhr -oa3m
../../results/Takeout_v_D4403N.a3m -p 0 -Z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -
-contxt /cluster/toolkit/production/biopros/tools/hh-suite-build/data/context_data.crf

No Hit           Prob E-value P-value  Score   SS Cols Query HMM  Template HMM
1 Q_Novo_D4403_p3/1-287  0.6   0.23   0.23   12.8  22.8  198  2-239  8-227 (287)

No 1
>Q_Novo_D4403_p3/1-287
Probab=0.62  E-value=0.23  Score=12.82  Aligned_cols=198  Identities=11%  Similarity=-0.003  Sum_probs=0.0  Template_Neff=8.900

Q ss_pred       HHHHHHHHHHHHHHccccCCCCccccc-----
Q Q_Takeout_p3  2 FAIAFAVVLCLLVSVDAKFPEDPKPCKYGDG-----ECIMKLCNTLFSENSAEGDPGINLMQLDPLKVD 65 (249)
Q Consensus     2 ~~~i~~~~~c~~~~d-----ci~~~~~r~~~~~G~p~g~IP~1DPL~i~ 65 (249)
T Consensus     8 ~~~~~l~~~c~~~~p~~~~~S~i~vpi~i~l~~l~~~in~~lp~l~~~~~ 82 (287)
T Q_Novo_D4403_p 8 TAAALTASLTLPACHRDRDEPPRAHDAIKVDPQASLITVPIHADIGNLAALAEERIPRTLWITDKPGQTCVPS 82 (287)
T ss_pred        HHHHHHHHHHHHHccccCCCCCCCCCCCCCCCCcEEEeeeeccccCCCCccccC-----

Q ss_pred       ceEEEcCCCCCCcEEEeeeeEEEEEccccCeeEEEEEeCcEEEEEEEEEeeeeeeEEE
Q Q_Takeout_p3  66 RMVISQGESSSPVGITLTFDTNLLYGKIDQRIVKVKGFRDLTAKHEVKIVTKTFSLVGPVNIQGKVLLPISGTCQSNN 145 (249)
Q Consensus     66 ~~~~~n~~~~Gls~~~i~~~~~p~~~~~l~~~~~g~y~~~g~~~~~i~g~g~~~ 145 (249)
T Consensus     83 -----rg~i~v~~~~~1~~~Pi~~~~~ 133 (287)


```



```

T ss_pred      -CCCCCceEEEEeeEEEEhHHhCCeEEEEEEeCCEEEeeeCc

Takeout vs. AsmA-N

Query      Q_AsmA1_180_p3
Match_columns 180
No_of_seqs 184 out of 186
Neff        10.5998
Searched_HMMs 1
Date        Thu Aug 16 12:57:40 2018
Command     hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/AsmA_N_v_Takeout.hhr -oa3m
../results/AsmA_N_v_Takeout.a3m -p 20 -Z 250 -loc -z 1 -b 1 -B 250 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -
context /cluster/toolkit/production/biopros/tools/hh-suite-build/data/context_data.crf

No Hit          Prob E-value P-value Score SS Cols Query HMM Template HMM
1 Q_Takeout_p3   3.0   0.038   0.038   15.3  2.1   18   1-18   1-18   (249)

No 1
>Q_Takeout_p3
Probab=2.98 E-value=0.038 Score=15.33 Aligned_cols=18 Identities=22% Similarity=0.263 Sum_probs=0.0 Template_Neff=10.000

Q ss_pred      ChHHHHHHHHHHHHHHHHHHH
Q Q_AsmA1_180_p3 1 MRRFLTTLMILLVILVAG 18 (180)
Q Consensus    1 mF~~~~~l~~~ 18 (180)
               ||.++..+++.++...+.
T Consensus    1 M~i~~~~~ 18 (249)
T Q_Takeout_p3 1 MFAIAFAVVVLCLLVSVDA 18 (249)
T ss_pred      CHHHHHHHHHHHHHHHhcc

```

Figure 4C

AsmA-N vs. Rv0817c-N – as above.

Chorein-N vs. Rv0817c-N

```

Query      Q_Rv0817c_p3/1-130
Match_columns 130
No_of_seqs 104 out of 126
Neff        8.2142
Searched_HMMs 1
Date        Mon Oct 22 16:46:50 2018
Command     hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/Rv0817c130_v_ChorN115_p3_1.hhr -oa3m
../results/Rv0817c130_v_ChorN115_p3_1.a3m -p 0 -Z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres
32000 -context /cluster/toolkit/production/biopros/tools/hh-suite-build/data/context_data.crf

No Hit          Prob E-value P-value Score SS Cols Query HMM Template HMM
1 Q_ChorN115_p3 54.6  0.00029  0.00029  24.0  1.8   37   59-100  50-86   (115)
2 Q_ChorN115_p3 6.4    0.022    0.022    14.8  4.6   39   92-130  33-73   (115)

