```
Trm1p     1  .......MEGFFRIP..LKRANLHGMLKAAIS...KIKANFTAYGAPRINIEDFNIVKEG
Trmt1p    1  MQGSSLWLSLTFRSARVLSRARFFEWQSPGLPNTAAMENGTGPYGEERPREVQETTVTEG

Trm1p    49  KAEILFPKKETVFYNPIQQFNRDLSVTCIKAWDNLYGEECGQKRNNKKSKKKRCAETNDD
Trmt1p   61  AAKIAFPSANEVFYNPVQEFNRDLTCAVITEFARIQLGAKGIQIKVPGEKDTQKVVVDLS

Trm1p   109  SSKRQ........KMGNGSPKEAVGNSNRNEPYINILEALSATGLRAIRYAHEIPHVREV
Trmt1p  121  EQEEEKVELKESENLASGDQPRTAAVGEICEEGLHVLEGLAASGLRSIREALEVPGLRSV

Trm1p   161  IANDLLPEAVESIKRNVEYNSVENIVKPNLDDANVLMYRNKATNNKFHVIDLDPYGTVTP
Trmt1p  181  VANDASTRAVDLIRRNVQLNDVAHLVQPSQADARMLMYQHQRVSERFDVIDLDPYGSPAT

Trm1p   221  FVDAAIQSIEEGGLMLVTCTDLSVLAGNGYPEKCFALYGGANMVSHESTHESALRLVLNL
Trmt1p  241  FLDAAVQAVSEGGLLCVTCTDMAVLAGN.SGETCYSKYG.AMALKSRACHEMALRIVLHS

Trm1p   281  LKQTAAKYKKTVEPLLSLSIDFYVRVFVKVKTSPIEVKNVMSSTMTTYHCSRCGSYHNQP
Trmt1p  299  LDLRANCYQRFVVPLLSISADFYVRVFVRVFTGQAKVKASASKQALVFQCVGCGAFHLQR

Trm1p   341  LGRISQREGRNNKTFTKYSVAQGPPVDTKCKFCEGTYHLAGPMYAGPLHNKEFIEEVLRI
Trmt1p  359  LGKASGVPSGR....AKFSAACGPPVTPECEHCGQRHQLGGPMWAEPIHDLDFVGRVLEA

Trm1p   401  NKEEHRDQDDTYGTRKRIEGMLSLAKNELSDSPFYFSPNHIASVIKLQVPPLKKVVAGLG
Trmt1p  415  VSANP....GRFHTSERIRGVLSVITEELPDVPLYYTLDQLSSTIHCNTPSLLQLRSALL

Trm1p   461  SLGFEGSLTHAQPSSLKTNAPWDAIWYVMQKCDDEK.KDLSKMNPNTTGYKILSAMPGWL
Trmt1p  471  HADFRVSLSHACKNAVKTDAPASALWDIMRCWEKECPVKRERLSETSPAFRILSVEPRLQ

Trm1p   520  S...............GTVKSEYDSKLSFAPNEQSG........NIEKLRKLKIVRYQEN
Trmt1p  531  ANFTIREDANPSSRQRGLKRFQANPEANWGPRPRARPGGKAADEAMEERRRLLQNKRKEP

Trm1p   557  PTKNWGPKARPNTS.............................................
Trmt1p  591  PEDVAQRAARLKTFPCKRFKEGTCQRGDQCCYSHSPPTPRVSADAAPDCPETSNQTPPGP
```

Figure S1. Sequence comparison between Trm1p from *Saccharomyces cerevisiae* and Trmt1p from *Homo sapines*. Uniport entries of Trm1p and Trmt1p are P15565 and Q9NXH9, respectively. The overall identity and similarity between these two sequences are 34.2% and 50.4%, respectively. The alignments illustrated in Fig. S1-S8 were generated by the ClustalW web server using BLOSUM as the weight matrix [1] and these figures were prepared using ESPript [2].

```
                 .         .         .         .         .         .         .
Trm2p      1     MYEQFEFSFFFFENSDNKVKYKAHLISSIKRWSIITCMRCFWTVQKSIFKARFFACRNFV
RHO4a      1     ..........................................MNTLLFKRKGGNCG...

                 .         .         .         .         .         .         .
Trm2p     61     KKHNYKLISTMTGSTEMVPPTMKHTVDNKRLSSPLTDSGNRRTKKPKLRKYKAKKVETTS
RHO4a     15     ...NESNIVSQGSPSSSNLPESPGTLDEKNLPRLPTPFARSLSTIP...SYEQMKRTNKL

                 .         .         .         .         .         .         .
