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Из списка с дрожжами я выбрала РММ.

Работала с файлом ptot.list в ~ (не стала создавать дополнительные директории)

Ниже приведены команды и полученные выводы stdout.

```
fufayevas@kodomo:~$ nano ptot.list
```

```
fufayevas@kodomo:~$ seqret @ptot.list ptot.fasta
```

```
fufayevas@kodomo:~$ less ptot.fasta
```

```
fufayevas@kodomo:~$ mafft ptot.fasta > ptot-al.fasta
```

```
fufayevas@kodomo:~$ hmmbuild ptot.hmm ptot-al.fasta
```

```
# hmmbuild :: profile HMM construction from multiple sequence alignments
```

```
# HMMER 3.3.2 (Nov 2020); http://hmmer.org/
```

```
# Copyright (C) 2020 Howard Hughes Medical Institute.
```

```
# Freely distributed under the BSD open source license.
```

```
# -----
```

```
# input alignment file:      ptot-al.fasta
```

```
# output HMM file:          ptot.hmm
```

```
# -----
```

```
# idx name          nseq alen mlen eff_nseq re/pos description
```

```
#-----
```

```
1      ptot-al          5  259  249  0.50 0.594
```

```
# CPU time: 0.12u 0.00s 00:00:00.12 Elapsed: 00:00:00.12
```

```
fufayevas@kodomo:~$ seqret sw:*_yeast yeast-proteins.fasta
```

```
fufayevas@kodomo:~$ wc -l yeast-proteins.fasta
```

```
60469 yeast-proteins.fasta
```

```
fufayevas@kodomo:~$ grep -c '>' yeast-proteins.fasta
```

```
6733
```

```
fufayevas@kodomo:~$ hmmsearch ptot.hmm yeast-proteins.fasta
```

```
# hmmsearch :: search profile(s) against a sequence database
```

```
# HMMER 3.3.2 (Nov 2020); http://hmmer.org/
```

```
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```

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```

```
# -----
```

```
# query HMM file:          ptot.hmm
```

```
# target sequence database: yeast-proteins.fasta
```

```
# -----
```

```
Query:      ptot-al [M=249]
```

```
Scores for complete sequences (score includes all domains):
```

```
--- full sequence --- --- best 1 domain --- -#dom-
```

```
      E-value score bias  E-value score bias  exp N Sequence Description
```

```
-----
```

```
3.1e-126 418.6 0.2 3.6e-126 418.3 0.2      1.0 1 PMM_YEAST P07283
```

```
Phosphomannomutase {ECO:0000303|PubMed:328
```

0.0031 15.6 0.0 0.0049 15.0 0.0 1.2 1 HXT4_YEAST P32467
Low-affinity glucose transporter HXT4 (Low

Domain annotation for each sequence (and alignments):

>> PMM_YEAST P07283 Phosphomannomutase {ECO:0000303|PubMed:3288631} (PMM)
(5.4.2.8 {ECO:0000269|PubMed:3288631}) (Aspar

#	score	bias	c-Value	i-Value	hmmfrom	hmm to	alifrom	ali to	envfrom	env to
1	418.3	0.2	1.1e-129	3.6e-126	5	247	9	253	4	
acc										

1 ! 418.3 0.2 1.1e-129 3.6e-126 5 247 .. 9 253 .. 4										
254 .] 0.98										

Alignments for each domain:

== domain 1 score: 418.3 bits; conditional E-value: 1.1e-129

ptot-al 5

rkkddvlfldvdgtlttaarkeiseelleflkkkrekvvvgvvggsdlvkiseqlgksvledydyvfsenglvaykkkgkligvqslkkylg
eekkelin 104

+ k+++l+lfvdvgtlt+ar+++see++++l klr+k +g+vggsdl+k+ eqlg++vl+++dy

fsengl+ay+ gk++++qs++++lgeek+++l

PMM_YEAST 9

KEKPETLVLFDDVDGTLTPARLTVSEEVKRLAKLRNKKCCIGFVGGSDLSKQLEQLGPNVLDE
FDYSFSENGLTAYRLGKELASQSFINWLGEKYNKLAV 108

45679*****
PP

ptot-al 105

ftlryiadldipikrgtfiefrkgmlnvspigrncsqeerdefekydkvhnirsklvevlkekfedlnltfsigggqisfdvfpkgwdktycl
yled..f 202

f+lry++++d+p +rgtf+efr+gm+nvspigrn+s+eer+efe+ydk h+ir

k+ve+lk++f+d++lftfsigggqisfdvfp gwdktycl+++e+ f

PMM_YEAST 109

FILRYLSEIDLPRKRGTFLEFRNGMINVSPIGRNASTEERNEFERDYDKEHQIRAKFVEALKKE
FPDYGLTFSIGGGQISFDVFPAGWDKTYCLQHVEKdgF 208

*****9889*
PP

ptot-al 203 eeihffgdktkyggndyeiyedertighsvtspddtvkqlkelfk 247

+eihffgdkt ggndyei+ dertighsv+spddtvk+l elf+

PMM_YEAST 209 KEIHFFGDKTMVGGNDYEIFVDERTIGHSVQSPDDTVKILTELFN 253

*****997 PP

>> HXT4_YEAST P32467 Low-affinity glucose transporter HXT4 (Low-affinity glucose
transporter LGT1)

#	score	bias	c-Value	i-Value	hmmfrom	hmm to	alifrom	ali to	envfrom	env to
acc										

1 ! 15.0 0.0 1.5e-06 0.0049 139 216 .. 36 113 .. 28 119 .. 0.87

Alignments for each domain:

== domain 1 score: 15.0 bits; conditional E-value: 1.5e-06

ptot-al 139

csqeerdefekydkvhnirsklvevlkekfedlnltfsigg.qisfdvfpkgwdktyclryledfeeihffgdktykgg 216

++ erd+++ +d h+ +++ve+ k+ + + +t si ++f f gwd ++ + + i fg k + g

HXT4_YEAST 36

SNKAERDDMKDFDENHEESNNYVEIPKKPASAY-VTVSICCMVAFGGFVFGWDTGTISGFV

AQTDFIRRFGMKHHDGT 113

5688*****9888776655.88999873689*****998875 PP

Internal pipeline statistics summary:

Query model(s): 1 (249 nodes)
Target sequences: 6733 (3025957 residues searched)
Passed MSV filter: 257 (0.0381702); expected 134.7 (0.02)
Passed bias filter: 161 (0.0239121); expected 134.7 (0.02)
Passed Vit filter: 14 (0.00207931); expected 6.7 (0.001)
Passed Fwd filter: 2 (0.000297044); expected 0.1 (1e-05)
Initial search space (Z): 6733 [actual number of targets]
Domain search space (domZ): 2 [number of targets reported over threshold]
CPU time: 0.08u 0.01s 00:00:00.09 Elapsed: 00:00:00.03
Mc/sec: 19645.15
//
[ok]