```
# hmmscan :: search sequence(s) against a profile database
# HMMER 3.2.1 (June 2018); http://hmmer.org/
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# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# query sequence file:             seq_YEAST05874.fa
# target HMM database:             /Users/ingo/src/protTrace/used_files/Pfam-A.hmm
# max ASCII text line length:      unlimited
# profile reporting threshold:     E-value <= 0.01
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

Query:        YEAST  [L=318]
Scores for complete sequence (score includes all domains):
   --- full sequence ---   --- best 1 domain ---   -#dom-
    E-value  score  bias    E-value  score  bias    exp  N  Model            Description
    -------  ------ -----    -------  ------ -----    ---- --  --------         -----------
    5.8e-80  268.2   0.1    6.9e-80  267.9   0.1    1.0  1  RrnaAD           Ribosomal RNA
adenine dimethylase
      3e-07   31.1   0.0    6.2e-07   30.0   0.0    1.6  1  Methyltransf_25  Methyltransferase
domain
    1.5e-05   25.5   0.0    3.5e-05   24.4   0.0    1.6  1  Methyltransf_11  Methyltransferase
domain
    0.00015   21.6   0.0    0.00029   20.7   0.0    1.4  1  PCMT             Protein-L-
isoaspartate(D-aspartate) O-methyltransferase (PCMT)
    0.00036   20.3   0.0    0.00061   19.6   0.0    1.3  1  Met_10           Met-10+ like-
protein
    0.0012   18.2   0.0     0.0031   16.8   0.0    1.6  2  CMAS             Mycolic acid
cyclopropane synthetase
    0.0021   17.9   0.0     0.0028   17.5   0.0    1.3  1  Methyltransf_23  Methyltransferase
domain
    0.0057   17.4   0.0      0.013   16.2   0.0    1.6  1  Methyltransf_12  Methyltransferase
domain
    0.0058   16.4   0.0      0.014   15.2   0.0    1.6  1  AAA_lid_4        RuvB AAA lid
domain
    0.0074   16.2   0.1       0.34   10.7   0.0    2.3  2  PRMT5            PRMT5 arginine-N-
methyltransferase


Domain annotation for each model (and alignments):
>> RrnaAD  Ribosomal RNA adenine dimethylase
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to    envfrom  env to
acc
 ---   ------ ----- --------- --------- -------  -------    ------- -------    ------- -------
----
   1 !  267.9   0.1   3.8e-83   6.9e-80        2     263 ..      28     280 ..      27
282 .. 0.98

  Alignments for each domain:
  == domain 1  score: 267.9 bits;  conditional E-value: 3.8e-83
            GCCXXGCG--EE--HHHHHHHHHHH-GGTTSEEEEES-TTTCCHHHHHCC-SEEEEE-S-
HHHHHHHHCHTT...TCCCEEEE-S-CCGHHHHHHHCTTTCCCCEEEEEEE--TTTHHHHHHHHHHHGGGGCEEEEEEEEEEHHHHHHHHH--
TTSTT-SHHHHHHHHHEEEEEEEEEC-GGCECS--SSSEEEEEEEE-SS-S--S-HHHHHHHHHHHHCTTTSBCCCHCCCTSTCHHHHHCTT.T--
TTTCCCCSGHHHHHHHHHHHH CS
  RrnaAD    2
nklrksygqnflknkkvineIldklnleekltvleigpGkGilTeeLakrakqvvvlElderLakllqkkls...kdeklkvvhqDflkfetpee
vtekdsihqeflvvanlPyeistqlvkqlleesrfglvkmllwlqkefarrllarpgskkrsrlsvlreaftdvklvakveksifsPppkvdsal
velerkdedlpqkdlkkyesvvrkllnrkrktlstslksllpggelqalsstgindnalvkklsaeqtldifkel 263
         +k+++++gq++lkn+ v+++I+dk+++++++ vle+gpG+G+lT++++++ak+vv++E+d+r+a++l+k+++     ++kl++
+  Df+k+e+p++          ++++n+Py+is++lv++l++++r++ + ++l++q+efa rllarpg+++++rls ++++++++v+++
+kv+k++f+Ppp+v+s++v+le+k+++ pq+d+++++ ++r+++++rk++t+s+ +ks++ ++ l++++++t++++n++++++++++++d++ke
