

## Appendix

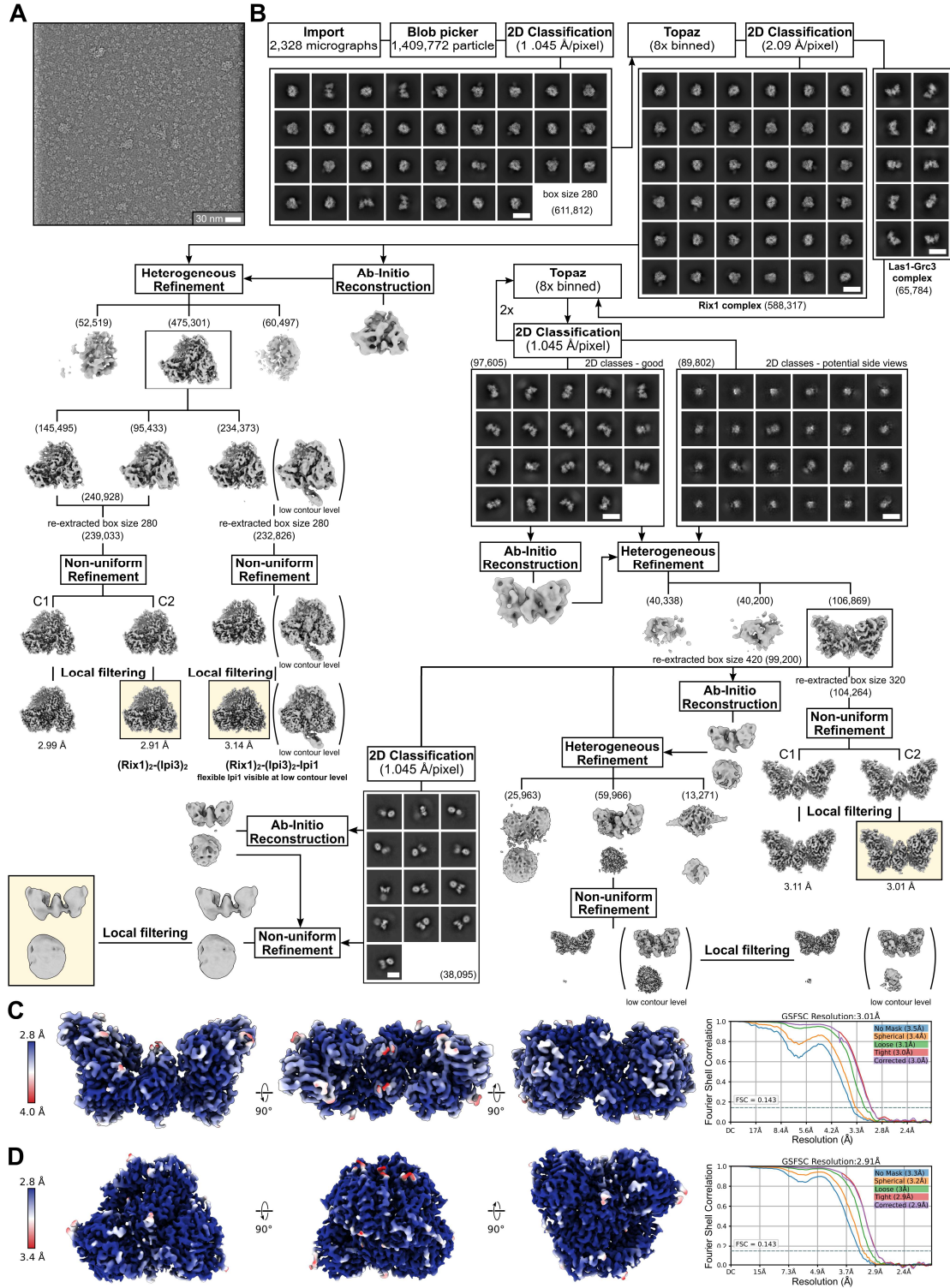
### Structural Insights into Coordinating 5S RNP Rotation with ITS2 pre-RNA Processing During Ribosome Formation