Trm2p    121     PMGVLEFEVNDLLKSQNLSREQVLNDVTSILNDKSSTDGPIVLQYHREVKNVKVLEITSN
RHO4a     69     PD........................................YHLKIVVVGDGAVGKT

                 .         .         .         .         .         .         .
Trm2p    181     GNGLALIDNPVETEKKQVVIIPFGLPGDVVNIKVFKTHPYYVESDLLDVVEKSPMRRDDL
RHO4a     87     CLLISYVQGTFPTD.....YIPTIFENYVTNIEGPN......................

                 .         .         .         .         .         .         .
Trm2p    241     IRDKYFGKSSGSQLEFLTYDDQLELKRKTIMNAYKFFAPRLVAEKLLPPFDTTVASPLQF
RHO4a    118     ..........GQIIELALWDTAGQEEYSRLR................PLSYTNADVLMV

                 .         .         .         .         .         .         .
Trm2p    301     GYRTKITPHFDMPKRKQKELSVRPPLGFGQKGRPQWRKDTLDIGGHGSILDIDECVLATE
RHO4a    151     CYSVGSKTSLKN..........VEDLWFP.............................

                 .         .         .         .         .         .         .
Trm2p    361     VLNKGLTNERRKFEQEFKNYKKGATILLRENTTILDPSKPTLEQLTEEASRDENGDISYV
RHO4a    170     ........EVKHFCPSTPIMLVGLKSDLYEADNLSDLVEP................SSA

                 .         .         .         .         .         .         .
Trm2p    421     EVEDKKNNVRLAKTCVTNPRQLVTEYVDGYTFNFSAGEFFQNNNSILPIVTKYVRDNLQA
RHO4a    205     ESLAKRLGAFAHIQCSARLKENIDEVFETAIHTLLSDSLYAPREPTHTIKNPFKRN....

                 .         .         .         .         .         .         .
Trm2p    481     PAKGDDNKTKFLVDAYCGSGLFSICSSKGVDKVIGVEISADSVSFAEKNAKANGVENCRF
RHO4a    261     .......TTRSDIDSSTGDTSVSISGTKRLRKNK........................

                 .         .         .         .         .         .         .
Trm2p    541     IVGKAEKLFESIDTPSENTSVILDPPRKGCDELFLKQLAAYNPAKIIYISCNVHSQARDV
RHO4a            ............................................................

                 .         .         .
Trm2p    601     EYFLKETENGSAHQIESIRGFDFFPQTHHVESVCIMKRI
RHO4a    288     ................................CIIM..
```

Figure S2. Sequence comparison between Trm2p from *Saccharomyces cerevisiae* and RHO4a protein from *Saccharomyces cerevisiae*. Uniport entries of Trm2p and RHO4a are P33753 and Q00246, respectively. The overall identity and similarity between these two sequences are 19.6% and 34.5%, respectively.

```
Trm3p      1  ................MVGGALICKYLPREEQLKLISDLIQNDSLEEVLELIETSPLDIT
TARBP1     1  MEWVLAEALLSQSRDPRALLGALCQGEASAERVETLRFLLQRLEDEEARGSGGAGALPEA

Trm3p     45  TDSNIETPIFEKITEQVIAYASIDG......EAREMFRSSRAEMNKALRTSAQLLCCLPS
TARBP1    61  AREVAAGYLVPLLRSLRGRPAGGPDPSLQPRHRRRVLRAAGAALRSCVRLAGRPQLAAAL

Trm3p     99  VWHKFQVWMSYRLNDIISENYKHLFNDN..FGKKIVQPFFDSFAEEQNANIK......HE
TARBP1   121  AEEALRDLLAGWRAPGAEAAVEVLAAVGPCLRPREDGPLLERVAGTAVALALGGGGDGDE

Trm3p    151  NLHLDILSLLHYLEVVYLFDECKNGISSKCLDFIIVPLLGCNSEEIADSCSKLMRWHIKY