  YEAST    28
FKFNTDLGQHILKNPLVAQGIVDKAQIRPSDVVLEVGPGTGNLTVRILEQAKNVVAVEMDPRMAAELTKRVRgtpVEKKLEIMLGDFMKTELPYF
D----------ICISNTPYQISSPLVFKLINQPRPP-
RVSILMFQREFALRLLARPGDSLYCRLSANVQMWANVTHIMKVGKNNFRPPPQVESSVVRLEIKNPR-
PQVDYNEWDGLLRIVFVRKNRTISAGFKSTTVMDILEKNYKTFLAMNNEMVDDTKGSMHDVVKEK 280

79***************************************************************999*****************7
7..........7*****************7.8899*******************************************************
*********.8***************************************************9986 PP


>> Methyltransf_25  Methyltransferase domain
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to    envfrom  env to
acc
 ---   ------ ----- --------- --------- -------  -------    ------- -------    ------- -------
----
   1 !   30.0   0.0   3.5e-10   6.2e-07        1      73 [.      60     129 ..      60
```

```
144 .. 0.88

  Alignments for each domain:
  == domain 1  score: 30.0 bits;  conditional E-value: 3.5e-10
                        EEEET-
TTSHHHHHHHCTSTSSEEEEEEESSHHHHHHHHHHHHHHTTT..TEEEEESBCCGBSSSTTTEEEEEEEST CS
  Methyltransf_25    1
vLdlGcGtGrltlalakrlgkakvtgvDiseemleaareraeeegl..nvefvqgdaedlpfedgsfDlvvssga 73
                        vL++G GtG+lt +++++   ++v++v+++++m ++  +r++   +  ++e++ gd+ + +++   fD+++s+
+
            YEAST  60 VLEVGPGTGNLTVRILEQA--KNVVAVEMDPRMAAELTKRVRGTPVekKLEIMLGDFMKTELPY--
FDICISN-T 129

9****************6..9****************88777999********9999886..***9995.3 PP

>> Methyltransf_11  Methyltransferase domain
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to    envfrom  env to
acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------    ------- -------
----
   1 !   24.4   0.0   1.9e-08   3.5e-05       1      68 [.      61     128 ..      61
138 .. 0.93

  Alignments for each domain:
  == domain 1  score: 24.4 bits;  conditional E-value: 1.9e-08
                        EEET-TTSHHHHHHHHHTTSEEEEEES-HHHHHHHHHHHCCHHT-..EEEETTEECCCTSS-TT-EEEEEEE CS
  Methyltransf_11    1 LdvGcGtGrlaealakrgarvvgvDlskemlklakekaseegl..kvefvvadaeklpfednsfDlvvss 68
                        L+vG GtG l+ + +++++vv+v+++++m +  +++++ ++ k+e++ +d+ k+ ++   fD+++s+
            YEAST  61 LEVGPGTGNLTVRILEQAKNVVAVEMDPRMAAELTKRVRGTPVekKLEIMLGDFMKTELPY--FDICISN
128

                        89*****************************999999999********988875..9999987 PP

>> PCMT  Protein-L-isoaspartate(D-aspartate) O-methyltransferase (PCMT)
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to    envfrom  env to
acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------    ------- -------
----
   1 !   20.7   0.0   1.6e-07   0.00029      59     160 ..      42     138 ..      18
144 .. 0.83

  Alignments for each domain:
  == domain 1  score: 20.7 bits;  conditional E-value: 1.6e-07
           HHHHHHHHHHTT--TT-EEEEES-TTSHHHHHHHHHHHCTTCEEEEEEESBHHHHHHHHHHHHHHHCTTC.SEEEEES-
GGGTTGGG-SEEEEEESSBBSS--HHHH CS
    PCMT  59
phmvalalellelkkgarvLevGsGsGyltavlarlvgekgrvvsierikelveeakrnlkkldle.nvivvvgDGrkGyeekaPYdaihvgaaa
peiPeali 160
           p +   +++  ++++ + vLevG G+G lt+   r++++ +vv++e +++++e +++++   +e ++ ++ gD    + +
PY  i ++ ++ +i  +l+