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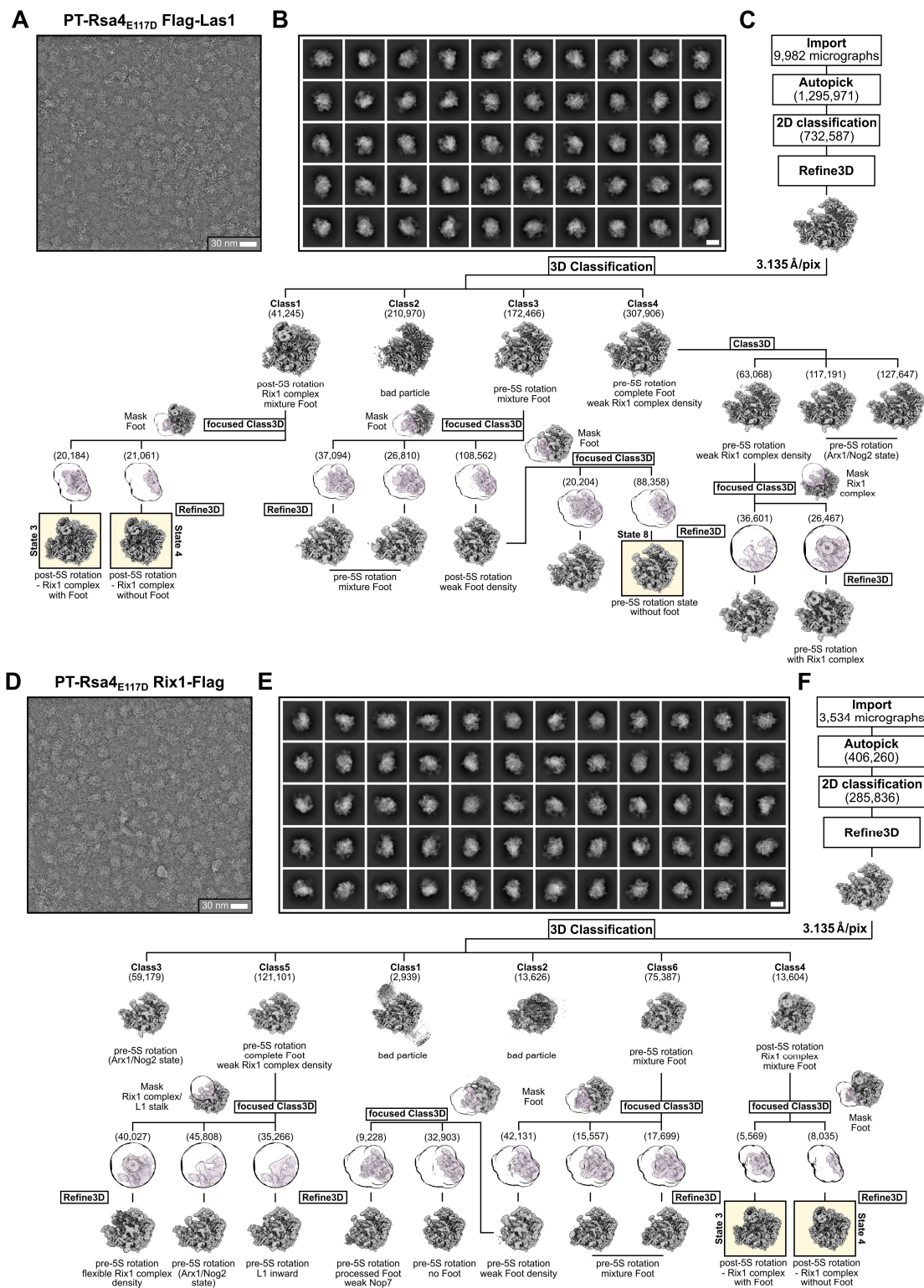




**Appendix Figure S2. Cryo-EM data processing scheme, local resolution and Fourier shell correlation of the PTF-Las1 rixosome dataset.**

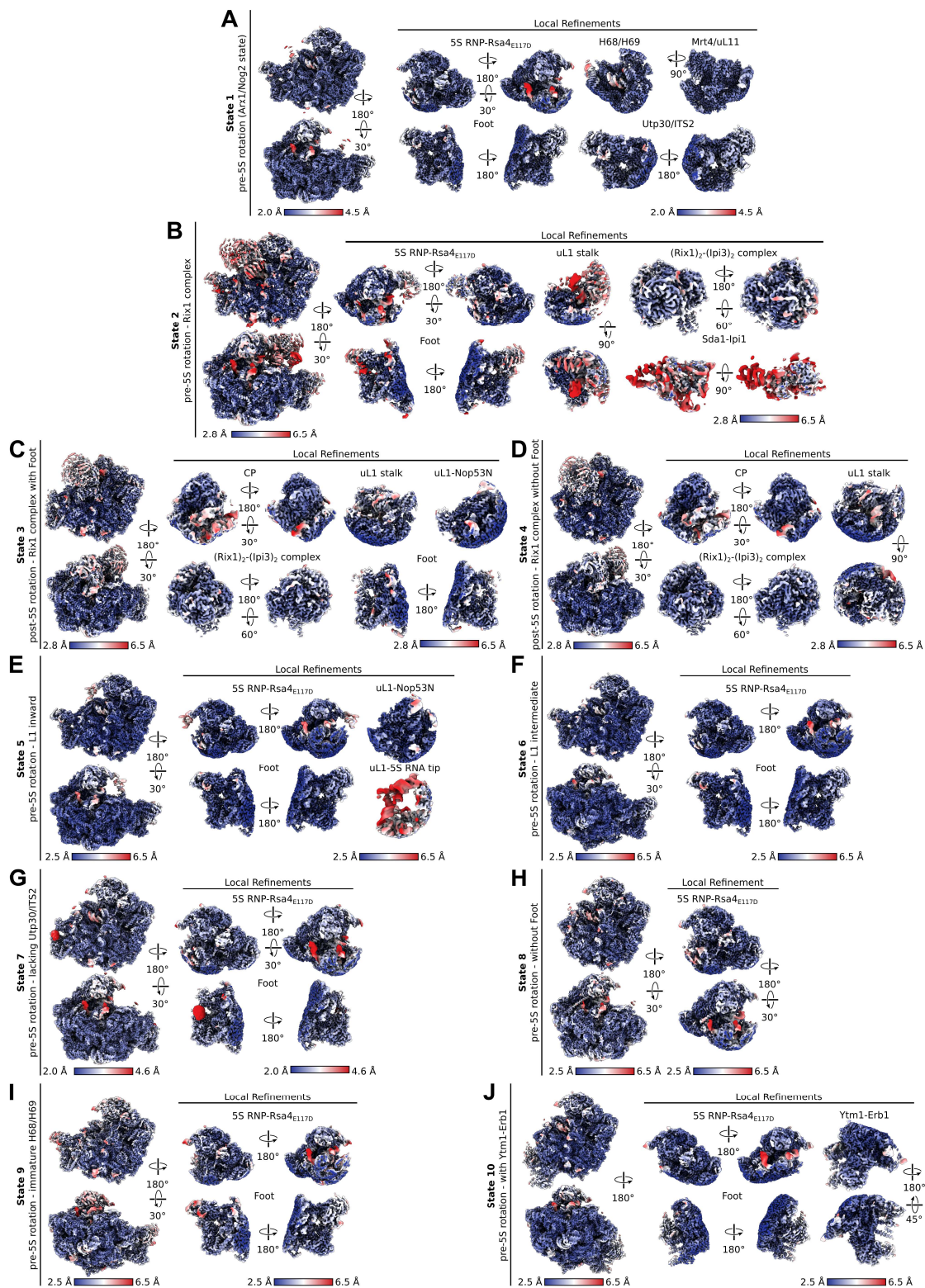
(A) Representative electron micrograph of the PTF-Las1 sample. Scale bar: 30 nm. (B) Data processing and classification scheme. Numbers in brackets indicate the respective particle count. Final classes of the Las1-Grc3 complex, the Rix1 complex and the low-resolution reconstruction of the rixosome are highlighted by yellow boxes. The scale bars for the different 2D classes correspond to 15 nm. (C-D) Local resolution filtered maps colored according to local resolution of the Las1-Grc3 complex (C) and the Rix1 complex (D) and the respective Fourier shell correlation (FSC) curves.