TARBP1   181  AGPAEDAAALVAGRLLPVLVQCGGAALRAVWGGLAAPGASLGSGRVEEKLLVLSALAEKL

Trm3p    211  LS..........KCCNTDSNFDKLIWTFIKQLYAEGSQQAWKQKNSLSFLLRFLLAAELS
TARBP1   241  LPEPGGDRARGAREAGPDARRCWRFWRTVQAGLGQADALTRKRARYLLQRAVEVSAELGA

Trm3p    261  PELITYIKTDAYWRHIQTELDNDVHEHRKLALSILKLTIQKLSSHGIT.....LQTTFYK
TARBP1   301  DCTCGPQEGNGPSLFWWSERKKDELLKFWENYILIMETLEGNQIHVIKPVLPKLNNLFEY

Trm3p    316  CNDLANIEMLGSWKKFTTLYEMIALDTSLNQIQAAKQDIIKIFDNEHLHHSWGLILLSTG
TARBP1   361  AVSEENGCWLFHPSWHMCIYKRMFESENKILSKEGVIHFLELYETKILPFSPEFSEFIIG

Trm3p    376  ......LKSSMESVRKYMMTLMFSITNMSAFSSNLPLLTKTLLPAAMSAHYFDVKGVSCP
TARBP1   421  PLMDALSESSLYSRSPGQPIGSCSPLGLKLQKFLVTYISLLPEEIKSSFLLKFIRKMTSR

Trm3p    430  HGEKLSLFVNNLLSQTTEGISDILFEILKLLVEKGTSFDPSRIYLSYGILVFFQNNKQKT
TARBP1   481  HWCAVPILFLSKALANVPRHKALGIDGLLALRDVIHCTMITHQILLRGAAQCYLLQTAMN

Trm3p    490  INSDHLSLIRKLYDFAAEEEVLETT..IQTIYLKFLLYIDPSVSASELLFTLVSHIKLKG
TARBP1   541  LLDVEKVSLSDVSTFLMSLRQEESLGRGTSLWTELCDWLRVNESYFKPSPTCSSIGLHKT

Trm3p    548  GTYKYVEPLFEDYR..............DLAVSHFDDLQAKENLTTNIGKDTIFDLLASI
TARBP1   601  SLNAYVKSIVQEYVKSSAWETGENCFMPDWFEAKLVSLMVLLAVDVEGMKTQYSGKQRTE

Trm3p    594  IFDFKDIDITPDFLIEVAKSKQDIPVYTSKAVTFLTQLLSGEPSNGYTYENATALLSYPN
TARBP1   661  NVLRIFLDPLLDVLMKFSTNAYMPLLKTDRCLQLLKLLNTCRLKGSSAQDDEVSTVLQN
```

```
Trm3p    654  FTISTWKSINVNNLFKSVMEKFS....LDKFKFFAEIYQKTYECRFDTIELNFNDLLSLY
TARBP1   721  FFMSTTESISEFILRRLTMNELNSVSDLDRCHLYLMVLTELINLHLKVGWKRGNPIWRVI

Trm3p    710  EMVKKSANQCSRESFKVKDSAYSSYFELLN.............................T
TARBP1   781  SLLKNASIQHLQEMDSGQEPTVGSQIQRVVSMAALAMVCEAIDQKPELQLDSLHAGPLES

Trm3p    741  FLKTYALNRDSSEGNDDELHILLRLVDENINKDNGN...........YLGNLAVCKLLYF
TARBP1   841  FLSSLQLNQTLQKPHAEEQSSYAHPLECSSVLEESSSSQGWGKIVAQYIHDQWVCLSFLL

Trm3p    790  IIDSYIHCST..........................SVSDDDIFIVKFIFEKFSFIWECI
TARBP1   901  KKYHTLIPTTGSEILEPFLPAVQMPIRTLQSALEALTVLSSDQVLPVFHCLKVLVPKLLT

Trm3p    824  NSERLVLKERDLHLMLIKGLFHPVILYFG.......SNQYIDTLTSKLEEHAQTIISLSY
TARBP1   961  SSESLCIESFDMAWKIISSLSNTQLIFWANLKAFVQFVFDNKVLTIAAKIKGQAYFKIKE

Trm3p    877  SRRSLLPLLGSQLRVFMKFYGKLLR...............EDVNYWWLINIIVGVFKQPQ
TARBP1  1021  IMYKIIEMSAIKTGVFNTLISYCCQSWIVSASNVSQGSLSSAKNYSELILEACIFGTVFR

Trm3p    922  MDVNLYKLKPVISSLFDHKLNNYYIKGDELYEKVYGPDEILARVSIIDSILYANDQLKIR
TARBP1  1081  RDQRLVQDVQTFIENLGHDCAANIVMENTKREDHYVRICAVKFLCLLDGSNMSHKLFIED

Trm3p    982  LIEKVTEKTNALYAIKRTDGAEALQR..LLQWQLLLLSLLTTNEKKLSETSMIRILKSIE
TARBP1  1141  LAIKLLDKDELVSKSKKRYYVNSLQHRVKNRVWQTLLVLFPRLDQNFLNGIIDRIFQAGF

Trm3p   1040  DESSPLVRVYKEWFISSKVVDYYKTG.........NPKFAEDYLFSLLEDHSKPVFVVSA
TARBP1  1201  TNNQASIKYFIEWIIILILHKFPQFLPKFWDCFSYGEENLKTSICIFLAVLSHLDIITQN

Trm3p   1091  EKICFMVLKDLRNDEKKYGFTQLLDR...FICTLVPNAASNKPLVRHFSNSLIISLWPTF
TARBP1  1261  IPEKKLILKQALIVVLQWCFNHNFSVRLYALVALKKLWTVCKVLSVEEFDALTPVIESSL

