**Table 2. Data collection and refinement statistics for the sweet potato PAP–phosphate complex**

| | |
|---|---|
| Data collection | |
| Temperature, K | 100 |
| Unit cell length, Å | $a = b$ =116.15 $c$ = 291.95 |
| Space group | $P6_522$ |
| Crystal mosaicity, ° | 0.42 |
| Resolution range, Å | 50.0–2.50 |
| Total observations, $I > 0\sigma(I)$ | 222,880 |
| Unique measurements, $I > 0\sigma(I)$ | 37,188 |
| Completeness,* % | 90.0 (56.5) |
| $R_{sym,}$*† % | 0.067 (0.310) |
| $I/\sigma(I)$* | 11.0 (3.0) |
| Dimers per asymmetric unit | 1 |
| Solvent content, % | 54 |
| Refinement | |
| Resolution range, Å | 50.0–2.50 |
| $R$ factor,‡ $F > 1\sigma(F)$ | 0.238 |
| $R_{free}$,‡ $F > 1\sigma(F)$ | 0.264 |
| rms deviations from ideal | |
| Bond length, Å | 0.007 |
| Bond angle, ° | 1.37 |
| Average B factor, Å$^2$ | 45.0 |
| Ramachandran plot statistics (%) | |
| Residues in most favoured regions | 83.4 |
| Residues in disallowed regions | 0.5 (2 from each subunit) |

*Values in parentheses are for the outer shell of data 2.60–2.50 Å.

†$R_{sym} = \sum| I - \langle I \rangle| / \sum \langle I \rangle$.

‡$R$ factor = $\sum||F_{obs}| - |F_{calc}|| / \sum|F_{obs}|$, where the $R$ factor is calculated based on the reflections used in the refinement (90% of the total data), and $R_{free}$ [Brünger, A. T. (1992)

*X-PLOR: A System for X-ray Crystallography and NMR* (Yale Univ. Press, New Haven, CT)] is calculated using the remaining 10% of the data.