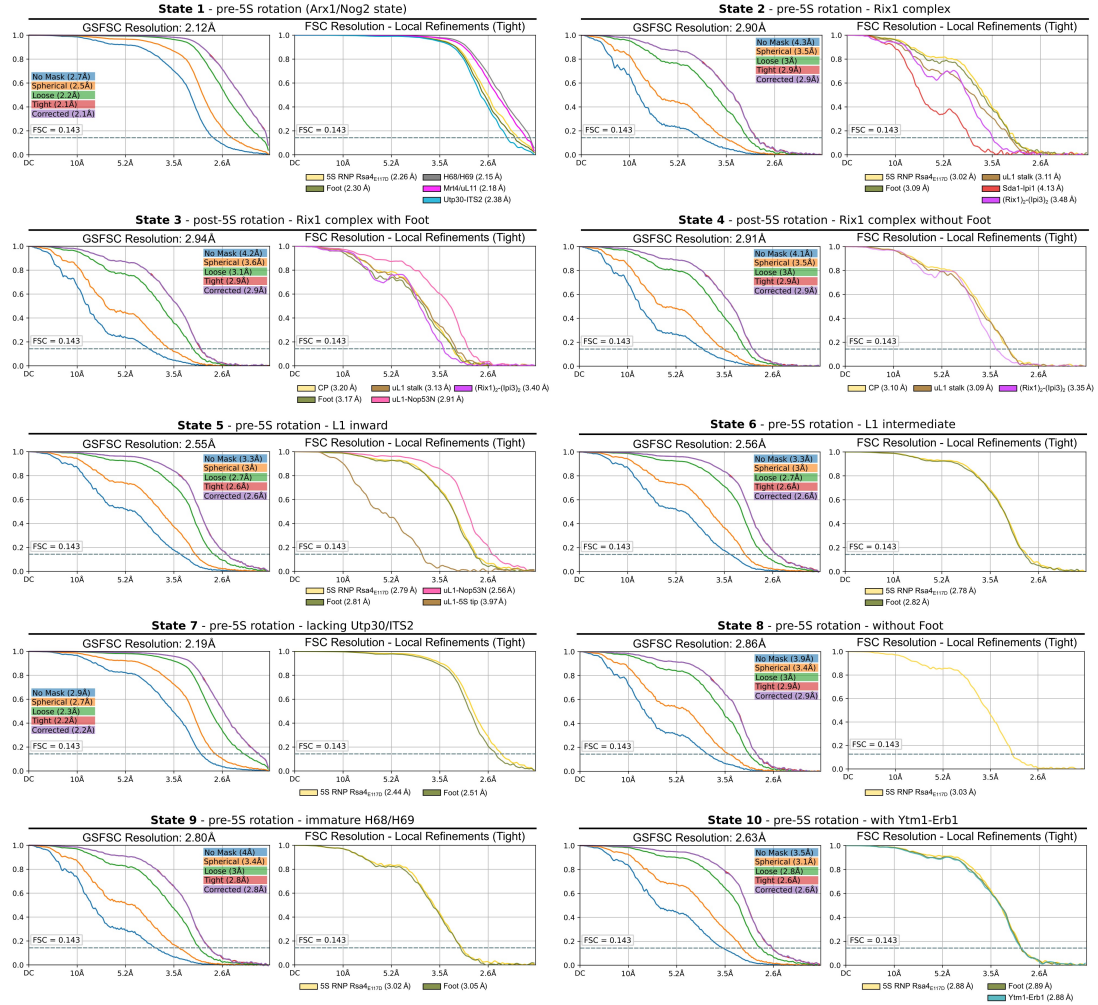
**Appendix Figure S4. Cryo-EM data processing scheme of the PT-Rsa4 E117D Rix-Flag and PT-Rsa4 E117D Flag-Las1 datasets.**

(A, B, D, E) Representative electron micrographs (A, D) and 2D class averages (B, E) of the PT-Rsa4 E117D Rix-Flag and PT-Rsa4 E117D Flag-Las1 datasets. The scale bars for the electron micrographs and the 2D class averages correspond to 30 nm and 15 nm, respectively. (C, F) Data processing and classification scheme of the PT-Rsa4 E117D Rix-Flag (C) and the PT-Rsa4 E117D Flag-Las1 (F) datasets. Particle numbers are shown in brackets and final classes used for undecimated refinement and subsequent local refinements are highlighted by yellow boxes.

