|  |  |  |
| --- | --- | --- |
|  | **Mp Eno** | **Mb Eno** |
| **Data collection** |  |  |
| Beamline | SSRF BL19U1 | SSRF BL19U1 |
| Space group | *P*1 21 1 | *I*4 |
| Cell dimensions |  |  |
|  *a*, *b*, *c* (Å) | 76.074, 106.548, 128.589 | 142.221, 142.221, 107.422 |
|   | 90.00, 103.15, 90.00 | 90.00, 90.00, 90.00 |
| Wavelength (Å) | 0.97853 | 0.97853 |
| Resolution (Å) | 19.84-1.8 (1.9-1.8) | 19.96-1.7 (1.79-1.7) |
| Total no. of reflections | 368478 (36808) | 115149 (9944) |
| *R*merge (%)  | 0.105 | 0.071 |
| **** | 6.55 (1.33) | 2.15 |
| Completeness (%) | 98.5(98.7) | 98.1(98.1) |
| Redundancy | 6.4 |  11.2 |
|  |  |  |
| **Refinement** |  |  |
| Resolution (Å)\* | 19.84-1.8 | 19.72-1.7 |
| No. reflections | 181,623 | 114,827 |
| R, R*free*  | 0.189 (0.223) | 0.158 (0.182) |
| No. atoms | 14,600 | 7,242 |
|  Protein | 13,715 | 6851 |
|  Water | 837 | 392 |
| Average *B*-factors (Å2) | 29.40 | 32.98 |
|  Protein | 29.08 | 32.83 |
|  Water | 34.21 | 35.62 |
| Rmsd values |  |  |
|  Bond lengths (Å) | 0.007 | 0.015 |
|  Bond angles () | 0.83 | 1.30 |
| Ramachandran plot (%) |  |  |
| Total favored | 98.04% | 97.75% |
| Total allowed | 1.85% | 1.91% |
| Outliers | 1.11% | 0.96% |

**Table 1. Data collection and refinement statistics.**

\*The values in parentheses are for the highest-resolution shell.

Rmerge = P | I - hIi| /PI, where I is the integrated intensity of a given reflection.R = P || Fobs | – | Fcalc | |/Phkl | Fobs |.Rfree was calculated using 5% of the data omitted from the refinement.I /σI = average (I /σI).