No 1
>Q_ChorN115_p3
Probab=54.57 E-value=0.00029 Score=23.96 Aligned_cols=37 Identities=11% Similarity=0.217 Sum_probs=0.0 Template_Neff=7.900

Q ss_pred      CCcchHHHhCcCcEEEEecccC
Q Q_Rv0817c_p3/1 59 RFPFIFQAMREHYAELIKAFAVEHAGSGTATL
Q Consensus    59 g~P~L~q1~~G~~~v~v~~~~~V~~ 100 (130)
               +..|.|.+..++|+|..|...+....+....|||+
T Consensus    50 ~lp~~~v~~g~ig~l~i~ip~~~w~~~s~pv~i~dv~i 86 (115)
T Q_ChorN115_p3 50 NLPV--IISKGILKTLEVEVP---WKS1KTDPFKIKKGHLI 86 (115)
T ss_pred      CCCE--EEEEEeEEEEE---chhcCCCCEEEeEEE

```

Chorein-N vs. AsmA-N

```

Query      Q_AsmA1_180_p3
Match_columns 180
No_of_seqs 184 out of 186
Neff        10.5998
Searched_HMMs 1
Date        Tue Aug 21 22:48:10 2018
Command     hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/AsmANP3_v_ChorNP3.hhr -oa3m
../results/AsmANP3_v_ChorNP3.a3m -p 0 -Z 250 -loc -z 1 -b 1 -B 250 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -
context /cluster/toolkit/production/biopros/tools/hh-suite-build/data/context_data.crf

No Hit          Prob E-value P-value Score SS Cols Query HMM Template HMM
1 Q_ChorN115_p3 92.7  1E-05   1E-05   30.0  6.4   89   31-122  1-97   (115)
2 Q_ChorN115_p3 0.1    0.47    0.47    7.8   6.3   39   142-180  50-92   (115)

No 1
>Q_ChorN115_p3
Probab=92.69 E-value=1e-05 Score=29.99 Aligned_cols=89 Identities=15% Similarity=0.121 Sum_probs=0.0 Template_Neff=7.900

Q ss_pred      HHHHHHHHHHHHHCeEE-ecCcEEcccEEEEEcccCCCCC-----EEEEEeEEEehHHhCCeEEE
Q Q_AsmA1_180_p3 31 FRDYMVKQVAARSGYQLQ-LDGPLRWHVWPQLSILSGRMSLTQGASQP-----LVRADNMRLDVALLPLLSHQLSVK 102 (180)
Q Consensus    31 ~~~~i~~~~~g~~v~i~~~~~p~~i~~~v~~~~~l~i~l~~~l~~~~~Ll~~~i~i~ 102 (180)
               ++.++..++..+=+ .++....-....++..++..++..+|+++,+
T Consensus    1 le~~~v~~~l~~L~g~y~i~~~~~l~~~l~i~G~i~L~n~l~l~~~~~lp~~~v~~g~ig~l~i~ip~w~l~s~pv--- 77 (115)
T Q_ChorN115_p3 1 FESLIADFLTKTIGKYIEDLDVNVSVSVLWNNGNVLKNLQVKKDACSALNLPVIISKGILKTLEVEVPWKS1KTDPF--- 77 (115)
T ss_pred      CHHHHHHHHHhHHHHhCChhcEEEeCeEEEEEeChhHHhCCCEEEEEEeEEEEEeChhCCC--~
               EEEEeCCEEeeCcCcCCCC
Q Q_AsmA1_180_p3 103 QVMLKGAVIDLPTQTEAVRS 122 (180)
Q Consensus    103 ~i~l~~~~v~l~~~~g~~~ 122 (180)

```


Q Q_AsmA1_180_p3	1 MRRFLTTL MILLV L VAGLS ALV LLV NP ND F RD YM V K QVA ARSGY QL Q LD GP LR WH V WP Q LS ILS GRMS LT A QG AS Q PLV	80 (180)
Q Consensus	1 mK~~~~~1~~~~~i~~~~~g~~~v~~~~~p~~~i~~~~~v~~~~~l	80 (180)
T Consensus	1 +. +++.+++++ .+++. .+ . +++. . +.+. +. +++.+++++ .+++. .+ . +++. . +.+	72 (150)
T Q_TamB1_150_p3	1 MK~~~r~~~~~l~i~~~~~l~t~g~~~~~l~i~~~~~G~l~~~~~l~v~~~~~l	72 (150)
T ss_pred	CchHHHHHHHHHHHHHHHHHHHHHHHHCCChhHHHHHHHHHHCCC-eEEEEeeec---cEEEeEEeC---CEE	
Q ss_pred	EEeeEEEehHHhCcEeEEEEeeecCCCCCCCCCCCCCCCcCCCCcccccccEEEee	
Q Q_AsmA1_180_p3	81 RADNMRLDVALLPLLSHQLSVKQVMLKGAVIQLTPQTEAVRSEDAPVAPRDNTLPDLSDDRGWSFDISSLKVADSVL VFQ	160 (180)
Q Consensus	81 ~i~~l~~~Ll~~~i~i~~l~~~v~~l~~~g~~~~~i~~~1~~~i~~~	160 (180)
T Consensus	73 ~~~~l~~~l~~~Ll~~~i~i~~l~~~i~~~i~~~i~~~~~1P~i~~i~~l~i~~~l~~~	148 (150)
T Q_TamB1_150_p3	73 KAGNLHLAVGLECLWNSSVCINDLALKDIQVNIDSKMPPSEQVEEEDSGPLDLS---TPYFIFTLTRVALDNVNIKID	148 (150)
T ss_pred	EEEEEeeeeCHhCcEEEEEeeccEEEecCCCCcccccccCCCCCCCC---CCceEEecEEEEee	
Q ss_pred	c	
Q Q_AsmA1_180_p3	161 H 161 (180)	
Q Consensus	161 d 161 (180)	
T Consensus	149 d 149 (150)	
T Q_TamB1_150_p3	149 D 149 (150)	
T ss_pred	C	

AsmA-N vs. TamB-N (BLASTx1)