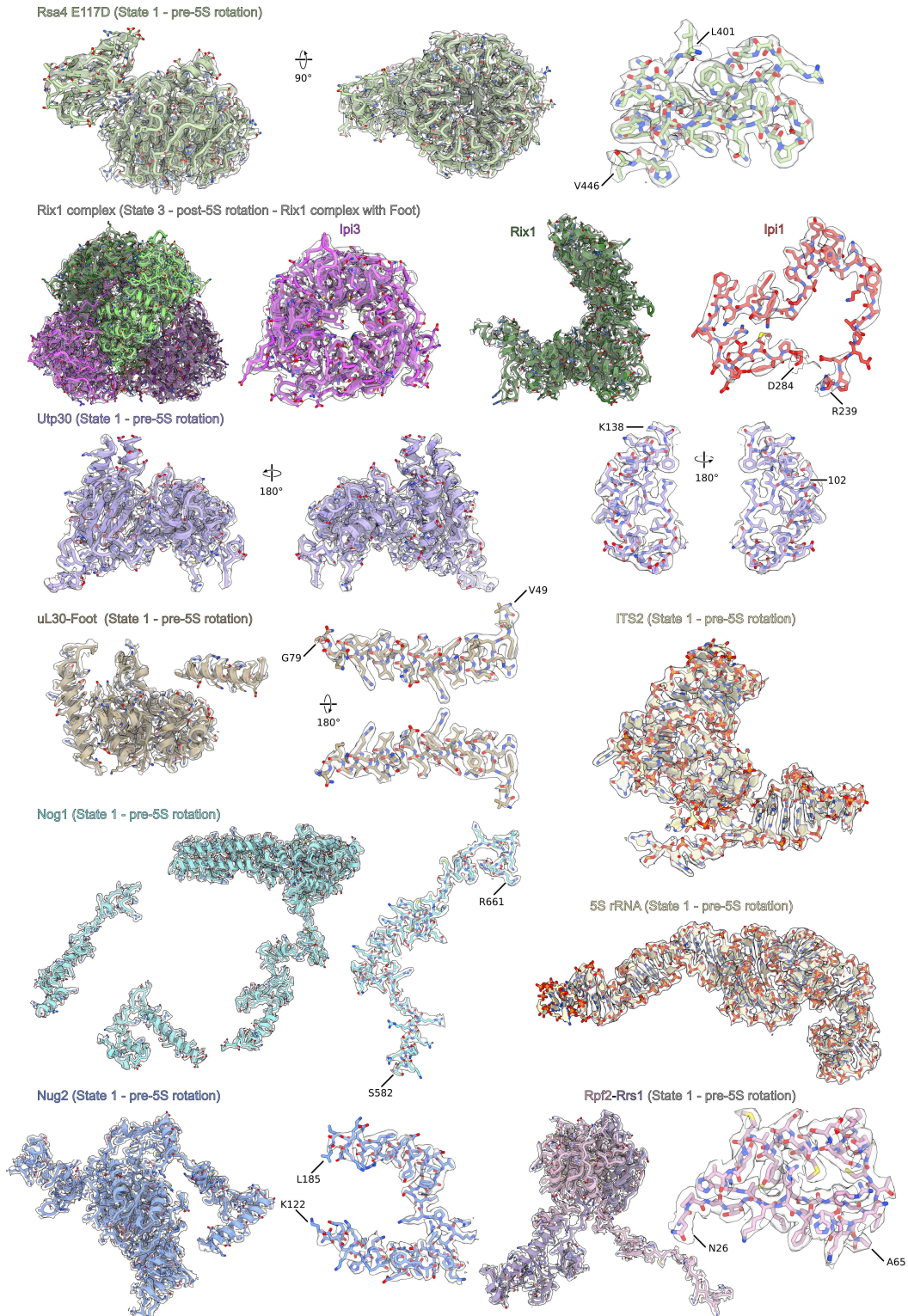


**Appendix Figure S5. Local resolution of the presented pre-60S states.**

For all states the local resolution filtered maps of the consensus densities and the individual local refinement maps are shown. The maps are colored according to local resolution.



**Appendix Figure S6. FSC curves of the presented states and corresponding local refinements.** For all states (see Appendix Figure S5) the FSC curves for the consensus reconstructions (left graphs) and the related local refinements (right graphs) are shown. (FSC – Fourier shell correlation)



## Appendix Figure S7. Model validation

Segmented cryo-EM densities and models of different biogenesis factors, ITS2 and 5S rRNA. The corresponding states are indicated in brackets.