    YEAST  42 PLVAQGIVDKAQIRPSDVVLEVGPGTGNLTV---RILEQAKNVVAVEMDPRMAAELTKRVRGTPVEkKLEIMLGDFM---
KTELPYFDICISNTPYQISSPLV 138

44445567778899**************9986...88889999*****************9998879******975...467888888888888
77777766 PP

>> Met_10  Met-10+ like-protein
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to    envfrom  env to
acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------    ------- -------
----
   1 !   19.6   0.0   3.4e-07   0.00061      97     163 ..      53     117 ..      16
140 .. 0.88

  Alignments for each domain:
  == domain 1  score: 19.6 bits;  conditional E-value: 3.4e-07
           T--TT-EEEET-TTTCCHHHCCHHTTSSEEEEEES-HHHHHHHHHHHHHHHTT-TTCEEEEES-GGG- CS
  Met_10  97 lveegevVvdvfAGiGpfaipiakyskakrvlaidlnPesvkylkeniklNkvekvvkpileDgrev 163
             ++++ +vV++v G G +++ i  +ak v+a++++P+   l++ ++ vek+++ +l+D +
    YEAST  53 QIRPSDVVLEVGPGTGNLTVRILE--QAKNVVAVEMDPRMAAELTKRVRGTPVEKKLEIMLGDFMKT 117
             6899****************99..9999*****************************9999997655 PP

>> CMAS  Mycolic acid cyclopropane synthetase
   #    score  bias  c-Evalue  i-Evalue hmmfrom   hmm to    alifrom  ali to    envfrom  env to
acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------    ------- -------
----
```

```
   1 !   16.8   0.0   1.7e-06    0.0031      54     126 ..      48     119 ..      44
128 .. 0.91
   2 ?   -2.3   0.0       1.2   2.2e+03     217     246 ..     250     279 ..     228
286 .. 0.58

  Alignments for each domain:
  == domain 1  score: 16.8 bits;  conditional E-value: 1.7e-06
           HHTTTT--TT-EEEEES-TTSHHHHHHHHHH--EEEEEES-HHHHHHHHHHHHTS-SSS-EEEEES-GGG--- CS
  CMAS   54 ileklelkpGmtlLdiGcGWGslvrraverydvkvvglTlSkeqaklakkrvdeldlerkvevklldyedlde 126
            i++k++++p + +L++G G G+l++r  e+  +vv++ +   a+   krv + +e+k e+ l d+   +
  YEAST  48 IVDKAQIRPSDVVLEVGPGTGNLTVRILEQ-AKNVVAVEMDPRMAAELTKRVRGTPVEKKLEIMLGDFMKTEL 119
            789*************************.99********************************99987665 PP

  == domain 2  score: -2.3 bits;  conditional E-value: 1.2
           E-HHHHHHHHHHHHHHHHHHTHHHHHHHHSHH CS
  CMAS  217 slrahYakTLkaWaealqenkdeaialvse 246
            l++Y++ L + +e + + k ++ ++v+e
  YEAST 250 ILEKNYKTFLAMNNEMVDDTKGSMHDVVKE 279
            3455555555555555555555555555 PP

>> Methyltransf_23  Methyltransferase domain
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to    envfrom  env to
acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------    ------- -------
----
   1 !   17.5   0.0   1.6e-06    0.0028      20      61 ..      54      95 ..      37
199 .. 0.86

  Alignments for each domain:
  == domain 1  score: 17.5 bits;  conditional E-value: 1.6e-06
  Methyltransf_23 20 lraggrvLdiGcGtGillevlrengfsvtgvDlspeaveiae 61
                     r++  vL++G+GtG+l+  + e+ ++v++v+++p++ +++
            YEAST 54 IRPSDVVLEVGPGTGNLTVRILEQAKNVVAVEMDPRMAAELT 95
                     577889*************9*9************9988764 PP

>> Methyltransf_12  Methyltransferase domain
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to    envfrom  env to
acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------    ------- -------
----
   1 !   16.2   0.0   7.3e-06     0.013       1      69 [.      61     124 ..      61