```

Query          Q_AsmA1_180_p3
Match_columns  180
No_of_seqs     184 out of 186
Neff           10.5998
Searched_HMMs 1
Date          Fri Aug 24 11:05:04 2018
Command         hhsearch -cpu 8 -i ..../results/full.a3m -d ..../results/db -o ..../results/AsmA_Np3_v_TamB_p1.hhr -oa3m
               ..../results/AsmA_Np3_v_TamB_p1.a3m -p 20 -Z 250 -loc -z 1 -b 1 -B 250 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -contxt /cluster/toolkit/production/bioprogs/tools/hh-suite-build/data/context_data.crf

      No Hit          Prob E-value P-value Score    SS Cols Query HMM   Template HMM
      1 Q_TamB1_150_p1    99.0 1.5E-14 1.5E-14   73.8  17.3  149    1-161    1-149 (150)

No 1
>Q_TamB1_150_p1
Prbab=99.01 E-value=1.5e-14 Score=73.79 Aligned_cols=149 Identities=12% Similarity=0.190 Sum_probs=0.0 Template_Neff=6.700

Q ss_pred       ChHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
Q Q_AsmA1_180_p3 1 MRRFLTTL MILLV L VAGLS ALV LLV NP ND F RD YM V K QVA ARSGY QL Q LD GP LR WH V WP Q LS ILS GRMS LT A QG AS Q PLV
Q Consensus     1 mK~~~~~1~~~~~i~~~~~g~~~v~~~~~p~~~i~~~~~v~~~~~l
T Consensus     1 |||+.|+++.+++++|||||||.+++.|||||.+|. +++.|||||. +.+.|||+.|+++.+++++|||||||.+++.|||||.+|. +++.|||||. +.+
T Q_TamB1_150_p1 1 M~~~kki~l~~~~~l1~~~~~l1~T~G~~~~~a~k~vpg-L~I~~~v~G~~~~~l~~~ltL~~~v~y~~~~~gv~v
T ss_pred       1 MSLWKRKISLGVVIVILLLGSAFLVGTGLHVFKAADRWVPG-LDIGKVTGG-WRD-LTLSDVRYEQP-GVAV
                CchHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCC-eEEEEeecc---ccc-cEEEeEEeC---CEE

Q ss_pred       EEeeEEEehHHhCcEeEEEEeeecCCCCCCCCCCCCCCCcCCCCcccccccEEEee
Q Q_AsmA1_180_p3 81 RADNMRLDVALLPLLSHQLSVKQVMLKGAVIQLTPQTEAVRSEDAPVAPRDNTLPDLSDDRGWSFDISSLKVADSVL VFQ
Q Consensus     81 ~i~~l~~~Ll~~~i~i~~l~~~v~~l~~~g~~~~~i~~~1~~~i~~~
T Consensus     73 ~~~~l~~~l~~~Ll~~~i~i~~l~~~i~~~i~~~i~~~~~1P~pI~l~~~l~n~i~l~id
T Q_TamB1_150_p1 73 KAGNLHLAVGLECLWNSSVCINDLALKDIQVNIDSKMPPSEQVEEEDSGPLDLS---TPYFIFTLTRVALDNVNIKID
T ss_pred       EEeeeEEEehHHhCcEEEEEeeccEEEecCCCCcccccccCCCCCCCC-eEEEeEEec--EE

Q ss_pred       c
Q Q_AsmA1_180_p3 161 H 161 (180)
Q Consensus     161 d 161 (180)
T Consensus     149 d 149 (150)
T Q_TamB1_150_p1 149 D 149 (150)
T ss_pred       C

```

Chorein-N vs. TamB-N

```

Query          Q_TamB1_150_p3
Match_columns  150
No_of_seqs     101 out of 104
Neff           9.26937
Searched_HMMs 1
Date          Mon Oct 22 17:17:55 2018
Command         hhsearch -cpu 8 -i ..../results/full.a3m -d ..../results/db -o ..../results/TamB150_v_ChorN115_p3.hhr -oa3m
               ..../results/TamB150_v_ChorN115_p3.a3m -p 0 -Z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -contxt /cluster/toolkit/production/bioprogs/tools/hh-suite-build/data/context_data.crf