**Appendix Table S1. *C. thermophilum* strains used in this study.**

| Experimental strain                                                                                                                                                                                | Source                | Identifier                                                             |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|------------------------------------------------------------------------|
| <i>Chaetomium thermophilum</i> wild-type strain                                                                                                                                                    | DMSZ,<br>Braunschweig | DSM No.: 1495<br><a href="https://www.dsmz.de">https://www.dsmz.de</a> |
| $P_{ACT1}\text{-}HPHNTI\text{-}T_{GPD} / P_{ACT1}\text{-}PT\text{-}RSA4$<br>$E117D\text{-}T_{GPD}$ , $P_{ACT1}\text{-}ERGI\text{-}T_{GPD} / P_{NOT7}\text{-}$<br>$NOP7\text{-}Flag\text{-}T_{GPD}$ | This study            | PT-Rsa4 E117D, Nop7-Flag                                               |
| $P_{ACT1}\text{-}HPHNTI\text{-}T_{GPD} / P_{ACT1}\text{-}PT\text{-}RSA4$<br>$E117D\text{-}T_{GPD}$ , $P_{ACT1}\text{-}ERGI\text{-}T_{GPD} / P_{RIX1}\text{-}RIX1\text{-}$<br>$Flag\text{-}T_{GPD}$ | This study            | PT-Rsa4 E117D, Rix1-Flag                                               |
| $P_{ACT1}\text{-}HPHNTI\text{-}T_{GPD} / P_{ACT1}\text{-}PT\text{-}RSA4$<br>$E117D\text{-}T_{GPD}$ , $P_{ACT1}\text{-}ERGI\text{-}T_{GPD} / P_{LASI}\text{-}Flag\text{-}$<br>$LASI\text{-}T_{GPD}$ | This study            | PT-Rsa4 E117D, Flag-LasI                                               |
| $P_{ACT1}\text{-}ERGI\text{-}T_{GPD} / P_{ACT1}\text{-}PTF\text{-}RSA4$ $E117D\text{-}$<br>$T_{GPD}$                                                                                               | This study            | PTF-Rsa4 E117D #14                                                     |
| $P_{ACT1}\text{-}ERGI\text{-}T_{GPD} / P_{ACT1}\text{-}PTF\text{-}RSA4$ $E117D\text{-}$<br>$T_{GPD}$                                                                                               | This study            | PTF-Rsa4 E117D #15                                                     |
| $P_{ACT1}\text{-}ERGI\text{-}T_{GPD} / P_{LASI}\text{-}PTF\text{-}LASI\text{-}T_{GPD}$                                                                                                             | This study            | PTF-LasI                                                               |
| $P_{ACT1}\text{-}ERGI\text{-}T_{GPD} / P_{NOT7}\text{-}NOP7\text{-}Flag\text{-}T_{GPD}$                                                                                                            | This study            | Nop7-Flag                                                              |
| $P_{ACT1}\text{-}HPHNTI\text{-}T_{GPD} / P_{ACT1}\text{-}PT\text{-}RSA4$<br>$E117D\text{-}T_{GPD}$                                                                                                 | This study            | PT-Rsa4 E117D                                                          |

