**Supplementary File 2. Cryo-EM data collection and refinement statistics of DEPTOR-mTORC1 complex**

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| DEPTOR-mTORC1 |
|  | Dimer (map4, Fig. 1-S2a) | Protomer(map5, Fig. 1-S2a) | DEPt-Protomer(map6, Fig. 1-S2a) |
| *Data acquisition and processing* |
| EMDB accession # | 13350 | 13351 | 13352 |
| Magnification |  |
| Voltage (kV) | 200 |
| Exposure (e-/ Å2) | 50 |
| Frames | 40 |
| Defocus range (µM) | -1.0 to -2.5 |
| Pixel size (Å) | 0.556 |
| Symmetry imposed | C1 |
| Initial particles | 2,156,602 |
| Final particles | 425,076 | 850152 | 211021 |
| FSC resolution (masked, Å)\* | 4.07 | 3.67 | 4.24 |
| *Model refinement* |
| PDB ID | 7PEA | 7PEB | 7PEC |
| Model resolution (Å) | 6.3/4.0 | 4.3/3.6 | 4.7/4.1 |
| FSC threshold | 0.50/0.143 | 0.50/0.143 | 0.50/0.143 |
|  |  |  |  |
| Bond length (Å) | 0.002 | 0.002 | 0.002 |
| Bond angle (°) | 0.455 | 0.505 | 0.470 |
| Favored (%) | 95.26 | 94.86 | 95.43 |
| Allowed (%) | 4.71 | 5.09 | 4.54 |
| Disallowed (%) | 0.03 | 0.06 | 0.03 |
| Rotamer Outliers (%) | 4.24 | 2.69 | 4.99 |
| MolProbity score | 1.99 | 1.91 | 2.13 |
| Clashscore | 3.95 | 4.50 | 5.32 |

\*gold-standard FSC criterion: 0.143