      No Hit          Prob E-value P-value Score    SS Cols Query HMM   Template HMM
      1 Q_ChorN115_p3   94.6 1.9E-06 1.9E-06   34.1   6.9   85  29-116   3-99 (115)
      2 Q_ChorN115_p3   4.3   0.031   0.031    14.0   3.1   21  128-148   48-68 (115)

No 1
>Q_ChorN115_p3
Prbab=94.62 E-value=1.9e-06 Score=34.13 Aligned_cols=85 Identities=9% Similarity=0.177 Sum_probs=0.0 Template_Neff=7.900

Q ss_pred       hhHHHHHHHHHHHHCCCeEEEEeecc-C-EEEEeEEEEEeCCEE-----EEEEEeeeeHHHHhCcEEEEE
Q Q_TamB1_150_p3 29 TSGLHLVFKAADRWVPGLDIGKVTGGWR-D-LTLSDVRYEQPGVA-----VKAGNLHLAVGLECLWNSSVCINDL
Q Consensus     29 ~g~~~~~l~~~~~i~~~G~l~~~~~i~~~~~v~~~~~l~~~l~i~~~l~~~~~Ll~~~l~i~~~l
                ..-+--+..+...+++-+...+ | +--+|+..+.-.++-+...+--+|...+--+|.-+..+...+--+
T Consensus     3 ~v~~~l~~~Lg~yi~~~~~l~~~~~l~G~i~L~n~L~~~~~lp~v~y~g~ig~l~i~Pw~s~p~-i
T Q_ChorN115_p3 3 SLIADFLTKTIGKYIEDLDVNSVSVLWNNGVLQNLQVKKDACSAFNLPVIISKGLKTLEVEVPWPKS1KTPF---KI
T ss_pred       HHHHHHHHHHhHHHHhCcChhCeeEEEeeeeEEEeeeeHHHHhCCCEEEEEEchhcCCCC--EE

```

```

Q ss_pred          EEEcceEEEEecCCCCCccc
Q Q_Tamb1_150_p3   97 ALKDIQVNIDSKKMPPSEQV  116 (150)
Q Consensus        97 ~~~~~~i~~~~~ 116 (150)
                           ++++++.+.+....+
T Consensus        80 ~i~dv~i~l~p~~~~~ 99 (115)
T Q_ChorN115_p3    80 KIKGLHIIISQPQTVFVFDAE  99 (115)
T ss_pred          EEEEeEEEEEEeCCcCCCCCHH

```

Chorein-N vs. TambB-N (BLASTx1)

```

Query          Q_Tamb1_150_p1
Match_columns  150
No_of_seqs     102 out of 106
Neff           6.69682
Searched_HMMs 1
Date           Fri Aug 24 11:03:23 2018
Command        hhsearch -cpu 8 -i ../results/full.a3m -d ..../results/db -o ..../results/Tamb150p1_v_ChorN115_p3.hhr -oa3m
..../results/Tamb150p1_v_ChorN115_p3.a3m -p 20 -Z 250 -loc -z 1 -b 1 -B 250 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres
32000 -context /cluster/toolkit/production/bioprogs/tools/hh-suite-build/data/context_data.crf

No Hit          Prob E-value P-value Score SS Cols Query HMM Template HMM
1 Q_ChorN115_p3 86.4 6.6E-05 6.6E-05 29.2 6.0 83 33-118 7-101 (115)

No 1
>Q_ChorN115_p3
Probab=86.37  E-value=6.6e-05  Score=29.23  Aligned_cols=83  Identities=12%  Similarity=0.256  Sum_probs=0.0  Template_Neff=7.900

Q ss_pred          HHHHHHHHHHHCCCCCCCCCC-cEEEEEchHHhhCCeEEEEEECCE-----
Q Q_Tamb1_150_p1   33 HLVFKAADRWVPGLDIGKVTGG-WRD-LTLSDRVYEQPGV-----AVKAGNLHLAVGLECLWNSSVCINDALKD 100 (150)
Q Consensus        33 ~~~~a~k~vpgL-I~~v~G~l~~-itL~~v~y~~gv-----v~~~l~L~l~~~CL~~~1C1~~~1~~~ 100 (150)
                           .++-+...++,.++-+-.++= |++ ++|+|+.++-+-.++-+..+.| .+|
T Consensus        7 ~~~~Lg~y~i~~~~~l~~~l~~~G~i~L~n~L~~~~~lp~~v~g~ig~l~i~Pw~1~s~pv~1---i~d 83 (115)
T Q_ChorN115_p3    7 DFLTKTIGKYIEBDLVNSVSVSLWNGNVQLKNLQVKKDACS AFNLPVIISK GILKTLEVEVPWKSIKTD FKI---KIKG 83 (115)
T ss_pred          HHHHHHHHHHHhCcHHhceEEEEEchHHhCCCCCCCC--EEe