Trm3p   1148  KAYLSDHTLRNIIENLYSNAKKTQIFGQYRAGDANIWDLKGDRKLTNMFGGVLKKVTDHD
TARBP1  1321  HQVESMHGAGNAKKNWQRIQEHFFFATFHPLKDYCLETIFYILPRLSGLIEDEWITIDKF

Trm3p   1208  CPYISESVFEKYLQEKDIVPIGTDERSLWLDKRD.TNTESVNNANISCDTSPLQTKSGAW
TARBP1  1381  TRFTDVPLAAGFQWYLSQTQLSKLKPGDWSQQDIGTNLVEADNQAEWTDVQKKIIPWNSR
```

```
Trm3p   1267  ETVLDLDNKKSNDVVTR....SELIVVSSLVDKPPNLGGICRLCDVLGVGLLTVQDIKVK
TARBP1  1441  VSDLDLELLFQDRAARLGKSISRLIVVASLIDKPTNLGGLCRTCEVFGASVLVVGSLQCI

Trm3p   1323  NHPQFKNVAVTADRWMPMEEVALDEIASFMKEKKKEGYTLIGLEQTDKSVKLDNNFQFPK
TARBP1  1501  SDKQFQHLSVSAEQWLPLVEVKPPQLIDYLQQKKTEGYTIIGVEQTAKSLDLT.QYCFPE

Trm3p   1383  KSLILLGTEAFGIPGTLLSELDLCLEIQQFGVIRSMNIQTATAVIVHSYTVQHM......
TARBP1  1560  KSLLLLGNEREGIPANLIQQLDVCVEIPQQGIIRSLNVHVSGALLIWEYTRQQLLSHGDT
```

```
                    .         .         .         .         .         .
Trm3p    121  HLFNDNFGKKIVQPFFDSFAEEQNANIKHENLHLDILSLLHYLEVVYLFDECKNGISSKC
TARBP2     1  ................MSEEEQGS.............................GTTTGC

                    .         .         .         .         .         .
Trm3p    181  LDFIIVPLLGCNSEEIADSCSKLMRWHIKYLSKCCNTDSNFDKLIWTFIKQLYAEGSQQA
TARBP2    15  GLPSIEQMLAANP..............................................

                    .         .         .         .         .         .
Trm3p    241  WKQKNSLSFLLRFLLAAELSPELITYIKTDAYWRHIQTELDNDVHEHRKLALSILKLTIQ
TARBP2        ............................................................

                    .         .         .         .         .         .
Trm3p    301  KLSSHGITLQTTFYKCNDLANIEMLGSWKKFTTLYEMIALDTSLNQIQAAKQDIIKIFDN
TARBP2    28  .............GKTPISLLQEYGTRIGKTPVYDLLKAEG..................

                    .         .         .         .         .         .
Trm3p    361  EHLHHSWGLILLSTGLKSSMESVRKYMMTLMFSITNMSAFSSNLPLLTKTLLPAAMSAHY
TARBP2    56  .......................QAHQPNFTFRVT........................

                    .         .         .         .         .         .
Trm3p    421  FDVKGVSCPHGEKLSLFVNNLLSQTTEGISDILFEILKLLVEKGTSFDPSRIYLSYGILV
TARBP2    68  ..VGDTSCTG...............................................

                    .         .         .         .         .         .
Trm3p    481  FFQNNKQKTINSDHLSLIRKLYDFAAEEEVLETTIQTIYLKFLLYIDPSVSASELLFTLV
TARBP2    76  ..............................................QGPSKKAAKHKAAEV

                    .         .         .         .         .         .
Trm3p    541  SHIKLKGGTYKYVEPLFEDYRDLAVSHFDDLQAKENLTTNIGKDTIFDLLASIIFDFKDI
TARBP2    91  ALKHLKGG..SMLEPALEDS.......................................

                    .         .         .         .         .         .
Trm3p    601  DITPDFLIEVAKSKQDIPVYTSKAVTFLTQLLSGEPSNGYTYENATALLSYPNFTISTWK
TARBP2   109  ........................SSFSPLDSSLPEDIPVFTAAAAATPVP........

                    .         .         .         .         .         .
