**Supplementary File 3. X-ray data collection and refinement for DEPTOR DEPt**

| DEPt(PDB 7PED) |
| --- |
| X-ray data collection |
|  Space group | P 1 21 1 |
|  Cell dimensions |
|   a, b, c (Å) | 50.9, 99.0, 68.2 |
|   α, β, γ (°) | 90.0, 109.7, 90.0 |
|  Resolution (Å) | 99.01-1.93 (1.98-1.93) \* |
|  Rmerge | 0.036 (1.41) |
|  CC1/2  | 0.999 (0.405) |
|  I/σI | 14.2 (0.6) |
|  Completeness (%) | 97.4 (87.6) |
|  Redundancy | 4.3 (3.1) |
| Refinement |
|  Resolution (Å) | 49.51-1.93 |
|  No. reflections | 46,321(4,170) |
|  Rwork/Rfree | 0.211/0.226 |
|  No. atoms |
|   Protein | 3572 |
|   Water | 204 |
|  B-factors |
|   Protein | 63.35 |
|   Water | 56.97 |
|  R.m.s. deviations |
|   Bond lengths (Å) | 0.006 |
|   Bond angles (°) | 1.04 |
| Ramachandranplot |  |
|   favored (%) | 98.6 |
|   allowed (%) | 1.4 |
|   outliers (%) | 0.0 |

\*Values in parentheses are for highest-resolution shell