Q ss_pred          eEEEcCCCCCCCCCCC
Q Q_Tamb1_150_p1   101 IQVNIDSKKMPPSEQVEE 118 (150)
Q Consensus        101 ~~v~l~~~p~~~~~ 118 (150)
                           .+.-+...++..+++
T Consensus        84 v~i~l~p~~~~~ 101 (115)
T Q_ChorN115_p3    84 LHIISQPQTVFVFDAEQY 101 (115)
T ss_pred          EEEEeCcCCCCCCCCHHH

```

Mdm31p (131-312) vs. Rv0817c

```

Query          Q_Mdm31_b3/131-312
Match_columns  182
No_of_seqs     104 out of 136
Neff           6.14424
Searched_HMMs 1
Date           Thu Jul 11 16:23:47 2019
Command        hhsearch -cpu 8 -i ..../results/full.a3m -d ..../results/db -o ..../results/Mdm31cut_v_Rv0817cdTMH.hhr -oa3m
..../results/Mdm31cut_v_Rv0817cdTMH.a3m -p 0 -Z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -realign -mact 0.3 -
maxres 32000 -context /cluster/toolkit/production/bioprogs/tools/hh-suite-build/data/context_data.crf

No Hit          Prob E-value P-value Score SS Cols Query HMM Template HMM
1 Q_Rv0817c_p3/30-130 0.2 0.38 0.38 9.1 8.9 39 17-57 10-49 (101)

No 1
>Q_Rv0817c_p3/30-130
Probab=0.19  E-value=0.38  Score=9.13  Aligned_cols=39  Identities=8%  Similarity=0.089  Sum_probs=16.9  Template_Neff=8.500

Q ss_pred          HHHHHHHHHhCcEEEcCc-CCCCCCCCeEEEEEE
Q Q_Mdm31_b3/131  17 LASKIGKFITKNESLSIVFESA-IVPDWSSKGISFQKVVFVSR 57 (182)
Q Consensus        17 va~~ig~~lt~~tGi~V-Fesa-ivP-Wkdc~I-f~NV~V~~
                           ++-+.-+....|.|+.++|..-|++ ..|..-
T Consensus        10 va~~l~~~l~~~p~V~i~g~P~L~q~l~~~v~i~~ 49 (101)
T Q_Rv0817c_p3/3  10 LSTTVRKAANLRSDFFVAILRFPFIPQAMREHY--AELEIKA 49 (101)
T ss_pred          HHHHHHHCCCCCCCC--EEeCcchHHHHcccc--ceEEEEEe
Confidence        3333333222233345555542 4555556554 4444433

```

Mdm31p (131-312) vs. Chorein-N

```

Query          Q_Vps13chorN_p3
Match_columns  127
No_of_seqs     128 out of 132
Neff           7.9632
Searched_HMMs 1
Date           Thu Jul 11 16:19:52 2019
Command        hhsearch -cpu 8 -i ..../results/full.a3m -d ..../results/db -o ..../results/ChoreindNp3_v_Mdm31cut.hhr -oa3m
..../results/ChoreindNp3_v_Mdm31cut.a3m -p 0 -Z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -realign -mact 0.3 -
maxres 32000 -context /cluster/toolkit/production/bioprogs/tools/hh-suite-build/data/context_data.crf

No Hit          Prob E-value P-value Score SS Cols Query HMM Template HMM
1 Q_Mdm31_b3/131-312 56.9 0.0019 0.0019 22.4 7.9 63 30-92 43-138 (182)
2 Q_Mdm31_b3/131-312 0.7 0.17 0.17 12.0 4.4 28 16-43 96-129 (182)

No 1
>Q_Mdm31_b3/131-312
Probab=56.92  E-value=0.0019  Score=22.41  Aligned_cols=63  Identities=6%  Similarity=0.125  Sum_probs=36.6  Template_Neff=6.100