Trm3p    661  SINVNNLFKSVMEKFSLDKFKFFAEIYQKTYECRFDTIELNFNDLLSLYEMVKKSANQCS
TARBP2   136  ....................................SVVLTRSPPMELQPPVSPQQSECN
```

```
Trm3p    721  RESFKVKDSAYSSYFELLNTFLKTYALNRDSSEGNDDELHILLRLVDENINKDNGNYLGN
TARBP2   160  .........PVGALQELVVQKG.....................................

Trm3p    781  LAVCKLLYFIIDSYIHCSTSVSDDDIFIVKFIFEKFSFIWECINSERLVLKERDLHLMLI
TARBP2        ............................................................

Trm3p    841  KGLFHPVILYFGSNQYIDTLTSKLEEHAQTIISLSYSRRSLLPLLGSQLRVFMKFYGKLL
TARBP2        ............................................................

Trm3p    901  REDVNYWWLINIIVGVFKQPQMDVNLYKLKPVISSLFDHKLNNYYIKGDELYEKVYGPDE
TARBP2   173  ......WRLPEYTVTQESGP......................................

Trm3p    961  ILARVSIIDSILYANDQLKIRLIEKVTEKTNALYAIKRTDGAEALQRLLQWQLLLLSLLT
TARBP2        ............................................................

Trm3p   1021  TNEKKLSETSMIRILKSIEDESSPLVRVYKEWFISSKVVDYYKTGNPKFAEDYLFSLLED
TARBP2        ............................................................

Trm3p   1081  HSKPVFVVSAEKICFMVLKDLRNDEKKYGFTQLLDRFICTLVPNAASNKPLVRHFSNSLI
TARBP2   187  ......................AHRKEFTMTCRVERFIEIGSG...TSKKLAKRNAAAKM

Trm3p   1141  ISLWPTFKAYLSDHTLRNIIENLYSNAKKTQIFGQYRAGDANIWDLKGDRKLTNMFGGVL
TARBP2   222  LLRVHTVPLDARDGNEVEPDDDHFSIGVGSRLDGLRNRGPGCTWDS..............

Trm3p   1201  KKVTDHDCPYISESVPEKYLQEKDIVPIGTDERSLWLDKRDTNTESVNNANISCDTSPLQ
TARBP2   268  ..........LRNSVGEKILSLR.............................SCSLGSLG

Trm3p   1261  TKSGAWETVLDLDNKKSNDVVTRSELIVVSSLVDKPPNLGGICRLCDVLGVGLLTVQDIK
TARBP2   289  ALGPACCRVLSELSEE........QAFHVSYLDIEELSLSGLCQCLVELST.........

Trm3p   1321  VKNHPQFKNVAVTADRWMPMEEVALDEIASFMKEKKKEGYTLIGLEQTDKSVKLDNNFQF
TARBP2   332  ....................................QPATVCHGSATTREAARGEAARRA

Trm3p   1381  PKKSLILLGTEAFGIPGTLLSELDLCLEIQQFGVIRSMNIQTATAVIVHSYTVQHM
TARBP2   356  LQYLKIMAGSK.........................................
```

Figure S3. Sequence comparison between Trm3p from *Saccharomyces cerevisiae* and TRBP isoforms from *Homo sapiens*. Uniport entries of Trm3p, TARBP1, and TARBP2 are Q07527, Q13395, and Q15633, respectively. The overall identity and similarity between Trm3p and TARBP1 sequences are 15.9% and 33.4%, respectively. The overall identity and similarity between Trm3p and TARBP2 sequences are 21.9% and 39.9%, respectively.

```
Trm4p  121  PKTVIRKNEQFAKTQRFLVVENAVGNISRQEAVSMIPPIVLEVKPHHTVLDMCAAPGSKT
Pmt1     1  ..........MLSTKRLRVLELYSG.................IGGMHYALNLANIP....

Trm4p  181  AQLIEALHKDTDEPSGFVVANDADARRSHMLVHQLKRLNSANLMVVNHDAQFFPRIRLHG
Pmt1    30  ADIVCAIDINPQANEIYNLNHGKLAKHMDISTLTAKDFDAFDCKLWTMSPSCQPFTRIG.

Trm4p  241  NSNNKNDVLKFDRILCDVPCSGDGTMRKNVNVWKDWNTQAGLGLHAVQLNILNRGLHLLK
Pmt1    89  ...NRKDILDPR.............SQAFLNILNVLPHVNNLPEYILIENVQGFEESKAA

Trm4p  301  NNGRLVYSTCSLNPIENEAVVAEALRKWGDKIRLVNCDDKLPGLIRSKGVSKWPVYDRNL
Pmt1   133  EECRKVLRNCGYNLIEGILSPNQFN........IPNSRSRWYGLARLNFKGEWSIDDVFQ

Trm4p  361  TEKTKGDEGTLDSFFSPSEEEASKFNLQNCMRVYPHQQNTGGFFITVFEKVEDSTEAATE
Pmt1   185  FSEVAQKEGEVKRIR.............................................

