**Supplementary File 3.** **Crystallographic data collection and refinement statistics (molecular replacement)**

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|  | ***Ct*Vps391-500 (SAD)**(pdb code: XXX) |
| **Data collection** |  |
| X-ray source | EMBL, Hamburg, Germany, P13 |
| Wavelength (Å)Space groupCell dimensions | 0.97937P21212 |
|  *a*, *b*, *c* (Å) | 64.70, 102.75, 59.56 |
| Resolution (Å) | 43.82‑2.89 (3.07‑2.89)\* |
| Total reflectionsMultiplicityUnique reflectionsCompleteness (%)*R*meas (%)CC(1/2)*I* / *I* | 114239 (16970)6.72 (6.48)17010 (2619)99.1 (94.8)23.1 (124.3)99.3 (76.6)7.70 (1.80) |
| Mosaicity (°)Wilson *B*-factor (Å2) | 0.52358.48 |
| **Refinement** |  |
| Resolution (Å) | 40.23‑2.89 |
| Reflections (working, test set) | 9264, 463 |
| *R*factor, *R*free | 0.269, 0.298 |
| Completeness for range (%)No. atoms | 99.1 |
|  Protein SolventProtein residues | 268110345 |
| R.m.s. deviations |  |
|  Bond lengths (Å) | 0.003 |
|  Bond angles (°)mean *B* value (Å2) | 0.55158.1 |

\*Values in parentheses are for highest-resolution shell.