Q ss_pred          EEecEEEEEEeEEECHHHHH-----CCCEEEEEEeEEEEEEehhh-cccccE

```

Q_Q_Vps13chorN_p	30	VWNGKVRLDNLLEQLREALDQ-----LKLPINVIGHGLGHLVLIHPWKT-LASEQV	78 (127)
Q_Consensus	30	l~~~G~i~l~n~l~~~~l~~~~~1p~~~v~~~g~Ig~l~i~i~Pw~~~l~s~p~	78 (127)
T_Consensus	43	.~.~ .+++ .~.~+~-..	
T_Q_Mdm31_b3/131	43	WkdG~I~f~NV~V~~~~~n~t~fdl~Id~idvtLs1~kWl~GkGL	122 (182)
T_ss_pred		WSGGKISFQKVFSRPPKVSRGFTKGSQQDALQRAKLALSERILVNQQDFDNGNYTQFDLTIDQVDISLNFRKWINGKGI	122 (182)
Confidence		cCCCCeeeeEEEEEccccCCCCCccccCchHHHHHHHHhhhhhhcccccCChHHHHHHHHHHHHHH	
		001122245688888886444 333332	

Q_ss_pred		--EEEEEEEEEeC	
Q_Q_Vps13chorN_p	79	--KINIEDVFLLASPK	92 (127)
Q_Consensus	79	--~i~i~~v~1~l~~~	92 (127)
T_Consensus	123	.~+ .~ ~.~+~.~+	
T_Q_Mdm31_b3/131	123	I-d~~~I~GvrG~Vdr~	138 (182)
T_ss_pred		LDEVTINGLRGVIDRT	138 (182)
Confidence		eeEEEeceeEEECC	
		4778887777543	

No 2
>Q_Mdm31_b3/131-312
Probab=0.69 E-value=0.17 Score=12.04 Aligned_cols=28 Identities=25% Similarity=0.420 Sum_probs=15.4 Template_Neff=6.100

Q_ss_pred		HHHh-CCHHhC--eEEEE---ecEEEEeeEEC	
Q_Q_Vps13chorN_p	16	MVKV-NFDFPKQL--KWEVW---NGKVRLDNLLEQ	43 (127)
Q_Consensus	16	~yi~~~l~~~l~~~l~~~G~i~l~n~l~	43 (127)
T_Consensus	96	.~.~ .+++ .~.~+~-..	
T_Q_Mdm31_b3/131	96	n~t~fdl~Id~idvtLs1~kWl~GkGLI~d~I~	129 (182)
T_ss_pred		NYTQFDLTIDQVDISLNFRKWINGKILDEVTIN	129 (182)
Confidence		CeeeeEEEEEeeeeHHHhCCCCeeEEEe	
		3443 3444444 44553 58777777765	

Mdm31p (131-312) vs. AsmA-N

Query	Q_Mdm31_b3/131-312									
Match_columns	182									
No_of_seqs	104 out of 136									
Neff	6.14424									
Searched_HMMs	1									
Date	Thu Jul 11 16:26:32 2019									
Command	hhsearch -cpu 8 -i/results/full.a3m -d/results/db -o/results/Mdm31cut_v_AsmALLdNr.hhr -oa3m/results/Mdm31cut_v_AsmALLdNr.a3m -p 0 -z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -realign -mact 0.3 -maxres 32000 -context /cluster/toolkit/production/biopros/tools/hh-suite-build/data/context_data.crf									
No Hit		Prob	E-value	P-value	Score	SS	Cols	Query HMM	Template HMM	
1 Q_AsmA_p3/26-123		87.9	0.00016	0.00016	27.6	9.5	85	16-137	5-90 (98)	
No 1 >Q_AsmA_p3/26-123										
Probab=87.89 E-value=0.00016 Score=27.59 Aligned_cols=85 Identities=7% Similarity=0.058 Sum_probs=56.7 Template_Neff=8.100										
Q_ss_pred		HHHHHHHHHHhCcCEEEeCCCCCccccCchHHHHHHHHHHHHHHHHHHHH								
Q_Q_Mdm31_b3/131	16	YLASKIGKFITKNESSLIVFESAIVPDW-SSKGKISFQKVFSRPRKVSRGFTKGSQQDALQRAKLALSERILVNQQDFDN	94 (182)							
Q_Consensus	16	~va~~ig~~Lt~~~tGi~v~FesAivP~W~kdg~I~f~NV~v~~~~~								
T_Consensus	5	.~.~ ...++ .~.~+~.~+~.~ =.~ ++ ~.~+....								
T_Q_AsmA_p3/26-1	5	~k~i~~~v~~~tGr~~~I~G~l~~~P~i~~~v~~~								
T_ss_pred		DFRDYMKVQVAARSGYQLQLDGPLRWHVWPQLSILSGRMSLTAOGA-----								
Confidence		hHHHHHHHHHHHHHHCCCCeeCCCeeEEEecccCCCC-----								
		34456777788899999887543221 12225666666643110								
Q_ss_pred		CeeEEEEEeeeeEEEEEeHHHhCCCCeeEEEecccCCCC-----								
Q_Q_Mdm31_b3/131	95	GNYTQFDLTIDQVDISLNFRKWINGKILDEVTINGLRGVIDR	137 (182)							
Q_Consensus	95	n~t~fdl~Id~idvtLs1~kWl~GkGLI~d~I~GvrG~Vdr	137 (182)							
T_Consensus	51	-----l~pLl~g~i~~~l~i~~~l~p~i~l~	90 (98)							
T_Q_AsmA_p3/26-1	51	-SQPLVRADNMRLDVALLPLSLHQLSVQVMKGAVIDLTP	90 (98)							
T_ss_pred		-----CCCCeeeeEEEEEeHHHhCCCCeeEEEecccCCCC-----								
Confidence		1223789999999999999999999999988654433								

Mdm31p (131-312) vs. TamB-N

Query	Q_TamB1_150_p3/27-150									
Match_columns	124									
No_of_seqs	100 out of 104									
Neff	9.57656									
Searched_HMMs	1									
Date	Thu Jul 11 16:16:02 2019									
Command	hhsearch -cpu 8 -i/results/full.a3m -d/results/db -o/results/TamB_deLT_v_Mdm31cut.hhr -oa3m/results/TamB_deLT_v_Mdm31cut.a3m -p 0 -z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -context /cluster/toolkit/production/biopros/tools/hh-suite-build/data/context_data.crf									
No Hit		Prob	E-value	P-value	Score	SS	Cols	Query HMM	Template HMM	
1 Q_Mdm31_b3/131-312		96.7	1.8E-07	1.8E-07	39.9	12.9	118	1-121	9-174 (182)	
2 Q_Mdm31_b3/131-312					1.7	0.075	0.075	13.2	2.0	11 105-115 100-110 (182)
No 1 >Q_Mdm31_b3/131-312										
Probab=96.73 E-value=1.8e-07 Score=39.91 Aligned_cols=118 Identities=8% Similarity=0.184 Sum_probs=0.0 Template_Neff=6.100										
Q_ss_pred		CChhHHHHHHHHHHhCC--CcEEEEEeeeeC---c~EEEEEecccC-----								
Q_Q_TamB1_150_p3	1	GTTSLGHLVFKAADRWVP---GLDIGKVTGGWR---D-LTLSDVRYEQP-----								
Q_Consensus	1	~t~g~~~l~~~l~~~l~~~G~1~~~l~~~l~~~l~~~v~~~								
T_Consensus	9	+ -..++...++... ++ .-+-.-+... +++++ .~.~								
T_Q_Mdm31_b3/131	9	Nt~~~qe~v~a~~ig~~Lt~~~tGi~v~FesAivP~W~kdg~I~f~NV~v~~~								
T_ss_pred		NTVFAQEYLAASKIGKFITKNESSLIVFESAIVPDWSSKGKISFQKVFSRPRKVSRGFTKGSQQDALQRAKLALSERILVN								
Confidence		hhhhcHHHHHHHHHHHHhCCCCeeCCCccccCCCCeeEEEecccCCCC-----								