Trm4p  421  KLSSETPALESEGPQTKKIKVEEVQKKERLPRDANEEPFVFVDPQHEALKVCWDFYGIDN
Pmt1   200  ......DYLEIERDWSSYMVLESVLNKWGHQFDIVKP......................

Trm4p  481  IFDRNTCLVRNATGEPTRVVYTVCPALKDVIQANDDRLKIIYSGVKLFVSQRSDIECSWR
Pmt1   231  ..DSSSCCCFTRG.............YTHLVQGAG............SILQMSDHENTHE

Trm4p  541  IQSESLPIMKHHMKSNRIVEANLEMLKHLLIESFPNFDDIRSKNIDNDFVEKMTKLSSGC
Pmt1   264  QFERNRMALQLRYFTAREVAR.........LMGFPESLEWSKSNVT..............

Trm4p  601  AFIDVSRNDPAKENLFLPVWKGNKCINLMVCKEDTHELLYRIFGIDANAKATPSAEEKEK
Pmt1   301  ....................................EKCMYRLLGNSINVKVVSYLISLLL

Trm4p  661  EKETTESPAETTTGTSTEAPSAAN
Pmt1   326  EPLNF...................
```

Figure S4. Sequence comparison between Trm4p from *Saccharomyces cerevisiae* and Pmt1

protein from *Schizosaccharomyces pombe*. Uniport entries of Trm4p and Pmt1 are P38205 and P40999, respectively. The overall identity and similarity between these two sequences are 17.9% and 37.0%, respectively.

```
Trm5p    1  MKIALPVFQKENRLISSCKMSGVFPYNPPVNRQMRELDRSFFITKIPMCAVKFPEPKNIS
TrmD     1  ..MKIDILILEPEMFSPLEHSIVG..........................KAREKGLLD

Trm5p   61  VFSKNFKNCILRVPRIPHVVKLNSSKPKDELTSVQNKKLKTADGNNTPVTKGVLLHESIH
TrmD    32  IQYHNFR...ENAEKARHVDDE........................PYGGGQGMLLRAQ

Trm5p  121  SVEDAYGKLPEDALAFLKENSAEIVPHEYVLDYDFWKAEEILRAVLPEQFLEEVPTGFTI
TrmD    64  PIFDSFDAIEKKNPRVILLD................PAGKQFDQAYAEDLAQEEELIFIC

Trm5p  181  TGHIAHLNLRTEFKPFDSLIGQVILDKNNKIECVVDKVSSIATQFRTFPMKVIAGKSDSL
TrmD   108  G..........HYEGYDERIKTLVTDEISLGDYVLTGGELAAMTMIDATVRLIPEVIGKE

Trm5p  241  VVEQKESNCTFKFDFSKVYWNSRLHTEHERLVKQYFQPGQVVCDVFAGVGPFAVPAGKKD
TrmD   158  SSHQDDS.............FSSGLLEYPQYTRPYDYRGMVVPDVLMSG...........

Trm5p  301  VIVLANDLNPESYKYLKENIALNKVAKTVKSFNMDGADFIRQSPQLLQQWIQDEEGGKIT
TrmD   194  ..........................................HHEKIRQWRLYES.....

Trm5p  361  IPLPLKKRHRSQQHNDQQPPQPRTKELIIPSHISHYVMNLPDSAISFLGNFRGIFAAHTK
TrmD   207  LKKTYERR......................PDLLEHYQLIVEE..................

Trm5p  421  GATDTIQMPWVHVHCFEKYPPGDQVTEDELHARVHARIIAALKVTADDLPLNAVSLHLVR
TrmD   228  ....................................EKMLAEIKENKE.............
```

Figure S5. Sequence comparison between Trm5p from *Saccharomyces cerevisiae* and TrmD from *Streptococcus pneumoniae*. Uniport entries of Trm5p and TrmD are P38793 and B8ZND2, respectively. The overall identity and similarity between these two sequences are 17.6% and 38.9%, respectively.

```
Trm12p   1  MSDETMPVEFLVSDKRLLKTIKVKLETNGLFVTPIYSDNDNKVIKSSIEDLNHPLAVEIN
VP39     1  ....................MDVVSLDKPFMYFEEIDNELDYEPESANEVAKKLPYQGQLK

Trm12p  61  NIAGVKARFHESGNLERSEGHLKHQSNSITEFTKSFLKDHGLANDKIFLSHLLDHLPLKY
VP39    42  LLLGELFFLSKLQRHGILDGATVVYIGSAPGTHIRYLRDHFYNLGVIIKWMLIDGRHHDP

Trm12p 121  TIYPPVVLFNNSTVRSFNHPIWQKAFQLKLFDPNEYYRELLCFLSPGKPSKGTSLHPNNR
VP39   102  ILNG..................LRDVTLVTRFVDEEYLRSIKKQLHP..............