**Appendix Table S2. Data collection, refinement and model statistics**

|                                                     | <b>State 1</b><br>Pre-5S rotation<br>(EMD-17956)<br>(PDB-8PV7) | <b>State 2</b><br>Pre-5S rotation –<br>Rix1 complex<br>(EMD-17953)<br>(PDB-8PV4) | <b>State 3</b><br>Post-5S rotation –<br>Rix1 complex<br>with Foot<br>(EMD-17955)<br>(PDB-8PV6) | <b>State 4</b><br>Post-5S rotation –<br>Rix1 complex<br>without Foot<br>(EMD-17957)<br>(PDB-8PV8) | <b>State 5</b><br>Pre-5S rotation –<br>L1 inward<br>(EMD-17969)<br>(PDB-8PVK) |
|-----------------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------|
| <b>Data collection &amp; processing</b>             |                                                                |                                                                                  |                                                                                                |                                                                                                   |                                                                               |
| Camera                                              | Gatan K2                                                       | Gatan K2                                                                         | Gatan K2                                                                                       | Gatan K2                                                                                          | Gatan K2                                                                      |
|                                                     | Summit                                                         | Summit                                                                           | Summit                                                                                         | Summit                                                                                            | Summit                                                                        |
| Magnification                                       | 130,000                                                        | 130,000                                                                          | 130,000                                                                                        | 130,000                                                                                           | 130,000                                                                       |
| Voltage (kV)                                        | 300                                                            | 300                                                                              | 300                                                                                            | 300                                                                                               | 300                                                                           |
| Electron exposure (e <sup>-</sup> /Å <sup>2</sup> ) | 45.6                                                           | 45.6                                                                             | 46.0                                                                                           | 46.0                                                                                              | 45.6                                                                          |
| Defocus range (μm)                                  | 0.5 - 3.5                                                      | 0.5 - 3.5                                                                        | 0.4 - 3.5                                                                                      | 0.4 - 3.5                                                                                         | 0.5 - 3.5                                                                     |
| Pixel size (Å)                                      | 1.045                                                          | 1.045                                                                            | 1.045                                                                                          | 1.045                                                                                             | 1.045                                                                         |
| Symmetry imposed                                    | C1                                                             | C1                                                                               | C1                                                                                             | C1                                                                                                | C1                                                                            |
| Micrographs collected (no.)                         |                                                                |                                                                                  |                                                                                                |                                                                                                   |                                                                               |
| Initial particle images (no.)                       | 1,975,074                                                      | 1,975,074                                                                        | 1,018,423                                                                                      | 1,018,423                                                                                         | 1,975,074                                                                     |
| Final particle images (no.)                         | 745,895                                                        | 25,363                                                                           | 25,753                                                                                         | 29,096                                                                                            | 74,129                                                                        |
| Map resolution (Å)                                  | 2.12                                                           | 2.90                                                                             | 2.94                                                                                           | 2.91                                                                                              | 2.55                                                                          |
| FSC threshold                                       | 0.143                                                          | 0.143                                                                            | 0.143                                                                                          | 0.143                                                                                             | 0.143                                                                         |
| <b>Refinement</b>                                   |                                                                |                                                                                  |                                                                                                |                                                                                                   |                                                                               |
| Model resolution (Å)                                | 2.1                                                            | 3.0                                                                              | 2.9                                                                                            | 2.9                                                                                               | 2.5                                                                           |
| FSC threshold                                       | 0.5                                                            | 0.5                                                                              | 0.5                                                                                            | 0.5                                                                                               | 0.5                                                                           |
| Map sharpening B factor (Å <sup>2</sup> )           | -65                                                            | -55                                                                              | -55                                                                                            | -60                                                                                               | -60                                                                           |
| Model composition                                   |                                                                |                                                                                  |                                                                                                |                                                                                                   |                                                                               |
| Non-hydrogen atoms                                  | 157,262                                                        | 178,878                                                                          | 172,014                                                                                        | 163,368                                                                                           | 160,598                                                                       |
| Protein residues                                    | 10,514                                                         | 13,274                                                                           | 12,679                                                                                         | 11,673                                                                                            | 10,777                                                                        |
| Nucleotide residues                                 | 3,435                                                          | 3,493                                                                            | 3,374                                                                                          | 3,350                                                                                             | 3,495                                                                         |
| Ligands                                             | 10                                                             | 10                                                                               | 10                                                                                             | 10                                                                                                | 10                                                                            |
| R.m.s deviations                                    |                                                                |                                                                                  |                                                                                                |                                                                                                   |                                                                               |
| Bond lengths (Å)                                    | 0.005                                                          | 0.003                                                                            | 0.003                                                                                          | 0.003                                                                                             | 0.004                                                                         |
| Bond angles (°)                                     | 0.753                                                          | 0.678                                                                            | 0.683                                                                                          | 0.689                                                                                             | 0.718                                                                         |
| Validation                                          |                                                                |                                                                                  |                                                                                                |                                                                                                   |                                                                               |
| Molprobability score                                | 1.04                                                           | 1.16                                                                             | 1.16                                                                                           | 1.18                                                                                              | 1.10                                                                          |
| Clash score                                         | 2.54                                                           | 3.71                                                                             | 3.69                                                                                           | 3.88                                                                                              | 3.07                                                                          |
| Poor rotamers (%)                                   | 0.91                                                           | 0.00                                                                             | 0.02                                                                                           | 0.04                                                                                              | 0.02                                                                          |
| Ramachandran plot                                   |                                                                |                                                                                  |                                                                                                |                                                                                                   |                                                                               |
| Favored (%)                                         | 98.69                                                          | 98.37                                                                            | 98.30                                                                                          | 98.32                                                                                             | 98.46                                                                         |
| Allowed (%)                                         | 1.31                                                           | 1.63                                                                             | 1.70                                                                                           | 1.67                                                                                              | 1.53                                                                          |
| Disallowed (%)                                      | 0.00                                                           | 0.00                                                                             | 0.01                                                                                           | 0.02                                                                                              | 0.01                                                                          |
| Map vs. Model CC (mask)                             | 0.88                                                           | 0.88                                                                             | 0.88                                                                                           | 0.88                                                                                              | 0.88                                                                          |
| <b>Local &amp; Consensus Refinements</b>            |                                                                |                                                                                  |                                                                                                |                                                                                                   |                                                                               |
|                                                     | EMD-17881                                                      | EMD-17887                                                                        | EMD-17893                                                                                      | EMD-17899                                                                                         | EMD-17903                                                                     |
|                                                     | EMD-17882                                                      | EMD-17888                                                                        | EMD-17894                                                                                      | EMD-17900                                                                                         | EMD-17904                                                                     |
|                                                     | EMD-17883                                                      | EMD-17889                                                                        | EMD-17895                                                                                      | EMD-17901                                                                                         | EMD-17905                                                                     |
|                                                     | EMD-17884                                                      | EMD-17890                                                                        | EMD-17896                                                                                      | EMD-17902                                                                                         | EMD-17906                                                                     |
|                                                     | EMD-17885                                                      | EMD-17891                                                                        | EMD-17897                                                                                      |                                                                                                   | EMD-17907                                                                     |
|                                                     | EMD-17886                                                      | EMD-17892                                                                        | EMD-17898                                                                                      |                                                                                                   |                                                                               |