```

Q ss_pred      -----CEEEEEEEEEEeHHHhcCeEEEEEEEcceCCCCccccccccCCCCCCCCCcEEEEE
Q Q_TamB1_150_p3 43 -----GVAVKAGNLHLAGVLECLWNSSVCINDLALKDIQVNIDSKKMPPSEQVEEEEDSGPLDLSTPYFITLDRV 112 (124)
Q Consensus    43 -----~l~~~l~~~l~~~l~~~~~i~~~l~~~~~i~~~~~i~~~~~i~~~~~i~~~~~i~~~~~i~~~~~lP~~~i~~~l 112 (124)
          ...+++++.+ .+++.+.+=|=+.+.|+.+.+.+-.
T Consensus    89 ~~~~~~n+t-fdl~Id~idvTLS1~kW1~GKGLI~d~I~GvG~Vdr~~v~~~p~~~r~~~gdfel~~~ 165 (182)
T Q_Mdm31_b3/131 89 QQDFDNGNYTQFDLTIQVDSLNRKWINKGKILDEVTINGLRGVIDRTHVVWK--KDDDPKNLYNQPGDFEISKF 165 (182)
T ss_pred       cccccCCCeeEEEEEEEEEHHHHcCCCCeeEEEEecccCCCCcccC---CCChhHhccCCCCeeEee

Q ss_pred      EEEeeeEEE
Q Q_TamB1_150_p3 113 ALDNVNNIKI 121 (124)
Q Consensus    113 ~i~~~l~~ 121 (124)
          .|+|+.+++
T Consensus    166 ki~D~~vtv 174 (182)
T Q_Mdm31_b3/131 166 TMNDVLCTL 174 (182)
T ss_pred       EEEEEEEE

```

```

No 2
>Q_Mdm31_b3/131-312
Probab=1.73 E-value=0.075 Score=13.20 Aligned_cols=11 Identities=18% Similarity=0.619 Sum_probs=0.0 Template_Neff=6.100

Q ss_pred      ceEEEeeeEEE
Q Q_TamB1_150_p3 105 YFITLTRVALD 115 (124)
Q Consensus    105 ~~i~i~~1~i~ 115 (124)
          |++.|+++.|+
T Consensus    100 fdl~Id~idvt 110 (182)
T Q_Mdm31_b3/131 100 FDLTIDQVDIS 110 (182)
T ss_pred       EEEEEEEE

```

Mdm31p (131-312) vs. TamB-N (BLASTx1)