Trm12p 181  LLTHLAINNPITEADVLRRPFNIQPLYGKLIDDSILDDNDNTLWENPSQEQLNSSIWCKV
VP39   131  .......SKIILISDVRSKRGGNEPSTADLLSN..........................YA

Trm12p 241  IQNGVTQIWSPVFTMFSRGNIKEKKRVLTTFPDICNNDVVDLYAGIGYFTFSYLTKGART
VP39   159  LQNVMISILNPVASSLKWR.........CPFPDQWIKDFYIPHGNKMLQPFAPSYSAEMR

Trm12p 301  LFAFELNPWSVEGLKRGLKANGFNKSGNCHVFQESNEMCVQRLTEFLSQNPGFRLRIRHI
VP39   210  LLSIYTG..ENMRLTRVTKSDAVNYEKKMYYLNKIVRNKVVVNFDYPNQEYDYFHMYFML

Trm12p 361  NLGLLPSSKQGWPLAIKLIYLQGASLEKVTMHIHENVHIDAIEDGSFEKNVIVELDAINE
VP39   268  RTVYCNKTFPTTKAKVLFLQQSIFRFLNIPTTSTEKVSHEPIQRKISSKNSMSKNRNSKR

Trm12p 421  SIALIRNRGIKLQFVRSKLERIKTFAPDIWHVCVDVDVIVST
VP39   328  SVRSNK...................................
```

Figure S6. Sequence comparison between Trm12p from *Saccharomyces cerevisiae* and VP39 protein from *Vaccinia virus*. Uniport entries of Trm12p and VP39 are Q04235 and P07617, respectively. The overall identity and similarity between these two sequences are 14.4% and 27.6%, respectively.

```
Trm13p     1  MLQDNNGPAVKRAKPSERLQCEYFMEKKKRRCGMTRSSQNLYCSEHLNLMKKAANSQVHN
U11-48K    1  .MEGEPPPVEERR....RLQEELNEFVESG............CRTLEEVTASLGWDLDSL

Trm13p    61  KNGSEAEKERERVPCPLDPNHTVWADQLKKHLKKCNKTKLSHLNDDKPYYEPGYNGENGL
U11-48K   44  DPGEEEAAEDEVVICPYDSNHHMPKSSLAKHMASCRLRKMGYTKEE..............

Trm13p   121  LSSSVKIDITAEHLVQSIELLYKVFEGESMDELPLRQLNNKLMSLKRFPQLPSNTKHAVQ
U11-48K   90  ...........EDEMYNPEFFYENVKIPSITLNKDSQF...........QIIKQARTAVG

Trm13p   181  QSSLIENLVDAGAFERPESLNFIEFGCGRAEFSRYVSLYLLTQLTSLPAEHSGSNSNEFV
U11-48K  128  KDSDCYNQRIYSSLPVEVPLNHKRFVCDLTQADRLALYDFVVEETKKKRSDSQIIENDSD

Trm13p   241  LIDRATNRMKFDKKIKDDFSEIKSNSPSKPISCPSIKRIKIDIRDLKMDPILKSTPGDDI
U11-48K  188  LFVDLAAKINQDNSRK...............SPKSYLEILAEVRDYKRR.........RQ

Trm13p   301  QYVCISKHLCGVATDLTLRCIGNSSILHGDDNNGCNPKLKAICIAMCCRHVCDYGDYVNR
U11-48K  224  SYRAKNVHITKKSYTEVIRDVIN.....................VHMEELSNHWQEEQEK

Trm13p   361  SYVTSLVEKYRAHGSILTYETFFRVLTKLCSWGTCGRKPGTAITDIVNVVESFEGAEPYT
U11-48K  263  AEDDAEKNEERRSASVDSRQSGGSYLDAECSR...........................

Trm13p   421  ITIKERENIGLMARRVIDEGRLVYVKEKFTEFNAELIRYVESDVSLENVAMLVYKK.
U11-48K  295  ............HRRDRSRSPHKRKRNKDKDKNCESRRKERDGERHHSHKRRKQKI
```

Figure S7. Sequence comparison between Trm13p from *Saccharomyces cerevisiae* and U11-48K protein from *Homo sapiens*. Uniport entries of Trm13p and U11-48K are Q12383 and Q6IEG0, respectively. The overall identity and similarity between these two sequences are 19.8% and 31.6%, respectively.

