Previously, we have determined the 2.44 Å crystal structure of FtsH in its ADP-bound form by selenomethionine-MAD at BM14, ESRF Grenoble (Bieniossek et al., Proc Natl Acad Sci U S A 103**:** 3066-3071; 2006). In order gain insight into the nucleotide-driven conformational changes, we have now solved a different nucleotide state employing selenomethionine SAD at ID29 and ID14-1 (experiments MX-522, MX-523). Experimental phasing was essential because molecular replacement calculations failed to reveal the position of the AAA domains. The new crystal from shows a radically different arrangement of the AAA domains compared to the ADP-form. Additionally, new features in the protease domain are observed. An inhibitor complex reveals the mechanism of substrate fixation and cleavage. This new structure gives a first insight into the conformational changes that transform the chemical energy stored in ATP into a mechanical force.

*Table: Data Collection and Refinement Statistics*

| **Crystal** | Inhibitor Complex | SeMet |
|---|---|---|
| Unit cell (P622)<br>a, b, c (Å)<br>α, β, γ (degrees) | <br>190.64, 190.65, 152.21<br>90.0, 90.0, 120.0 | <br>191.20, 191.20, 152.63<br>90.0, 90.0, 120.0 |
| ***Data collection*** | D*TREK | MOSFLM |
| Beamline | ID-29, ESRF Grenoble | ID-29, ESRF, Grenoble |
| Wavelength (Å) | 0.987 | 0.987 |
| Resolution range (Å) | 34.0 - 2.60 (2.74 -2.60) | 50- 3.20 (3.37 -3.20) |
| No. unique reflections | 50,585 | 27,700 |
| Redundancy | 10.5 (9.3) | 13.7 (14.3) |
| Completeness (%) | 99.9 (100.0) | 100.0 (100.0) |
| Rsym (%) | 8.7 (69.2) | 9.5 (44.2) |
| I/σ (I) | 13.9 (4.1) | 24.3 (6.5) |
| ***Refinement*** | | |
| Resolution range (Å) | 34.0 - 2.60 | |
| No. reflections / test set | 50,576 / 2,001 | |
| No. atoms<br>total<br>Water molecules / $Zn^{2+}$<br>TAPI | <br>10,068<br>24 / 3<br>87 | |
| R/R-free (%) | 21.3 / 28.7 | |
| RMS bonds (Å) | 0.006 | |
| RMS angles (deg.) | 0.97 | |
| Ramachandran outliers (%) | 8.5 | |