```

Query      Q_TamB1_150_p1/27-150
Match_columns 124
No_of_seqs 101 out of 106
Neff      6.74852
Searched_HMMs 1
Date        Thu Jul 11 16:17:17 2019
Command     hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/TamB_dTp1_v_Mdm31cut.hhr -oa3m
../results/TamB_dTp1_v_Mdm31cut.a3m -p 0 -Z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000
-ctxt /cluster/toolkit/production/bioprosgs/tools/hh-suite-build/data/context_data.cr
No Hit      Prob E-value P-value Score SS Cols Query HMM  Template HMM
1 Q_Mdm31_b3/131-312 91.2 2.9E-05 2.9E-05 33.0 7.9 77 44-123 100-176 (182)
2 Q_Mdm31_b3/131-312 1.3 0.094 0.094 14.0 2.0 14 60-73 43-56 (182)

No 1
>Q_Mdm31_b3/131-312
Probab=91.23 E-value=2.9E-05 Score=33.00 Aligned_cols=77 Identities=8% Similarity=0.239 Sum_probs=0.0 Template_Neff=6.100

Q ss_pred      EEEEEEchHHhccCeEEEEEEEcceEEEcCcCCCCCccccccccCCCCCCCCccccccccCCCCCCCCCcEEEEE
Q Q_TamB1_150_p1 44 VAVKAGNLHLAGVLECLWNSSVCINDLALKDIQVNIDSKKMPPSEQVEEEEDSGPLDLSTPYFITLDRV 123 (124)
Q Consensus    44 v-v~~~l~L~L~~~CL~~~1C1~~~l~~~~~v~~~~~i~~~~~p~~~~~s~~~~~i~~~~~i~~~~~lP~~~i~~~l~~~L~n~i~~~l~idd 123 (124)
          .+++++.+.|++.=.+.+-=|+++.+.|++-.|....-.|+....-.|-.+++.++|+.|.+
T Consensus    100 fdl~Id~idvtLS1~kW1~GKGLI~d~I~GvG~Vdr~~v~~~p~~~r~~~gdfel~~~ki~D~~vtv~q 176 (182)
T Q_Mdm31_b3/131 100 FDLTIDQVDISLNFRKWINKGKILDEVTINGLRGVIDRTHVVWK--KDDDPKNLYNQPGDFEISKF 176 (182)
T ss_pred       EEEEEEEEHHHHcCCCCeeEEEEecccCCCCCc---CCChhHhccCCCCeeEeeEEEEEEE

```

ALSO: BPI_N vs. BPI_C

```

Query      Q_BPI_N_p3
Match_columns 230
No_of_seqs 105 out of 119
Neff      9.811
Searched_HMMs 1
Date        Mon Jul  8 14:29:35 2019
Command     hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/BPI_N_v_C.hhr -oa3m ../results/BPI_N_v_C.a3m
-p 20 -Z 250 -loc -z 1 -b 1 -B 250 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -ctxt /cluster/toolkit/production/bioprosgs/tools/hh-suite-build/data/context_data.cr
No Hit      Prob E-value P-value Score SS Cols Query HMM  Template HMM
1 Q_BPI_C_p3 41.7 0.0044 0.0044 22.0 12.4 99 108-207 106-204 (237)

No 1
>Q_BPI_C_p3
Probab=41.73 E-value=0.0044 Score=22.01 Aligned_cols=99 Identities=9% Similarity=0.025 Sum_probs=0.0 Template_Neff=9.600

Q ss_pred      EEEEEEeEEEEEEEEEeEEEEEeEEEEEEeCCCCCCeEEEeeeeEEEEEeCcchHHHHH
Q Q_BPI_N_p3 108 KFSISANANIKISGKWAQRFKLMSGNFDLSIEGMSISADLKLSNPFTSGKPTITTCSRSSHINSVHHSKSKVGLIQ 187 (230)
Q Consensus    108 ~~~~~~i~g~~~~~g~~~~~i~~~~~l~~~~~g~~~v~~~C~~~i~v~i~~~~~l~n 187 (230)
          .+++...+.+..+...+.+...+.+...+.+...+.+...+.+...+.+...+.+...+.+...+.+...
T Consensus    106 ~~~~~~i~~~~~l~~~~~v~~~~~s~~~~~i~~~~~l~~~ 184 (237)
T Q_BPI_C_p3 106 HLSVQPTGLTFYPAVDVQAFAVLPNSS-LASLFLIGMHTGSMEVSAESNRVLGVGELKLDRLLELKHSNIGPFPVELLQD 184 (237)
T ss_pred       eEEEeCCCCeEEEEEEEEEeCCCC-eEEEEEEEEEeCCCC-eCCCCCCCCCCCCCCHHHHH

Q ss_pred      HHHHHHHHHHHHHHHHHHH
Q Q_BPI_N_p3 188 LFHKKKIESALRNKMNSQVCE 207 (230)
Q Consensus    188 ~~~~~i~~~i~~~v~~~i~~~l~ 207 (230)
          .+...+...+...+...
T Consensus    185 ~i~~~l~~~i~p~ln~~~l~ 204 (237)
T Q_BPI_C_p3 185 IMNYIVPILVLPFRNEKLQK 204 (237)
T ss_pred       HHHHHHhccHHHHHHHH

```