**Additional file 6**

**Table S2** Data collection and refinement statistics for *Rd*FucI

|  |  |  |
| --- | --- | --- |
| **Data collection** | *Rd*FucI | *Rd*FucI-Mn2+ |
| Space group | P212121 | P212121 |
| Cell dimensions |  |  |
| *a*, *b*, *c* (Å) | 113.98, 127.61, 257.29 | 116.27, 163.27, 196.34 |
| Resolution (Å) | 50.0–2.50 (2.54–2.50)a | 30.0-2.95 (3.00–2.95)a |
| Completeness | 96.4 (95.4)a | 93.8 (85.9)a |
| Redundancy | 4.1 (3.2)a | 4.4. (3.3)a |
| I/σ(I) | 7.65 (1.59)a | 17.34 (2.29)a |
| Rmergeb | 0.115 (0.357)a | 0.120 (0.463)a |
| **Refinement statistics** |  |  |
| Resolution (Å) | 50.0–2.50 | 30.0–2.96 |
| Rwork / Rfree (%)c | 17.65/23.33 | 19.26/25.19 |
| B-factor (Averaged) |  |  |
| Protein | 36.22 | 60.69 |
| Water | 29.25 | 38.77 |
| R.M.S. deviations |  |  |
| Bond lengths (Å) | 0.011 | 0.010 |
| Bond angles (°) | 1.394 | 1.320 |
| Ramachandran plot(%) |  |  |
| favored | 95.9 | 95.1 |
| allowed | 3.7 | 4.3 |
| Outliers | 0.4 | 0.6 |

aThe highest resolution shell is shown in parentheses

b*R*merge = Σ*h*Σ*i*|I*i*(hkl)\_<*I*(hkl)>|/Σ*h*Σ*i*I*i*(hkl), where *Ii*(hkl) is the intensity of the ‘ith’ measurement of reflection hkl and <*I*(hkl)> is the weighted mean of all measurements of hkl

c*R*work = Σ||*F*obs|-|*F*calc||/Σ|*F*obs|, where *F*obs and *F*calc are the observed and calculated structure-factor amplitudes, respectively. Rfree was calculated as Rwork using a randomly selected subset (5.1%) of unique reflections not used for structure refinement