**Table S1 Data collection and refinement statistics of AtGPRAT2**

|  |  |  |
| --- | --- | --- |
|  |  | **AtGPRAT2** |
| **Data collection** |  |  |
| Space Group |  | P3121 |
| Unit Cell (Å)  α, β, γ (°) |  | 179.74, 179.74, 109.20  90, 90, 120 |
| Wavelength (Å) |  | 0.979 |
| Resolution (Å) |  | 3.07 (3.18-3.07) |
| Rmerge % |  | 9.9 (73.2) |
| I/sigma |  | 18.3 (3.11) |
| Completeness (%) |  | 99.9 (100.0) |
| Redundancy |  | 6.0 (6.0) |
| **Refinement** |  |
| Rwork |  | 0.1933 |
| Rfree |  | 0.2131 |
| No. protein atoms |  | 6887 |
| Overall B factors: |  | 58.56 |
| RMSD bond lengths |  | 0.007 |
| RMSD bond angles |  | 0.91 |
| Ramachandran plot statistics (%) |  |
| In favored regions |  | 95.16 |
| In allowed regions |  | 4.62 |
| Outliers |  | 0.23 |
| PDB code |  | 6LBP |

Values in parentheses are for the highest resolution shell. *Rmerge*=ΣhΣi|*Ih,i*-*Ih*|/ΣhΣi*Ih,i*, where *Ih* is the mean intensity of the *i* observations of symmetry related reflections of *h*. *R*=Σ|*Fobs*-*Fcalc*|/Σ*Fobs*, where *Fcalc* is the calculated protein structure factor from the atomic model (Rfree was calculated with 5% of the reflections selected).