|                                                     | State 6<br>Pre-5S rotation – L1<br>intermediate<br>(EMD-17950)<br>(PDB-8PV1) | State 7<br>Pre-5S rotation –<br>lacking Utp30/TTS2<br>(EMD-17970)<br>(PDB-8PVL) | State 8<br>Pre-5S rotation –<br>without Foot<br>(EMD-17954)<br>(PDB-8PV5) | State 9<br>Pre-5S rotation –<br>immature H68/H69<br>(EMD-17952)<br>(PDB-8PV3) | State 10<br>Pre-5S rotation –<br>with Ytm1-Erb1<br>(EMD-17951)<br>(PDB-8PV2) |
|-----------------------------------------------------|------------------------------------------------------------------------------|---------------------------------------------------------------------------------|---------------------------------------------------------------------------|-------------------------------------------------------------------------------|------------------------------------------------------------------------------|
| <b>Data collection &amp; processing</b>             |                                                                              |                                                                                 |                                                                           |                                                                               |                                                                              |
| Camera                                              | Gatan K2<br>Summit                                                           | Gatan K2<br>Summit                                                              | Gatan K2<br>Summit                                                        | Gatan K2<br>Summit                                                            | Gatan K2<br>Summit                                                           |
| Magnification                                       | 130,000                                                                      | 130,000                                                                         | 130,000                                                                   | 130,000                                                                       | 130,000                                                                      |
| Voltage (kV)                                        | 300                                                                          | 300                                                                             | 300                                                                       | 300                                                                           | 300                                                                          |
| Electron exposure (e <sup>-</sup> /Å <sup>2</sup> ) | 45.6                                                                         | 45.6                                                                            | 46.0                                                                      | 45.6                                                                          | 45.6                                                                         |
| Defocus range (μm)                                  | 0.5 - 3.5                                                                    | 0.5 - 3.5                                                                       | 0.4 - 3.5                                                                 | 0.5 - 3.5                                                                     | 0.5 - 3.5                                                                    |
| Pixel size (Å)                                      | 1.045                                                                        | 1.045                                                                           | 1.045                                                                     | 1.045                                                                         | 1.045                                                                        |
| Symmetry imposed                                    | C1                                                                           | C1                                                                              | C1                                                                        | C1                                                                            | C1                                                                           |
| Micrographs collected (no.)                         |                                                                              |                                                                                 |                                                                           |                                                                               |                                                                              |
| Initial particle images (no.)                       | 1,975,074                                                                    | 1,975,074                                                                       | 732,587                                                                   | 1,975,074                                                                     | 1,975,074                                                                    |
| Final particle images (no.)                         | 74,642                                                                       | 276,213                                                                         | 88,358                                                                    | 35,432                                                                        | 66,943                                                                       |
| Map resolution (Å)                                  | 2.56                                                                         | 2.19                                                                            | 2.86                                                                      | 2.80                                                                          | 2.63                                                                         |
| FSC threshold                                       | 0.143                                                                        | 0.143                                                                           | 0.143                                                                     | 0.143                                                                         | 0.143                                                                        |
| <b>Refinement</b>                                   |                                                                              |                                                                                 |                                                                           |                                                                               |                                                                              |
| Model resolution (Å)                                | 2.5                                                                          | 2.2                                                                             | 2.9                                                                       | 2.8                                                                           | 2.6                                                                          |
| FSC threshold                                       | 0.5                                                                          | 0.5                                                                             | 0.5                                                                       | 0.5                                                                           | 0.5                                                                          |
| Map sharpening B factor (Å <sup>2</sup> )           | -65                                                                          | -60                                                                             | -65                                                                       | -60                                                                           | -60                                                                          |
| Model composition                                   |                                                                              |                                                                                 |                                                                           |                                                                               |                                                                              |
| Non-hydrogen atoms                                  | 157,250                                                                      | 152,760                                                                         | 144,398                                                                   | 155,443                                                                       | 155,881                                                                      |
| Protein residues                                    | 10,512                                                                       | 10,162                                                                          | 9,204                                                                     | 10,501                                                                        | 10,783                                                                       |
| Nucleotide residues                                 | 3,435                                                                        | 3,356                                                                           | 3,331                                                                     | 3,355                                                                         | 3,328                                                                        |
| Ligands                                             | 10                                                                           | 10                                                                              | 10                                                                        | 10                                                                            | 10                                                                           |
| R.m.s deviations                                    |                                                                              |                                                                                 |                                                                           |                                                                               |                                                                              |
| Bond lengths (Å)                                    | 0.003                                                                        | 0.008                                                                           | 0.003                                                                     | 0.004                                                                         | 0.005                                                                        |
| Bond angles (°)                                     | 0.680                                                                        | 0.920                                                                           | 0.682                                                                     | 0.688                                                                         | 0.733                                                                        |
| Validation                                          |                                                                              |                                                                                 |                                                                           |                                                                               |                                                                              |
| Molprobrity score                                   | 1.10                                                                         | 1.02                                                                            | 1.20                                                                      | 1.13                                                                          | 1.11                                                                         |
| Clash score                                         | 3.09                                                                         | 2.41                                                                            | 4.20                                                                      | 3.37                                                                          | 3.15                                                                         |
| Poor rotamers (%)                                   | 0.02                                                                         | 0.91                                                                            | 0.01                                                                      | 0.02                                                                          | 0.02                                                                         |
| Ramachandran plot                                   |                                                                              |                                                                                 |                                                                           |                                                                               |                                                                              |
| Favored (%)                                         | 98.42                                                                        | 98.58                                                                           | 98.26                                                                     | 98.51                                                                         | 98.24                                                                        |
| Allowed (%)                                         | 1.57                                                                         | 1.42                                                                            | 1.73                                                                      | 1.49                                                                          | 1.76                                                                         |
| Disallowed (%)                                      | 0.01                                                                         | 0.00                                                                            | 0.01                                                                      | 0.00                                                                          | 0.00                                                                         |
| Map vs. Model CC (mask)                             | 0.88                                                                         | 0.90                                                                            | 0.81                                                                      | 0.86                                                                          | 0.89                                                                         |
| <b>Local &amp; Consensus Refinements</b>            |                                                                              |                                                                                 |                                                                           |                                                                               |                                                                              |
|                                                     | EMD-17908                                                                    | EMD-17911                                                                       | EMD-17914                                                                 | EMD-17916                                                                     | EMD-17919                                                                    |
|                                                     | EMD-17909                                                                    | EMD-17912                                                                       | EMD-17915                                                                 | EMD-17917                                                                     | EMD-17920                                                                    |
|                                                     | EMD-17910                                                                    | EMD-17913                                                                       |                                                                           | EMD-17918                                                                     | EMD-17921                                                                    |
|                                                     |                                                                              |                                                                                 |                                                                           |                                                                               | EMD-17922                                                                    |