```
Trm44p     1  MTGDGSAHISKNNQNQHKDRFKFIVNDKS....ILGPQWLSLYQTDGKVTFAKSHFEQAM
Trmt44p    1  MAEVGRTGISYPGALLPQGFWAAVEVWLERPQVANKRLCGARLEARWSAALPCAEARGPG

Trm44p    57  MNVIREPNINSTVILRADILKEINHAAEAGSEPKFDESVLKKFEIDNGNESGEEDVKKIN
Trmt44p   61  TSAGSEQKERGPGPGQGSPGGGPGPRSLSGPEQGTACCELEEAQGQCQQEEAQREAASVP

Trm44p   117  IEDLNIR.....SCETSESLKLSPVHEFVRRIIPRNFYKDAIINQTCLILNSKDPNFQET
Trmt44p  121  LRDSGHPGHAEGREGDFPAADLDSLWEDFSQSLAR.GNSELLAFLTSSGAGSQPEAQREL

Trm44p   172  SLIVYTPHINSEKDCPFYIPRTQSVGILLHQSVLSVHYIPFPEDKTAFTDES........
Trmt44p  180  DVVLRTVIPKTSPHCPLTTPRREIVVQDVLNGTITFLPLEEDDEGNLKVKMSNVYQIQLS

Trm44p   224  ......................ERVVRTAYRLLQTANKHSKGVMQGYEKRVNHDQVVNKV
Trmt44p  240  HSKEEWFISVLIFCPERWHSDGIVYPKPTWLGEELLAKLAKWSVENKKSDFKSTLSLISI

                                   Motif X
Trm44p   262  NFQNTYIVLKKKYSKFLVENWAESTDPKKHVFEDIAIAAELIELWIKVYGPDFRSKMQ.F
Trmt44p  300  MKYSKAYQELKEKYKEMVKVWPEVTDPEKFVYEDVAIAAYLLILWEEERAERRLTARQSF

              Motif I                Motif II               Motif III
Trm44p   321  RDLGCGNGALCYILLSESIKGLGIDARKRKSWSIYPPEVQSSLKEQVIIPSILLRPHPAL
Trmt44p  360  VDLGCGNGLLVHILSSEGHPGRGIDVRRRKIWDMYGPQTQ..LEEDAITPNDKTLFPDVD

Trm44p   381  KRQVPHLEHNGRFFPVKVTHEVIAPATVVYSSEDLLKSFQVN...........TAEFPP
Trmt44p  418  WLIGNHSDELTPWIPVIAARSSYNCRFFVLPCCFFDFIGRYSRRQSKKTQYREYLDFIKE

                Motif IV
Trm44p   429  DTFIIGNHSDELTCWIP......LLGHPYMVIPCCSHNFSGQRVRFNVRKR.........
Trmt44p  478  VGFTCGFHVDEDCLRIPSTKRVCLWGKSRTYPSSREASVDEKRTQYIKSRRGCPVSPPGW

Trm44p   474  ............................................................SPRSNEIK
Trmt44p  538  ELSPSPRWVAAGSAGHCDGQQALDARVGCVTRAWAAEHGAGPQAEGPWLPGFHPREKAER

Trm44p   482  NQNNSKSTYSGLVDHVEYISSRVGWKVEKEMLRIPSTRNAAIIGVPNATLKHFP....TQ
Trmt44p  598  VRNCAALPRDFIDQVVLQVANLLLGGKQLNTRSSRNGSLKTWNGGPSLSLAEVANELDTE

Trm44p   538  AVYDMIWEDGGAEGWIQNTMSLLKRN.................................
Trmt44p  658  TLRRLKREGGLQTLLRNSHQVFQVVNGRVHIRDWREETLWKTKQPEAKQRLLSEACKTR

Trm44p   564  ...................PRNH................
Trmt44p  718  LCWFFMHHPDGCALSTDCCPFAHGPAELRPPRTTPRKKIS
```

Figure S8. Sequence comparison between Trm44p from *Saccharomyces cerevisiae* and Trmt44p from *Homo sapiens*. Uniport entries of Trm44p and Trmt44p are Q02648 and Q8IYL2, respectively. The overall identity and similarity between these two sequences are 18.1% and 32.3%, respectively. The motifs conserved in DUF1613 proteins are indicated above the sequences.

References

[1] Thompson, J.D., Gibson, T.J., Higgins, D.G., 2002. Multiple sequence alignment usingClustalW and ClustalX. Curr. Protoc. Bioinf. Chap. 2, Unit 2.3.

[2] Robert, X., Gouet, P., 2014. Deciphering key features in protein structures with the new ENDscript server. Nucleic Acids Res. 42, W320-324.