

| Taxonomy                                         | Number of hits       | Number of Organisms |
|--------------------------------------------------|----------------------|---------------------|
| [-] Eukaryota                                    | <a href="#">1055</a> | 722                 |
| [-] Opisthokonta                                 | <a href="#">779</a>  | 585                 |
| [-] Fungi                                        | <a href="#">285</a>  | 224                 |
| [-] Dikarya                                      | <a href="#">278</a>  | 220                 |
| [-] Ascomycota                                   | <a href="#">222</a>  | 173                 |
| [-] saccharomyceta                               | <a href="#">210</a>  | 165                 |
| [-] Saccharomycetales                            | <a href="#">88</a>   | 44                  |
| [-] Pezizomycotina                               | <a href="#">122</a>  | 121                 |
| [-] Taphrinomycotina                             | <a href="#">12</a>   | 8                   |
| [-] Basidiomycota                                | <a href="#">56</a>   | 47                  |
| [-] Chytridiomycetes                             | <a href="#">2</a>    | 2                   |
| [-] <i>Phycomyces blakesleeanus</i> NRRL 1555(-) | <a href="#">3</a>    | 1                   |
| [-] <i>Mitosporidium daphniae</i>                | <a href="#">2</a>    | 1                   |
| [-] Metazoa                                      | <a href="#">487</a>  | 356                 |
| [-] Ichthyosporea                                | <a href="#">3</a>    | 2                   |
| [-] Salpingoecidae                               | <a href="#">2</a>    | 2                   |
| [-] Fonticula alba                               | <a href="#">2</a>    | 1                   |
| [-] Viridiplantae                                | <a href="#">204</a>  | 83                  |
| [-] Rhodophyta                                   | <a href="#">5</a>    | 3                   |
| [-] <i>Guillardia theta</i> CCMP2712             | <a href="#">1</a>    | 1                   |
| [-] Alveolata                                    | <a href="#">27</a>   | 22                  |
| [-] Stramenopiles                                | <a href="#">20</a>   | 12                  |
| [-] <i>Trichomonas vaginalis</i> G3              | <a href="#">2</a>    | 1                   |
| [-] Amoebozoa                                    | <a href="#">6</a>    | 5                   |
| [-] <i>Emiliana huxleyi</i> CCMP1516             | <a href="#">2</a>    | 1                   |
| [-] <i>Thecamonas trahens</i> ATCC 50062         | <a href="#">1</a>    | 1                   |
| [-] Trypanosomatidae                             | <a href="#">8</a>    | 8                   |

Figure S1. Taxonomy report from PSI-blast search of Utp30/Cic1 homologs.