134 .. 0.74

  Alignments for each domain:
  == domain 1  score: 16.2 bits;  conditional E-value: 7.3e-06
  Methyltransf_12   1 LeiGcGtGsllralleklpdieytgvDispsaiedakeklakrennnnnnveleald lldldggssfDl 69
                      Le+G GtG+l+ ++le+    +++++v+ +p++ +   ++ +      +++e+   d +++ + +fD+
            YEAST  61 LEVGPGTGNLTVRILEQ--AKNVVAVEMDPRMAAELTKRVRGTP--VEKKLEIMLGDFMKTELP-YFDI 124
                      8****************..*************55555555444..344555555555555555.6666 PP

>> AAA_lid_4  RuvB AAA lid domain
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to    envfrom  env to
acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------    ------- -------
----
   1 !   15.2   0.0   7.7e-06     0.014       8      37 ..      73     102 ..      68
116 .. 0.93

  Alignments for each domain:
  == domain 1  score: 15.2 bits;  conditional E-value: 7.7e-06
  AAA_lid_4   8 eivkrsakilgveieeegaaeiarRsRGTP 37
                +i++++ +++ ve+++  aae+++R RGTP
      YEAST  73 RILEQAKNVVAVEMDPRMAAELTKRVRGTP 102
                6999999*********************** PP

>> PRMT5  PRMT5 arginine-N-methyltransferase
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to    envfrom  env to
acc
 ---   ------ ----- --------- --------- ------- -------    ------- -------    ------- -------
----
   1 !   10.7   0.0   0.00019      0.34      64     143 ..      56     127 ..      29
129 .. 0.82
   2 ?    3.2   0.0      0.04        71      93     132 ..     245     284 ..     227
299 .. 0.77

  Alignments for each domain:
```

```
   == domain 1  score: 10.7 bits;  conditional E-value: 0.00019
            -EEEEEEES-TTSHHHHHHHHHHHHHHCCCEEEEEEEES-HHHHHHHHHHHHHHTTCCGCEEEES-CCCCCHCC-ECEEEE CS
  PRMT5   64 kklvilvvGaGRGplvdralkaleetkvtkvkivavEKnpnavvtLqkkvneekWeekveviksdmrelkaeekvdllvs
143
             + v+l vG G G l  r+l+     +k    ++vavE p+    L+k+v+ +  e+k+e++  d+ + + +  +d+++s
  YEAST   56 PSDVVLEVGPGTGNLTVRILEQ---AK----NVVAVEMDPRMAAELTKRVRGTPVEKKLEIMLGDFMKTELPY-FDICIS
127

            4567888999*99998777654...44....689*****************************99998875.899998 PP


   == domain 2  score: 3.2 bits;  conditional E-value: 0.04
            EEEEEEEES-HHHHHHHHHHHHHHHTTCCGCEEEES-CCCC CS
  PRMT5   93 kvkivavEKnpnavvtLqkkvneekWeekveviksdmrel 132
            ++ + ++EKn ++++++++++  ++ ++  +v+k+ + ++
  YEAST  245 TTVMDILEKNYKTFLAMNNEMVDDTKGSMHDVVKEKIDTV 284
            4455689************98888877778888887665 PP




Internal pipeline statistics summary:
-------------------------------------
Query sequence(s):                     1  (318 residues searched)
Target model(s):                   17929  (3037991 nodes)
Passed MSV filter:                   584  (0.0325729); expected 358.6 (0.02)
Passed bias filter:                  488  (0.0272185); expected 358.6 (0.02)
Passed Vit filter:                    46  (0.00256568); expected 17.9 (0.001)
Passed Fwd filter:                    15  (0.000836633); expected 0.2 (1e-05)
Initial search space (Z):          17929  [actual number of targets]
Domain search space  (domZ):          10  [number of targets reported over threshold]
# CPU time: 0.99u 0.55s 00:00:01.54 Elapsed: 00:00:01.40
# Mc/sec: 689.18
//
[ok]
```