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|  | ***P. syringae* SsdAtox / SsdAI SAD peaka** |
| PDB accession code  | 7JTU  |
| **Data Collection**  |  |
| Space group  | I4122  |
| Cell dimension  *a, b, c* (Å)  | 93.07, 93.07, 383.49  |
|  a, b, g (°)  | 90, 90, 90  |
| Wavelength (Å)  | 0.9790  |
| Resolution (Å)  | 33.4 - 3.0 (3.15-3.0)b |
| No. unique reflections  | 17597 (434)  |
| Rmerge  | 0.12  |
| I/sI  | 22.9 (2.7)  |
| Completeness (%) Total  | 100 (100)  |
|  Anomalous  | 100 (100)  |
| Redundancy  | 28.6 (29.6)  |
| Wilson B-factor (Å2)  | 79.6  |
| **Refinement**  |  |
| Resolution (Å)  | 33.4 – 3.0 (3.1 – 3.0)  |
| No. reflections  | 17248 (1193)  |
| Rwork/Rfree (%)  | 20.2 / 23.5 (32.3 / 40.5)  |
| No. atoms  Protein  | 2717  |
|  Ligand/ion  | 0  |
|  Water  | 3  |
| B-factors(Å2) Protein | 79.6  |
| Ligand/ion  | N/A  |
|  Water  | 63.9  |
| rmsd Bond lengths (Å)  | 0.009  |
| Bond angles (°)  | 1.086  |
| Missing residues chain A  | 245-257, 409 |
|  chain B  | none |

aAll data collected from a single crystal

bValues in parentheses are for the highest resolution shell