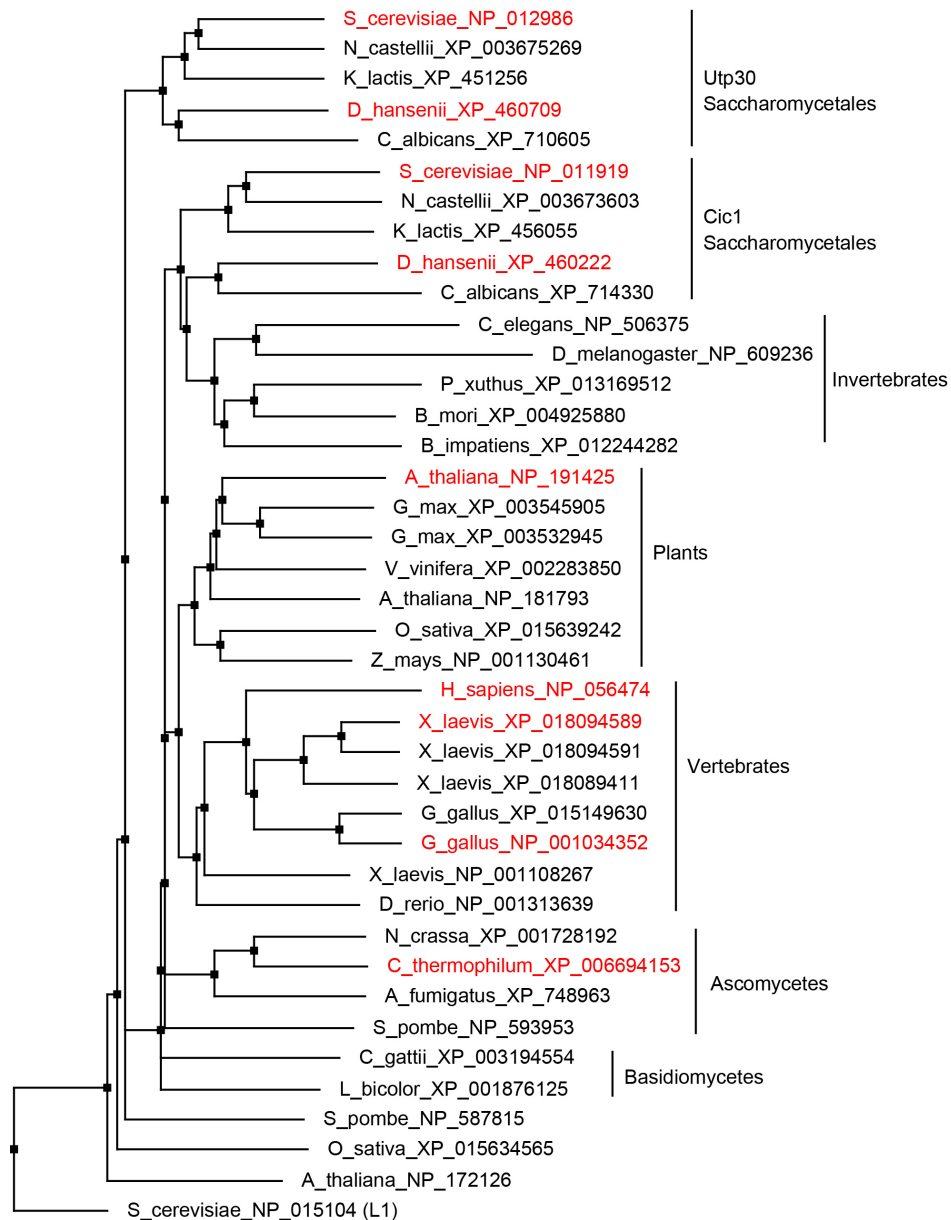


Figure S2. Unrooted phylogenetic tree of Utp30/Cic1 homologs from representative species. The ribosomal L1 protein was included as a distant sequence. Each sequence is designated by binomial name of organism and protein ID. The sequences in red are aligned in Figure 1C.

Table S1. Statistics of data collection and structural refinement

|                                   | Native                | Se-labeled            |
|-----------------------------------|-----------------------|-----------------------|
| Data collection                   |                       |                       |
| Beamline                          | BL19U                 | BL17U                 |
| Wavelength (Å)                    | 0.97776               | 0.97919               |
| Space group                       | C222 <sub>1</sub>     | C222 <sub>1</sub>     |
| Unit cell dimensions              |                       |                       |
| a, b, c (Å)                       | 72.4, 90.9, 157.2     | 72.9, 91.0, 159.0     |
| $\alpha$ , $\beta$ , $\gamma$ (°) | 90.0, 90.0, 90.0      | 90.0, 90.0, 90.0      |
| Resolution (Å)                    | 50.0-2.65 (2.70-2.65) | 50.0- 3.0 (3.05-3.00) |
| Unique reflections                | 15291 (1432)          | 10898 (1036)          |
| Completeness (%)                  | 98.7 (95.4)           | 99.7 (97.0)           |
| Redundancy                        | 11.4 (8.4)            | 7.4 (5.9)             |
| $\langle I/\sigma(I) \rangle$     | 21.4 (2.0)            | 24.2 (3.2)            |
| Rmerge                            | 0.168(0.765)          | 0.139(0.767)          |
| CC1/2                             | (0.768)               | (0.850)               |
| Refinement                        |                       |                       |
| Resolution (Å)                    | 46.0-2.65 (2.85-2.65) |                       |
| Number of reflections             | 15282 (2894)          |                       |
| Number of atoms                   | 3897                  |                       |
| R-work                            | 0.200 (0.274)         |                       |
| R-free                            | 0.266 (0.359)         |                       |
| RMSD bond length (Å)              | 0.009                 |                       |
| RMSD bond angles (°)              | 1.081                 |                       |

\*Numbers in parenthesis are for the highest resolution shell

Table S2. Statistics of real space refinement of remodeled Utp30 in  $\Delta$ Mtr4 90S cryo-EM density

|                       |        |
|-----------------------|--------|
| Resolution (Å)        | 4.5    |
| Map CC (around atoms) | 0.6299 |
| RMSD bonds (Å)        | 0.005  |
| RMSD Angles (°)       | 1.017  |
| Clashscore            | 6.87   |
| Rotamers outliers (%) | 0.44   |
| Ramachandran plot     |        |
| Favored (%)           | 91.3   |
| Allowed (%)           | 8.7    |
| Outliers (%)          | 0      |

Supplementary Dataset 1. Mass spectrometric data for 90S particles. The SCPHR and RSAF values of identified proteins are displayed in two separate sheets. The RSAF is normalized against six UTPB proteins. The top rows include the summed SCPHR or RSAF values for 90S proteins, pre-40S proteins, pre-60S proteins, small subunit ribosomal proteins (RPS), large subunit ribosomal proteins (RPLs) and total identified proteins, the total spectral counts (SpC) of reference proteins and the molar percentages of 90S AFs over all detected proteins. (Excel table)