|                                                     | <b>Las1-Grc3<br/>complex</b><br>(EMD-17949)<br>(PDB-8PUW) | <b>Rix1-complex</b><br>(Rix1) <sub>2</sub> -(Ipi3) <sub>2</sub><br>(EMD-17879)<br>(PDB-8PTW) | <b>Rix1-complex</b><br>(Rix1) <sub>2</sub> -(Ipi3) <sub>2</sub> -<br>Ipi1<br>(EMD-17923) | <b>Rixosome</b><br>(EMD-17880) |
|-----------------------------------------------------|-----------------------------------------------------------|----------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------|--------------------------------|
| <b>Data collection &amp; processing</b>             |                                                           |                                                                                              |                                                                                          |                                |
| Camera                                              | Gatan K2<br>Summit                                        | Gatan K2<br>Summit                                                                           | Gatan K2<br>Summit                                                                       | Gatan K2<br>Summit             |
| Magnification                                       | 130,000                                                   | 130,000                                                                                      | 130,000                                                                                  | 130,000                        |
| Voltage (kV)                                        | 300                                                       | 300                                                                                          | 300                                                                                      | 300                            |
| Electron exposure (e <sup>-</sup> /Å <sup>2</sup> ) | 43.6                                                      | 43.6                                                                                         | 43.6                                                                                     | 43.6                           |
| Defocus range (μm)                                  | 0.5 - 3.5                                                 | 0.5 - 3.5                                                                                    | 0.5 - 3.5                                                                                | 0.5 - 3.5                      |
| Pixel size (Å)                                      | 1.045                                                     | 1.045                                                                                        | 1.045                                                                                    | 1.045                          |
| Symmetry imposed                                    | C2                                                        | C2                                                                                           | C1                                                                                       | C1                             |
| Micrographs collected (no.)                         |                                                           |                                                                                              |                                                                                          |                                |
| Initial particle images (no.)                       | 187,407                                                   | 588,317                                                                                      | 588,317                                                                                  | 104,264                        |
| Final particle images (no.)                         | 104,264                                                   | 239,033                                                                                      | 232,826                                                                                  | 38,095                         |
| Map resolution (Å)                                  | 3.01                                                      | 2.91                                                                                         | 3.14                                                                                     | 10.02                          |
| FSC threshold                                       | 0.143                                                     | 0.143                                                                                        | 0.143                                                                                    | 0.143                          |
| <b>Refinement</b>                                   |                                                           |                                                                                              |                                                                                          |                                |
| Model resolution (Å)                                | 3.0                                                       | 3.0                                                                                          |                                                                                          |                                |
| FSC threshold                                       | 0.5                                                       | 0.5                                                                                          |                                                                                          |                                |
| Map sharpening B factor (Å <sup>2</sup> )           | -80                                                       | -80                                                                                          |                                                                                          |                                |
| Model composition                                   |                                                           |                                                                                              |                                                                                          |                                |
| Non-hydrogen atoms                                  | 11,160                                                    | 14,242                                                                                       |                                                                                          |                                |
| Protein residues                                    | 1,442                                                     | 1,878                                                                                        |                                                                                          |                                |
| Nucleotide residues                                 | 0                                                         | 0                                                                                            |                                                                                          |                                |
| Ligands                                             | 0                                                         | 0                                                                                            |                                                                                          |                                |
| R.m.s deviations                                    |                                                           |                                                                                              |                                                                                          |                                |
| Bond lengths (Å)                                    | 0.004                                                     | 0.04                                                                                         |                                                                                          |                                |
| Bond angles (°)                                     | 0.693                                                     | 0.784                                                                                        |                                                                                          |                                |
| Validation                                          |                                                           |                                                                                              |                                                                                          |                                |
| Molprobrity score                                   | 1.10                                                      | 1.18                                                                                         |                                                                                          |                                |
| Clash score                                         | 3.07                                                      | 3.99                                                                                         |                                                                                          |                                |
| Poor rotamers (%)                                   | 0.00                                                      | 0.00                                                                                         |                                                                                          |                                |
| Ramachandran plot                                   |                                                           |                                                                                              |                                                                                          |                                |
| Favored (%)                                         | 98.44                                                     | 98.17                                                                                        |                                                                                          |                                |
| Allowed (%)                                         | 1.56                                                      | 1.83                                                                                         |                                                                                          |                                |
| Disallowed (%)                                      | 0.00                                                      | 0.00                                                                                         |                                                                                          |                                |
| Map vs. Model CC (mask)                             | 0.88                                                      | 0.81                                                                                         |                                                                                          |                                |